

PCTWORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification : C07K 14/47, C12N 5/10, 5/16, 15/12, 15/63, 15/64	A1	(11) International Publication Number: WO 00/61629 (43) International Publication Date: 19 October 2000 (19.10.00)
(21) International Application Number: PCT/US00/09071 (22) International Filing Date: 6 April 2000 (06.04.00) (30) Priority Data: 60/128,694 9 April 1999 (09.04.99) US 60/176,931 20 January 2000 (20.01.00) US (71) Applicants (for all designated States except US): HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US). ROSEN, Craig, A. [US/US]; 22400 Rolling Hill Road, Laytonsville, MD 20882 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): RUBEN, Steven, M. [US/US]; 18528 Heritage Hills Drive, Laytonsville, MD 20882 (US). KOMATSOUKIS, George [US/US]; 9518 Garwood Street, Silver Spring, MD 20901 (US). (74) Agents: HOOVER, Kenley, K. et al.; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 20850 (US).	(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i>	
(54) Title: 49 HUMAN SECRETED PROTEINS		
(57) Abstract The present invention relates to novel human secreted proteins and isolated nucleic acids containing the coding regions of the genes encoding such proteins. Also provided are vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The invention further relates to diagnostic and therapeutic methods useful for diagnosing and treating diseases, disorders, and/or conditions related to these novel human secreted proteins.		

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

49 Human Secreted Proteins

Field of the Invention

This invention relates to newly identified polynucleotides and the polypeptides encoded by these polynucleotides, uses of such polynucleotides and polypeptides, and their production.

Background of the Invention

Unlike bacterium, which exist as a single compartment surrounded by a membrane, human cells and other eucaryotes are subdivided by membranes into many functionally distinct compartments. Each membrane-bounded compartment, or organelle, contains different proteins essential for the function of the organelle. The cell uses "sorting signals," which are amino acid motifs located within the protein, to target proteins to particular cellular organelles.

One type of sorting signal, called a signal sequence, a signal peptide, or a leader sequence, directs a class of proteins to an organelle called the endoplasmic reticulum (ER). The ER separates the membrane-bounded proteins from all other types of proteins. Once localized to the ER, both groups of proteins can be further directed to another organelle called the Golgi apparatus. Here, the Golgi distributes the proteins to vesicles, including secretory vesicles, the cell membrane, lysosomes, and the other organelles.

Proteins targeted to the ER by a signal sequence can be released into the extracellular space as a secreted protein. For example, vesicles containing secreted proteins can fuse with the cell membrane and release their contents into the extracellular space - a process called exocytosis. Exocytosis can occur constitutively or after receipt of a triggering signal. In the latter case, the proteins are stored in secretory vesicles (or secretory granules) until exocytosis is triggered. Similarly,

proteins residing on the cell membrane can also be secreted into the extracellular space by proteolytic cleavage of a "linker" holding the protein to the membrane.

Despite the great progress made in recent years, only a small number of genes encoding human secreted proteins have been identified. These secreted proteins
5 include the commercially valuable human insulin, interferon, Factor VIII, human growth hormone, tissue plasminogen activator, and erythropoietin. Thus, in light of the pervasive role of secreted proteins in human physiology, a need exists for identifying and characterizing novel human secreted proteins and the genes that encode them. This knowledge will allow one to detect, to treat, and to prevent
10 medical diseases, disorders, and/or conditions by using secreted proteins or the genes that encode them.

Summary of the Invention

The present invention relates to novel polynucleotides and the encoded
15 polypeptides. Moreover, the present invention relates to vectors, host cells, antibodies, and recombinant and synthetic methods for producing the polypeptides and polynucleotides. Also provided are diagnostic methods for detecting diseases, disorders, and/or conditions related to the polypeptides and polynucleotides, and therapeutic methods for treating such diseases, disorders, and/or conditions. The
20 invention further relates to screening methods for identifying binding partners of the polypeptides.

Detailed Description

Definitions

The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide. The term "isolated" does not refer to genomic or cDNA libraries, whole cell total or mRNA preparations, genomic DNA preparations (including those separated by electrophoresis and transferred onto blots), sheared whole cell genomic DNA preparations or other compositions where the art demonstrates no distinguishing features of the polynucleotide/sequences of the present invention.

In the present invention, a "secreted" protein refers to those proteins capable of being directed to the ER, secretory vesicles, or the extracellular space as a result of a signal sequence, as well as those proteins released into the extracellular space without necessarily containing a signal sequence. If the secreted protein is released into the extracellular space, the secreted protein can undergo extracellular processing to produce a "mature" protein. Release into the extracellular space can occur by many mechanisms, including exocytosis and proteolytic cleavage.

In specific embodiments, the polynucleotides of the invention are at least 15, at least 30, at least 50, at least 100, at least 125, at least 500, or at least 1000 continuous nucleotides but are less than or equal to 300 kb, 200 kb, 100 kb, 50 kb, 15 kb, 10 kb, 7.5 kb, 5 kb, 2.5 kb, 2.0 kb, or 1 kb, in length. In a further embodiment, polynucleotides of the invention comprise a portion of the coding sequences, as

disclosed herein, but do not comprise all or a portion of any intron. In another embodiment, the polynucleotides comprising coding sequences do not contain coding sequences of a genomic flanking gene (i.e., 5' or 3' to the gene of interest in the genome). In other embodiments, the polynucleotides of the invention do not contain
5 the coding sequence of more than 1000, 500, 250, 100, 50, 25, 20, 15, 10, 5, 4, 3, 2, or 1 genomic flanking gene(s).

As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence contained in SEQ ID NO:X or the cDNA contained within the clone deposited with the ATCC. For example, the polynucleotide can contain the
10 nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, with or without the signal sequence, the secreted protein coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having the translated amino acid sequence generated from the
15 polynucleotide as broadly defined.

In the present invention, the full length sequence identified as SEQ ID NO:X was often generated by overlapping sequences contained in multiple clones (contig analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X was deposited with the American Type Culture Collection ("ATCC"). As
20 shown in Table 1, each clone is identified by a cDNA Clone ID (Identifier) and the ATCC Deposit Number. The ATCC is located at 10801 University Boulevard, Manassas, Virginia 20110-2209, USA. The ATCC deposit was made pursuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for purposes of patent procedure.

25 A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to

sequences contained in SEQ ID NO:X, the complement thereof, or the cDNA within the clone deposited with the ATCC. "Stringent hybridization conditions" refers to an overnight incubation at 42 degree C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x

- 5 Denhardt's solution, 10% dextran sulfate, and 20 μ g/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65 degree C.

Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily

10 accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37 degree C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH_2PO_4 ; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 ug/ml

15 salmon sperm blocking DNA; followed by washes at 50 degree C with 1XSSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

Note that variations in the above conditions may be accomplished through the

20 inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above,

25 due to problems with compatibility.

Of course, a polynucleotide which hybridizes only to polyA+ sequences (such as any 3' terminal polyA+ tract of a cDNA shown in the sequence listing), or to a complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone generated using oligo dT as a primer).

The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

The polypeptide of the present invention can be composed of amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more

detailed monographs, as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in

5 a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation,

10 ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation,

15 gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES,

20 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth Enzymol 182:626-646 (1990); Rattan et al., Ann NY Acad Sci 663:48-62 (1992).)

"SEQ ID NO:X" refers to a polynucleotide sequence while "SEQ ID NO:Y"

25 refers to a polypeptide sequence, both sequences identified by an integer specified in Table I.

"A polypeptide having biological activity" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. In the case where dose dependency does
5 exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to
10 the polypeptide of the present invention.)

Many proteins (and translated DNA sequences) contain regions where the amino acid composition is highly biased toward a small subset of the available residues. For example, membrane spanning domains and signal peptides (which are also membrane spanning) typically contain long stretches where Leucine (L), Valine
15 (V), Alanine (A), and Isoleucine (I) predominate. Poly-Adenosine tracts (polyA) at the end of cDNAs appear in forward translations as poly-Lysine (poly-K) and poly-Phenylalanine (poly-F) when the reverse complement is translated. These regions are often referred to as "low complexity" regions.

Such regions can cause database similarity search programs such as BLAST to
20 find high-scoring sequence matches that do not imply true homology. The problem is exacerbated by the fact that most weight matrices (used to score the alignments generated by BLAST) give a match between any of a group of hydrophobic amino acids (L, V and I) that are commonly found in certain low complexity regions almost as high a score as for exact matches.

25 In order to compensate for this, BLASTX.2 (version 2.0a5MP-WashU) employs two filters ("seg" and "xnu") which "mask" the low complexity regions in a

particular sequence. These filters parse the sequence for such regions, and create a new sequence in which the amino acids in the low complexity region have been replaced with the character "X". This is then used as the input sequence (sometimes referred to herein as "Query" and/or "Q") to the BLASTX program. While this regime helps to ensure that high-scoring matches represent true homology, there is a negative consequence in that the BLASTX program uses the query sequence that has been masked by the filters to draw alignments.

Thus, a stretch of "X"s in an alignment shown in the following application does not necessarily indicate that either the underlying DNA sequence or the translated protein sequence is unknown or uncertain. Nor is the presence of such stretches meant to indicate that the sequence is identical or not identical to the sequence disclosed in the alignment of the present invention. Such stretches may simply indicate that the BLASTX program masked amino acids in that region due to the detection of a low complexity region, as defined above. In all cases, the reference sequence(s) (sometimes referred to herein as "Subject", "Sbjct", and/or "S") indicated in the specification, sequence table (Table 1), and/or the deposited clone is (are) the definitive embodiment(s) of the present invention, and should not be construed as limiting the present invention to the partial sequence shown in an alignment, unless specifically noted otherwise herein.

20

Polynucleotides and Polypeptides of the Invention

FEATURES OF PROTEIN ENCODED BY GENE NO: 1

It has been discovered that this gene is expressed primarily in Activated T-cell(12h)/Thiouridine-re-excision.

25

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:11 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 826 of SEQ ID NO:11, b is an integer of 15 to 840, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:11, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 2

The computer algorithm BLASTX has been used to determine that the translation product of this gene shares sequence homology with, as a non-limiting example, the sequence accessible through the following database accession no. gnllPIDle1346972 (all information available through the recited accession number is incorporated herein by reference) which is described therein as a *C. elegans* protein. A partial alignment demonstrating the observed homology is shown immediately below.

```
>gnl|PID|e1346972 cDNA EST yk478b4.5 comes from this gene; cDNA EST
EMBL:D74716
comes from this gene; cDNA EST yk456b12.5 comes from this
gene;
cDNA EST EMBL:T00892 comes from this gene [Caenorhabditis
elegans]
>sp|E1346972|E1346972 F52B11.1 PROTEIN.
Length = 523

Plus Strand HSPs:
```


Score = 139 (48.9 bits), Expect = 1.0e-15, Sum P(3) = 1.0e-15
 Identities = 36/141 (25%), Positives = 67/141 (47%), Frame = +2

```

5  Q: 1706 FCDVYNPQSKTYCKRLQVLCPEHSRDPKVPADDEVCGCP-----LVRDVFELTG 1849
      +C+ Y+ ++ ++CKRL+ LCPEH +          +VCG P          V ++ E+
S: 313 YCEKYDSRTNSFCKRLKSLCPEHRKLGDEQHLKVCGYPKKWEDGMIETAKTVSELIEMED 372

10 Q: 1850 DF----CRLPKRQCNRRHYCWELRRRAEVDLERVRVWYKLDELFEQERNVRTAMTNRAGLL 2017
      F    CR K C++H+ W    R ++LE+ ++ K+ EL + +          L
S: -373 PFGEEGCRTKKDACHKHKHWIPSLRGITIELEQACLFQKMYELCHEMHKLNAHAEWTTNAL 432

Q: 2018 ALMLHQTIQHDPLTTDLRSSA 2080
      ++M+H+ + + LR+ A
15 S: 433 SIMMHKQPSTEEKCSFFLRNFA 453
  
```

The segment of gnl|PIDle1346972 that is shown as "S" above is set out in the sequence listing as SEQ ID NO. 109.

Preferred polypeptides of the invention comprise a polypeptide having the
 20 amino acid sequence set out in the sequence listing as SEQ ID NO. 110 which corresponds to the "Q" sequence in the alignment shown above (gaps introduced in a sequence by the computer are, of course, removed).

It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: Soares infant brain 1NIB and to a lesser extent in
 25 NCI_CGAP_GCB1; Human Primary Breast Cancer Reexcision; Activated T-cell(12h)/Thiouridine-re-excision; Stratagene fetal spleen (#937205); Soares_parathyroid_tumor_NbHPA; normalized infant brain cDNA; Human Thymus; Rejected Kidney, lib 4; Human fetal brain S. Meier-Ewert; Activated T-Cell (12hs)/Thiouridine labelledEco; Soares_pregnant_uterus_NbHPU; T cell helper II;
 30 Human Cerebellum; Normal trachea; Corpus Callosum; Activated T-Cells, 8 hrs, subtracted; Human White Adipose; Healing Abdomen wound,70&90 min post incision; Supt Cells, cyclohexamide treated; Human adult small intestine,re-excision; Stratagene ovary (#937217); Myoloid Progenitor Cell Line; Human Adult Small Intestine; Human Thymus; Human Umbilical Vein Endothelial Cells, uninduced;

Human Activated T-Cells; Human Pancreas Tumor; Human Adult Testes, Large
Inserts, Reexcision; Human Heart; Human colorectal cancer; Soares_testis_NHT;
Soares_total_fetus_Nb2HF8_9w; Soares_fetal_liver_spleen_INFLS_S1; Stratagene
schizo brain S11; Stratagene lung carcinoma 937218; Human Pancreas Tumor,
5 Reexcision; Ulcerative Colitis; Human Testes Tumor, re-excision;
Hemangiopericytoma; Human Fetal Brain; Stratagene NT2 neuronal precursor
937230; Pancreas Islet Cell Tumor; Human T-Cell Lymphoma; Human Testes
Tumor; Colon Tumor II; H. Frontal cortex,epileptic,re-excision; Human Synovial
Sarcoma; Anergic T-cell; NCI_CGAP_SS1; NCI_CGAP_Co10; NCI_CGAP_Thy1;
10 Human Endometrial Tumor; Hodgkin's Lymphoma II; Nine Week Old Early Stage
Human; Soares placenta Nb2HP and Primary Dendritic Cells, lib 1.

Many polynucleotide sequences, such as EST sequences, are publicly
available and accessible through sequence databases. Some of these sequences are
related to SEQ ID NO:12 and may have been publicly available prior to conception of
15 the present invention. Preferably, such related polynucleotides are specifically
excluded from the scope of the present invention. To list every related sequence
would be cumbersome. Accordingly, preferably excluded from the present invention
are one or more polynucleotides comprising a nucleotide sequence described by the
general formula of a-b, where a is any integer between 1 to 2373 of SEQ ID NO:12, b
20 is an integer of 15 to 2387, where both a and b correspond to the positions of
nucleotide residues shown in SEQ ID NO:12, and where b is greater than or equal to a
+ 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 3

25 The computer algorithm BLASTX has been used to determine that the
translation product of this gene shares sequence homology with, as a non-limiting

example, the sequence accessible through the following database accession no. gnl|PID|e1343996 (all information available through the recited accession number is incorporated herein by reference) which is described therein as "similar to guanine nucleotide binding protein." A partial alignment demonstrating the observed

5--homology is shown immediately below.

```

>gnl|PID|e1343996 similar to guanine nucleotide binding protein; cDNA EST
      EMBL:T00917 comes from this gene; cDNA EST CEMSE07F comes from
this
10      gene; cDNA EST EMBL:T00918 comes from this gene; cDNA EST
      EMBL:D70900 comes from this gene; cDNA EST EMBL:D70636 comes >
      Length = 376

      Minus Strand HSPs:
15
      Score = 1216 (428.1 bits), Expect = 5.1e-123, P = 5.1e-123
      Identities = 222/323 (68%), Positives = 264/323 (81%), Frame = -2

20      Q: 1886 PTPSSSATQSKPTPV-----KPNYALKFTLAGHTKAVSSVKFSPNGEWLASSSADKLIK 1725
      . P P +SA      P      NY L  TL GHK++SS KFSP G++L +SSADK +K
      S: 53 PAPGASAQTPNPNAAGASASGSANYKLMCTLEGHTKSISSAKFSPCGKYLGTSSADKTVK 112

      Q: 1724 IWGAYDGKFEKTISGHKLGISDAWSSDSNLLVSASDDKTLKIWDVSSGKCLKTLKGHSN 1545
      IW      E+T++GHKLG++D+AWSSDS +VSASDDKTLKI+++ + + KTLKGH+N
25      S: 113 IWNMDHMICERTLTGHKLGVNDAWSSDSRCVVSASDDKTLKIFEIVTSRMTKTLKGHN 172

      Q: 1544 YVFCCNFNPQSNLIVSGSFDESRIWDVKTGKCLKTLPAHSDPVSAVHFNRDGSILVSSS 1365
      YVFCCNFNPQS+L+VSGSFDESRIWDVKTG C+KTLPAHSDPVSAV FNRDGLI S S
30      S: 173 YVFCCNFNPQSSLVSGSFDESRIWDVKTGMCIKTLPAHSDPVSAVSFNRDGLIASGS 232

      Q: 1364 YDGLCRIWDTASGQCLKTLIDDDNPPVSFVKFSPNGKYILAATLDNTLKLWDYSKGKCLK 1185
      YDGL RIWDTA+GQC+KTL+DD+NPPV+FVKFSPNGKYILA+ LD+TLKLWD+SKGK LK
      S: 233 YDGLVRIWDTANGQCIKTLVDDENPPVAFVKFSPNGKYILASNLDSTLKLWDFSKGKTLK 292

35      Q: 1184 TYTGHKNEKYCIFANFSVTGGKWIVSGSEDNLVYIWNLQTKIIVQKLQGHTDVVISTACH 1005
      YTGH+N KYCIFANFSVTGGKWI+SGSED +YIWNLQT+EIVQ L+GHT V+++ CH
      S: 293 QYTGHENSKYCIFANFSVTGGKWIISGSEDCKIYIWNLQTREIVQCLEGHTQPVLASDCH 352

40      Q: 1004 PTENIIASAALENDKTIKLWKS D 936
      P +NIIAS ALE D I +W+SD
      S: 353 PVQNIISGALEPDNKIHIWRS D 375
  
```

The segment of gnl|PID|e1343996 that is shown as "S" above is set out in the sequence listing as SEQ ID NO. 111.

Preferred polypeptides of the invention comprise a polypeptide having the amino acid sequence set out in the sequence listing as SEQ ID NO. 112 which corresponds to the "Q" sequence in the alignment shown above (gaps introduced in a sequence by the computer are, of course, removed).

- 5 It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: CD34 positive cells (Cord Blood) and to a lesser extent in NCI_CGAP_GCB1; Soares fetal liver spleen 1NFLS; Soares_pregnant_uterus_NbHPU; Stratagene colon (#937204); LNCAP, differential expression; Amniotic Cells - TNF induced; Human Soleus; Human Skin Tumor;
- 10 Human Pineal Gland; Soares adult brain N2b4HB55Y; Human Stomach, re-excision; Jurkat T-Cell, S phase; Apoptotic T-cell; Human Jurkat Membrane Bound Polysomes; Human Adult Testes, Large Inserts, Reexcision; Epithelial-TNF α and INF induced; Human Testes Tumor, re-excision; Bone Marrow Stromal Cell, untreated; Smooth muscle, serum induced, re-exc; Pancreas Islet Cell Tumor; 12 Week Old Early
- 15 Stage Human; Adipocytes; Human Testes, Reexcision; Human Adult Pulmonary, re-excision; NCI_CGAP_GC3; Colon Normal III; Soares_multiple_sclerosis_2NbHMSP; Human Bone Marrow, treated; Activated T-cell(12h)/Thiouridine-re-excision; Nine Week Old Early Stage Human; Human Cerebellum; Soares_fetal_liver_spleen_1NFLS_S1; Primary Dendritic Cells, lib 1
- 20 and Soares infant brain 1NIB.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 62 as residues: Gly-30 to Thr-44.

- Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are
- 25 related to SEQ ID NO:13 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically

excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2050 of SEQ ID NO:13, b
 5 is an integer of 15 to 2064, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:13, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 4

10 The computer algorithm BLASTX has been used to determine that the translation product of this gene shares sequence homology with, as a non-limiting example, the sequence accessible through the following database accession no. gil2149634 (all information available through the recited accession number is incorporated herein by reference) which is described therein as "terminal
 15 deoxynucleotidyltransferase [Monodelphis domestica]." A partial alignment demonstrating the observed homology is shown immediately below.

```

20 >gi|2149634 terminal deoxynucleotidyltransferase [Monodelphis domestica]
    Length = 518

    Minus Strand HSPs:

    Score = 216 (76.0 bits), Expect = 4.7e-32, Sum P(4) = 4.7e-32
25 Identities = 42/83 (50%), Positives = 62/83 (74%), Frame = -3

    Q: 1896 VEVRRSERYQTMKLTQIFGVGVKTADRWYREGLRTLDDLR-EQPQKLTQQQKAGLQHH 1720
        V+ V   ERYQ+ KLFT +FGVG+KTAD+WYR G RTL+ +R ++ KLT+ QKAGL ++
    S: 239 VQAVLNDERYQSFKLFTSVFGVGLKTADKWYRMGFRTLKIRSDKTLKLTQMOKAGLCYY 298

30 Q: 1719 QDLSTPVLRSDDVDALQQVVEEAV 1651
        +DL V +++ DA+ +V++AV
    S: 299 EDLIDCVSKAEADAVSLLVQDAV 321
  
```

The segment of gil2149634 that is shown as "S" above is set out in the sequence listing as SEQ ID NO. 113. Based on the structural similarity these homologous polypeptides are expected to share at least some biological activities. Such activities are known in the art, some of which are described elsewhere herein.

- 5 Assays for determining such activities are also known in the art, some of which have been described elsewhere herein.

Preferred polypeptides of the invention comprise a polypeptide having the amino acid sequence set out in the sequence listing as SEQ ID NO. 114 which corresponds to the "Q" sequence in the alignment shown above (gaps introduced in a
10 sequence by the computer are, of course, removed).

It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: NCI_CGAP_GCB1 and to a lesser extent in Soares_pregnant_uterus_NbHPU; Soares_multiple_sclerosis_2NbHMSP; Human Thymus Stromal Cells; Human Leukocytes; Human OB HOS treated (1 nM E2)
15 fraction I; Smooth muscle, IL1b induced; LNCAP prostate cell line; Brain Frontal Cortex, re-excision; Ovarian Tumor 10-3-95; Human Gall Bladder; NCI_CGAP_AA1; NCI_CGAP_Br2; NCI_CGAP_Co8; NCI_CGAP_Pr5; NCI_CGAP_Lei2; NCI_CGAP_Brn23; Colon Normal II; Human Synovial Sarcoma; Hodgkin's Lymphoma II and T cell helper II.

- 20 Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 63 as residues: Pro-26 to Met-35.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:14 and may have been publicly available prior to conception of
25 the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence

would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1884 of SEQ ID NO:14, b is an integer of 15 to 1898, where both a and b correspond to the positions of

5 nucleotide residues shown in SEQ ID NO:14, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 5

The computer algorithm BLASTX has been used to determine that the
10 translation product of this gene shares sequence homology with, as a non-limiting example, the sequence accessible through the following database accession no. gi1906596 (all information available through the recited accession number is incorporated herein by reference) which is described therein as "kinesin-73 [Drosophila melanogaster]." A partial alignment demonstrating the observed
15 homology is shown immediately below.

>gi1906596 kinesin-73 [Drosophila melanogaster] >sp|001349|001349
KINESIN-73.

Length = 1921

Plus Strand HSPs:

Score = 1695 (596.7 bits), Expect = 2.3e-184, Sum P(2) = 2.3e-184
Identities = 339/504 (67%), Positives = 396/504 (78%), Frame = +1

25 Q: 166 ESFQRRCPGPAEVFAYDHCFWSMDES VK EYAGQDIVFKCLGENILQNAFXGYNACIFAY 345
E +R+ P + FA+DHCF+S++ E +A Q+ VF C+G IL NAF GYNACIFAY
S: 44 EKIERKQP---KTFAFDHCFYSLNPE-DENFASQETVFD CVGRGILDNAFQGYNACIFAY 99

30 Q: 346 GQTGSGKSYTMMGTADQPLIPRLCSGLFERTQKEGNEEQSFKEVVS YMEIYNEKVRDLL 525
GQTGSGKSYTMMGT + G+IPRLC LF + E +KVEVS YMEIYNEKV DLL
S: 100 GQTGSGKSYTMMGTQESKGIIPRLCDQLFSAIANKSTPELMYKVEVS YMEIYNEKVHDL 159

35 Q: 526 DPKGSRQTLK VREHSVLGPYVDGLSKLAVTSYKDIESLMSEG NKSRTVAATNMNEESSRS 705
DPK ++Q+LK VREH+V+GPYVDGLS+LAVTSY+DI++LM+EG NKSRTVAATNMN ESSRS
S: 160 DPKPNKQSLK VREHNVMG PYVDGLSQLAVTSYQDIDNLMTEG NKSRTVAATNMNAESSRS 219

Q: 706 HAVFKITLTHTLVDVKSGETSGEKVGKXSLVDLXGSERATKTGAAGDRLKEGSNINKSLTT 885
 HAVF + LT L D +G SGEKV + SLVDL GSERA KTGA GDRLKEGSNINKSLTT
 S: 220 HAVFSVLTQILTDQATGVSGEKVSRLSLVDLAGSERAVKTGAAGDRLKEGSNINKSLTT 279

5 Q: 886 LGLVISALADQSAGK-SXN-KFVPYRDSVLTWLLKDSLGGNSKXAMVATVSPAADNYDET 1059
 LGLVIS LADQS GK S N KFVPYRDSVLTWLLKD+LGGNS+ MVAT+SP+ADNY+ET
 S: 280 LGLVISKADQSNKGKSGNDKFVPYRDSVLTWLLKDNLGGNSRTVMVATISPSADNYEET 339

10 Q: 1060 LSTLRYADRAKHIVNHAVVNEDPNARIIRDLREEVEKLREQLTKAEAMKSPELKDRLEES 1239
 LSTLRYADRAK IVNHAVVNEDPNARIIR+LR EVE LR L A +++D+L ES
 S: 340 LSTLRYADRAKRIVNHAVVNEDPNARIIRELRHEVETLRSMKXATGSPVGDVQDKLAES 399

15 Q: 1240 EKLIQEMTVTWEEKLRKTEEIAQERQKQLESLSGSGIKVGDDKCFVLNADPALN 1419
 E L++++ TWEEKL KTE I ERQ+ LE +GIS+Q+SGIKV +K +LVNADNP+LN
 S: 400 ENLMKQISQTWEEKLVKTERIQNERQQALEKMGISVQASGIKVEKNKYLVNADNP+LN 459

20 Q: 1420 ELLVYYLKEHTLIG----SANSQDIQLCGMGILPEHCIIIDITSEGQVMLTPQKNRTFVN 1587
 ELLVYYLK+ TLIG S DIQL G+GI PEHC+I I G M P + R FVN
 S: 460 ELLVYYLKDRTLIGGRTISGQQPDIQLSGLGIQPEHCVITIEDSGLYM-EPVQGARCFVN 518

Q: 1588 GSSVSSPIQLHHGDRILWGNHFFRLNLP 1674
 GS+ L +GDRILWGN+HFFR+N P
 S: 519 GSAAVEKTPLQNGDRILWGNHFFRVNSP 547

25 The segment of gil1906596 that is shown as "S" above is set out in the sequence listing as SEQ ID NO. 115. Based on the structural similarity these homologous polypeptides are expected to share at least some biological activities. Such activities are known in the art, some of which are described elsewhere herein. Assays for determining such activities are also known in the art, some of which have
 30 been described elsewhere herein.

Preferred polypeptides of the invention comprise a polypeptide having the amino acid sequence set out in the sequence listing as SEQ ID NO. 116 which corresponds to the "Q" sequence in the alignment shown above (gaps introduced in a sequence by the computer are, of course, removed).

35 It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: Colon Normal II; Soares_fetal_liver_spleen_1NFLS_S1 and to a lesser extent in Pancreatic Islet; and Human Fetal Heart.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:15 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically
5 excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1687 of SEQ ID NO:15, b is an integer of 15 to 1701, where both a and b correspond to the positions of
10 nucleotide residues shown in SEQ ID NO:15, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 6

It has been discovered that this gene is expressed primarily in the following
15 tissues/cDNA libraries: Soares breast 2NbHBst; and Ovarian Tumor 10-3-95.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:16 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically
20 excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1161 of SEQ ID NO:16, b is an integer of 15 to 1175, where both a and b correspond to the positions of
25 nucleotide residues shown in SEQ ID NO:16, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 7

The computer algorithm BLASTX has been used to determine that the translation product of this gene shares sequence homology with, as a non-limiting example, the sequence accessible through the following database accession no. gnl|PID|e1321523 (all information available through the recited accession number is incorporated herein by reference) which is described therein as "ATP(GTP)-binding protein [Homo sapiens]." A partial alignment demonstrating the observed homology is shown immediately below.

10

```
>gnl|PID|e1321523 (AJ010842) ATP(GTP)-binding protein [Homo sapiens]
>sp|O76004|O76004 ATP(GTP)-BINDING PROTEIN (FRAGMENT).
Length = 358
```

15

Minus Strand HSPs:

```
Score = 1594 (561.1 bits), Expect = 4.3e-163, P = 4.3e-163
Identities = 319/358 (89%), Positives = 319/358 (89%), Frame = -1
```

20

```
Q: 1761 RHPVCLLVLMAGSGKTTTFVQRLTGHHLHAQGTTPPYVINLDPVHEVPFPANIDIRDTVKY
1582
```

```
S: 1 RHPVCLLVLMAGSGKTTTFVQRLTGHHLHAQGTTPPYVINLDPVHEVPFPANIDIRDTVKY
60
```

25

```
Q: 1581 KEVMKQYGLGPNGGIVTSLNLFATRFDQVMKFIKAQNMSKYVLIDTPGQIEVFTWSASG
1402
```

```
S: 61 KEVMKQYGLGPNGGIVTSLNLFATRFDQVMKFIKAQNMSKYVLIDTPGQIEVFTWSASG
120
```

30

```
Q: 1401 TIITEALASSFPTVVIYVMDTSRSTNPVTFMSNMLYACSIYKTKLPFIVVMNKTDIIDH
1222
```

35

```
S: 121 TIITEALASSFPTVVIYVMDTSRSTNPVTFMSNMLYACSIYKTKLPFIVVMNKTDIIDH
180
```

40

```
Q: 1221 SFAVEWMQDFAEQDALNQETTYVSNLTRMSLVLDEFYSSLRVVGSAVLGTGLDELFFV
1042
```

```
S: 181 SFAVEWMQDFAEQDALNQETTYVSNLTRMSLVLDEFYSSLRVVGSAVLGTGLDELFFV
240
```

45

```
Q: 1041 QVTSAXXXXXXXXXXXXXLKKSLANAESXXXXXXXXXXXXKMGVALDAGTAKDSLSPV
862
```

```

          QVTSAA          LKKSLANAES          KDMGSVALDAGTAKDSLSPV
S:   241 QVTSAAEEYEREYRPEYERLKKSLANAESQQQREQLERLRKDMGSVALDAGTAKDSLSPV
300
5       Q:   861 LHPSDLILTRGTLXXXXXXXXXXXXXXXXXHRVTEESHEEPAFQNFMQESMAQYWKRRNK
688
          LHPSDLILTRGTL          HRVTEESHEEPAFQNFMQESMAQYWKRRNK
S:   301 LHPSDLILTRGTLDEEDEEADSDTDDIDHRVTEESHEEPAFQNFMQESMAQYWKRRNK
358

```

10

The segment of gnl|PID|e1321523 that is shown as "S" above is set out in the sequence listing as SEQ ID NO. 117. Based on the structural similarity these homologous polypeptides are expected to share at least some biological activities. Such activities are known in the art, some of which are described elsewhere herein.

15 Assays for determining such activities are also known in the art, some of which have been described elsewhere herein.

Preferred polypeptides of the invention comprise a polypeptide having the amino acid sequence set out in the sequence listing as SEQ ID NO. 118 which corresponds to the "Q" sequence in the alignment shown above (gaps introduced in a

20 sequence by the computer are, of course, removed).

It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: Soares melanocyte 2NbHM and to a lesser extent in Stratagene ovarian cancer (#937219); Soares infant brain 1NIB; Soares placenta Nb2HP; NCI_CGAP_GCB1; Human Adult Small Intestine; Stratagene NT2 neuronal

25 precursor 937230; NTERA2 + retinoic acid, 14 days; Stratagene lung (#937210); 12 Week Old Early Stage Human; NCI_CGAP_Ew1; Anergic T-cell; Soares_fetal_liver_spleen_1NFLS_S1; Stratagene endothelial cell 937223; Keratinocyte; Human 8 Week Whole Embryo; Human Infant Adrenal Gland, Subtracted; H. Atrophic Endometrium; Adipocytes, re-excision; Human Thyroid;

30 Human Liver; Human Adult Heart, re-excision; Apoptotic T-cell, re-excision; H

Female Bladder, Adult; Healing groin wound, 7.5 hours post incision; Synovial hypoxia-RSF subtracted; Spleen metastatic melanoma; Ovarian Tumor 10-3-95; Fetal Liver, subtraction II; Human Prostate; Human Thymus; Human Uterine Cancer; T-Cell PHA 24 hrs; Human Ovarian Cancer Reexcision; Human Thymus Stromal Cells;

5 Epithelial-TNF α and INF induced; Human Testes Tumor, re-excision; Soares_NhHMPu_S1; Human Substantia Nigra; NCI_CGAP_AA1; NCI_CGAP_Lu5; Colon Normal II; Human Placenta; Adipocytes; Pancreatic Islet; Primary Dendritic cells,frac 2; Human Fetal Heart; human tonsils; Endothelial cells-control; Human Microvascular Endothelial Cells, fract. A; Monocyte activated; T Cell

10 helper I; Soares_pregnant_uterus_NbHPU and Stratagene hNT neuron (#937233).

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:17 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically

15 excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1813 of SEQ ID NO:17, b is an integer of 15 to 1827, where both a and b correspond to the positions of

20 nucleotide residues shown in SEQ ID NO:17, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 8

The computer algorithm BLASTX has been used to determine that the

25 translation product of this gene shares sequence homology with, as a non-limiting example, the sequence accessible through the following database accession no.

gil2197085 (all information available through the recited accession number is incorporated herein by reference) which is described therein as "ORF2-like protein [Homo sapiens]." A partial alignment demonstrating the observed homology is shown immediately below.

5

```

>gi|2197085 (AF003535) ORF2-like protein [Homo sapiens] >gi|2197085
(AF003535)
      ORF2-like protein [Homo sapiens] >sp|O00549|O00549 ORF2-LIKE
      PROTEIN (FRAGMENT).
10      Length = 573

      Plus Strand HSPs:

      Score = 176 (62.0 bits), Expect = 9.3e-17, Sum P(4) = 9.3e-17
15      Identities = 57/179 (31%), Positives = 90/179 (50%), Frame = +2

      Q: 1721 QTNLELISSRL*QGCRIKLNT*KXIPFLYTSXEPLEFEIKIXHH*XYQKREREXICIML 1900
          Q L+LIS+ + K+N K FLYT+ E +I KR + + I L
20      S: 230 QNLLKLISN-FSKVSGYKINVQKSQAFLYTNNRQTESQIMGELPFTIASKRIK-YLGIQL 287

      Q: 1901 TKXVXKVCEKNYKSLMK*IKGDLN*WKDKLC*WIRKLNLMVCQFIP--I*SIDSMQ-S*K 2071
          T+ V + ++NYK L+K IK D N WK+ C W+ ++N+V +P I +++
25      S: 288 TRDVKDLFKENYKPLLKEIKEDTNKWKNI PCSWVGRINIVKMAILPKVIYRFNAIPIKLP 347

      Q: 2072 ATLWTSAN*----F*GLHEKAKRCNSRNNIEEEQRSRTLLDFKSFYKATI IKIVVHW*KN 2239
          T +T F ++A+ S + + + TLLDFK +YKAT+ K W+W +N
30      S: 348 MTFTELEKTTLKFIWNQKRARI AKSILSQKNKAGGITLLDFKLYYKATVTKTAWYWYQN 407

      Q: 2240 R 2242
          R
      S: 408 R 408

```

The segment of gil2197085 that is shown as "S" above is set out in the sequence listing as SEQ ID NO. 119.

35 Preferred polypeptides of the invention comprise a polypeptide having the amino acid sequence set out in the sequence listing as SEQ ID NO. 120 which corresponds to the "Q" sequence in the alignment shown above (gaps introduced in a sequence by the computer are, of course, removed).

It has been discovered that this gene is expressed primarily in L428.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 67 as residues: Lys-89 to Glu-94.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:18 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2331 of SEQ ID NO:18, b is an integer of 15 to 2345, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:18, and where b is greater than or equal to a + 14.

15 FEATURES OF PROTEIN ENCODED BY GENE NO: 9

It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: Human Tonsils, Lib 2; and Keratinocyte.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:19 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 840 of SEQ ID NO:19, b is an integer of 15 to 854, where both a and b correspond to the positions of

nucleotide residues shown in SEQ ID NO:19, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 10

5 It has been discovered that this gene is expressed primarily in Adipocytes.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:20 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically
10 excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1436 of SEQ ID NO:20, b is an integer of 15 to 1450, where both a and b correspond to the positions of
15 nucleotide residues shown in SEQ ID NO:20, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 11

It has been discovered that this gene is expressed primarily in the following
20 tissues/cDNA libraries: Human Chronic Synovitis; NCI_CGAP_GCB1; Human Umbilical Vein Endothelial Cells, uninduced; NCI_CGAP_Kid5; and H. Frontal cortex, epileptic, re-excision.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are
25 related to SEQ ID NO:21 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically

excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1234 of SEQ ID NO:21, b
5 is an integer of 15 to 1248, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:21, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 12

10 When tested against fibroblast cell lines, supernatants removed from cells containing this gene activated the EGR1 assay. Thus, it is likely that this gene activates fibroblast cells through a signal transduction pathway. Early growth response 1 (EGR1) is a promoter associated with certain genes that induces various tissues and cell types upon activation, leading the cells to undergo differentiation
15 and proliferation

It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: Human Cerebellum and to a lesser extent in Stratagene pancreas (#937208); Human Substantia Nigra; Human B Cell Lymphoma; Primary Dendritic Cells, lib 1; Soares infant brain 1NIB; LNCAP + 0.3nM R1881;
20 Soares_multiple_sclerosis_2NbHMSP; prostate-edited; Human OB HOS treated (10 nM E2) fraction I; Human Tonsils, Lib 2; HEL cell line; pBMC stimulated w/ poly I/C; Human Uterine Cancer; Human Thymus Stromal Cells; Human T-Cell Lymphoma; Human Eosinophils; breast lymph node CDNA library; Bone marrow; human tonsils; Human Neutrophil, Activated; Activated T-Cell (12hs)/Thiouridine
25 labelledEco; Monocyte activated and neutrophils control.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 71 as residues: Arg-4 to Met-10, Gly-21 to Met-33, Leu-54 to Ser-62, Lys-67 to Arg-79.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:22 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3254 of SEQ ID NO:22, b is an integer of 15 to 3268, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:22, and where b is greater than or equal to a + 14.

15

FEATURES OF PROTEIN ENCODED BY GENE NO: 13

It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: Soares infant brain 1NIB and to a lesser extent in Pancreatic Islet; Soares_placenta_8to9weeks_2NbHP8to9W; Normal Prostate; Human Tonsils, Lib 2; B Cell lymphoma and Human Liver, normal.

20

Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 72 as residues: Glu-121 to Leu-126.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:23 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically

25

excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1659 of SEQ ID NO:23, b
5 is an integer of 15 to 1673, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:23, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 14

10 It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: CD34+ cell, I; Human Aortic Endothelium; Human Fetal Epithelium (Skin); Prostate BPH; Fetal Liver, subtraction II; Human Osteoblasts II; Human Adrenal Gland Tumor; Human adult testis, large inserts; Smooth muscle, serum induced, re-exc; Macrophage-oxLDL, re-excision; Smooth muscle, serum
15 treated; Human Synovial Sarcoma; Monocyte activated; Human B Cell Lymphoma; and Primary Dendritic Cells, lib 1.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:24 and may have been publicly available prior to conception of
20 the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 932 of SEQ ID NO:24, b
25 is an integer of 15 to 946, where both a and b correspond to the positions of

nucleotide residues shown in SEQ ID NO:24, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 15

5 It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: Neutrophils IL-1 and LPS induced; and Endothelial-induced.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 74 as residues: Asn-25 to Thr-33.

Many polynucleotide sequences, such as EST sequences, are publicly
10 available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:25 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention
15 are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 607 of SEQ ID NO:25, b is an integer of 15 to 621, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:25, and where b is greater than or equal to a + 14.

20

FEATURES OF PROTEIN ENCODED BY GENE NO: 16

When tested against K562 leukemia cell lines, supernatants removed from cells containing this gene activated the ISRE assay. Thus, it is likely that this gene activates leukemia cells through the Jak-STAT signal transduction pathway. The
25 interferon-sensitive response element is a promoter element found upstream of many genes which are involved in the Jak-STAT pathway. The Jak-STAT pathway is a

large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jak-STAT pathway, reflected by the binding of the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells.

5 It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: Jurkat T-Cell, S phase; and Neutrophils IL-1 and LPS induced.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are
10 related to SEQ ID NO:26 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the
15 general formula of a-b, where a is any integer between 1 to 1722 of SEQ ID NO:26, b is an integer of 15 to 1736, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:26, and where b is greater than or equal to a + 14.

20 **FEATURES OF PROTEIN ENCODED BY GENE NO: 17**

It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: Human adult testis, large inserts and to a lesser extent in Human Testes Tumor; Activated T-cell(12h)/Thiouridine-re-excision; Soares infant
brain 1NIB; Soares ovary tumor NbHOT; Palate normal; Whole 6 Week Old Embryo;
25 Human Colon, subtraction; Human Fetal Spleen; Human Liver; Human Synovium; Human Chronic Synovitis; T-Cell PHA 16 hrs; Human Fetal Kidney; Human Thymus

Stromal Cells; Human Adrenal Gland Tumor; Soares_pregnant_uterus_NbHPU;
Human Whole Six Week Old Embryo; Human T-Cell Lymphoma; Colon Carcinoma;
Adipocytes; T Cell helper I; Human Bone Marrow, treated; Bone Marrow Cell Line
(RS4,11) and Keratinocyte.

5 Preferred epitopes include those comprising a sequence shown in SEQ ID NO.
76 as residues: Pro-20 to Pro-28, Pro-36 to Cys-41.

Many polynucleotide sequences, such as EST sequences, are publicly
available and accessible through sequence databases. Some of these sequences are
related to SEQ ID NO:27 and may have been publicly available prior to conception of
10 the present invention. Preferably, such related polynucleotides are specifically
excluded from the scope of the present invention. To list every related sequence
would be cumbersome. Accordingly, preferably excluded from the present invention
are one or more polynucleotides comprising a nucleotide sequence described by the
general formula of a-b, where a is any integer between 1 to 1789 of SEQ ID NO:27, b
15 is an integer of 15 to 1803, where both a and b correspond to the positions of
nucleotide residues shown in SEQ ID NO:27, and where b is greater than or equal to a
+ 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 18

20 It has been discovered that this gene is expressed primarily in the following
tissues/cDNA libraries: Soares_multiple_sclerosis_2NbHMSP and to a lesser extent
in Human Hippocampus; Spinal cord; Human Manic Depression Tissue; Early Stage
Human Brain; Frontal lobe,dementia,re-excision; Alzheimers, spongy change; Human
Substantia Nigra; Soares infant brain 1NIB; Human Right Hemisphere of Brain;
25 Human colon cancer, metaticized to liver, subtraction; Human Kidney Cortex, re-
rescue; Supt Cells, cyclohexamide treated; NTERA2 teratocarcinoma cell

- line+retinoic acid (14 days); human corpus colosum; Human Amygdala, re-excision;
Spinal Cord, re-excision; Fetal Liver, subtraction II; Human
Hypothalamus, Schizophrenia; Human Fetal Brain; Human Whole Six Week Old
Embryo; Human Gall Bladder; Human Testes Tumor; Human Testes; Human
5 Endometrial Tumor and Nine Week Old Early Stage Human.

Many polynucleotide sequences, such as EST sequences, are publicly
available and accessible through sequence databases. Some of these sequences are
related to SEQ ID NO:28 and may have been publicly available prior to conception of
the present invention. Preferably, such related polynucleotides are specifically
10 excluded from the scope of the present invention. To list every related sequence
would be cumbersome. Accordingly, preferably excluded from the present invention
are one or more polynucleotides comprising a nucleotide sequence described by the
general formula of a-b, where a is any integer between 1 to 2273 of SEQ ID NO:28, b
is an integer of 15 to 2287, where both a and b correspond to the positions of
15 nucleotide residues shown in SEQ ID NO:28, and where b is greater than or equal to a
+ 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 19

- It has been discovered that this gene is expressed primarily in the following
20 tissues/cDNA libraries: Soares fetal liver spleen 1NFLS and to a lesser extent in
Colon Tumor II; Normal colon; Stratagene lung (#937210); Human Umbilical Vein
Endothelial Cells, uninduced; Soares_senescent_fibroblasts_NbHSF; Human
endometrial stromal cells-treated with progesterone; Osteoblasts; Endothelial cells-
control; Colon Normal III; Stratagene ovary (#937217); 12 Week Old Early Stage
25 Human; CD34 depleted Buffy Coat (Cord Blood), re-excision; H. Amygdala
Depression, subtracted; Activated T-cells; Human Colon, re-excision; Macrophage

- (GM-CSF treated); Colon Carcinoma; breast lymph node CDNA library; Neutrophils control, re-excision; Spleen, Chronic lymphocytic leukemia;
- Soares_fetal_lung_NbHL19W; Morton Fetal Cochlea; Soares adult brain
- N2b5HB55Y; Soares melanocyte 2NbHM; Anergic T-cell; Hodgkin's Lymphoma II;
- 5 T cell helper II; Primary Dendritic Cells, lib 1; Human endometrial stromal cells- treated with estradiol; Stratagene endothelial cell 937223; Stratagene endothelial cell 937223; NCI_CGAP_GC5; Human Fetal Dura Mater; Human Rhabdomyosarcoma; Soares_fetal_heart_NbHH19W; H Macrophage (GM-CSF treated), re-excision; Human Placenta; Bone marrow; NCI_CGAP_GC3;
- 10 Soares_parathyroid_tumor_NbHPA; Human Colon Cancer, subtracted; Weizmann Olfactory Epithelium; Stratagene endothelial cell 937223; Resting T-Cell, re-excision; Stomach cancer (human),re-excision; Human Hypothalamus,schizophrenia, re-excision; H Female Bladder, Adult; Human Adipose Tissue, re-excision; Human Brain, Striatum; Macrophage-oxLDL; Human Activated Monocytes; Colon Normal
- 15 II; Soares breast 3NbHBst; Adipocytes; Dendritic cells, pooled; Human Microvascular Endothelial Cells, fract. A; NCI_CGAP_Kid6; Human Bone Marrow, treated; Neutrophils IL-1 and LPS induced; Stratagene fibroblast (#937212); Osteoarthritis (OA-4); CD40 activated monocyte dendridic cells; Activated T-Cells, 8 hrs, subtracted; CD34+cells, II, FRACTION 2; Frontal Lobe, Dementia; Human
- 20 White Adipose; Hodgkin's Lymphoma I; Healing Abdomen wound,70&90 min post incision; Frontal lobe,dementia,re-excision; Aorta endothelial cells + TNF-a; HSA 172 Cells; Apoptotic T-cell, re-excision; Human Synovium; Synovial IL-1/TNF stimulated; H. Kidney Cortex, subtracted; Stratagene ovarian cancer (#937219); Human Osteosarcoma; Pancreas normal PCA4 No; Human endometrial stromal cells;
- 25 Jurkat T-cell G1 phase; Stratagene lung carcinoma 937218; Myoloid Progenitor Cell Line; Human Ovary; Spleen metastatic melanoma; Human Chronic Synovitis; Human

- Prostate; CD34 depleted Buffy Coat (Cord Blood); T-Cell PHA 16 hrs; Human Bone Marrow, re-excision; Apoptotic T-cell; Human Jurkat Membrane Bound Polysomes; Human Primary Breast Cancer Reexcision; T-Cell PHA 24 hrs; Stromal cell TF274; Human umbilical vein endothelial cells, IL-4 induced; Spinal cord; Synovial
- 5 Fibroblasts (control); Ulcerative Colitis; Human Thymus Stromal Cells; Human Whole Six Week Old Embryo; Macrophage-oxLDL, re-excision; Human Gall Bladder; Human T-Cell Lymphoma; Early Stage Human Brain; Clontech human aorta polyA+ mRNA (#6572); NCI_CGAP_Pr3; Human Fetal Lung III; Endothelial-induced; Bone Marrow Cell Line (RS4,11); Nine Week Old Early Stage Human;
- 10 Stratagene NT2 neuronal precursor 937230; Soares placenta Nb2HP; Human Pancreas; Activated T-Cells, 8 hrs, differentially expressed; Human Colon Cancer, differential; H. Leukocytes, normalized cot 500 A; Stratagene pancreas (#937208); Stratagene ovarian cancer (#937219); H. Primary Dendritic Cells, lib 3; Human Greater Omentum, flI remake; H. Leukocytes, normalized cot 500 B; Human
- 15 Astrocyte; Human Adult Spleen, fractionII; Thyroid Thyroiditis; Palate carcinoma; Rectum normal; Larynx Normal; Human Bone Marrow; Osteoclastoma-normalized A; Larynx Carcinoma; Larynx tumor; Colon Tumor; Liver Tumour Met 5 Tu; Colon, normal; Activated T-Cells, 8 hrs.; Brain Amygdala Depression; Human B Cell 8866; H. Adipose Tissue; Colorectal Tumor; Hypothalamus;
- 20 Soares_multiple_sclerosis_2NbHMSP; Human Adult Spleen; Soares retina N2b5HR; stomach cancer (human); A-14 cell line; Human Aortic Endothelium; Human Cerebellum, subtracted; Human Primary Breast Cancer, re-excision; Smooth Muscle Serum Treated, Norm; human colon cancer; Human Lung; Smooth Muscle- HASTE normalized; Human Pineal Gland; Human Normal Breast; Mesangial cell, frac 2;
- 25 Human Epididymus; Human Prostate Cancer, Stage C fraction; Alzheimers, spongy change; Healing groin wound, 7.5 hours post incision; Human Frontal Cortex,

Schizophrenia; Healing groin wound, 6.5 hours post incision; H. Ovarian Tumor, II, OV5232; Synovial hypoxia; Synovial Fibroblasts (II1/TNF), subt; Soares_pregnant_uterus_NbHPU; H. Meningima, M1; H. Lymph node breast Cancer; Stratagene endothelial cell 937223; Spinal Cord, re-excision; Temporal cortex-
 5 Alzheimer, subtracted; Human Fetal Kidney; Stratagene fetal spleen (#937205); HMI; NCI_CGAP_Br3; NCI_CGAP_Co9; NCI_CGAP_Pr7; NCI_CGAP_CNS1; NCI_CGAP_Co11; NCI_CGAP_Lar1; NCI_CGAP_Pr12; NCI_CGAP_Pr25; NCI_CGAP_Thy1; NCI_CGAP_Br1.1; Human Uterine Cancer; Human Activated T-Cells; Human Pancreas Tumor; Human Chondrosarcoma; Epithelial-TNF α and INF
 10 induced; Human Testes Tumor, re-excision; Human Thymus; Bone Marrow Stromal Cell, untreated; Human Fetal Brain; Human Liver, normal; Resting T-Cell Library,II; Neutrophils IL-1 and LPS induced; Human Substantia Nigra; NCI_CGAP_Lym3; Human Synovial Sarcoma; Primary Dendritic cells,frac 2; Human Neutrophil, Activated; Human Osteoclastoma; T Cell helper I; NCI_CGAP_Kid3; neutrophils
 15 control; NCI_CGAP_Pr1; NCI_CGAP_Lip2; Stratagene neuroepithelium NT2RAMI 937234; and Human 8 Week Whole Embryo.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 78 as residues: Cys-22 to Ser-27.

Many polynucleotide sequences, such as EST sequences, are publicly
 20 available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:29 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention
 25 are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 913 of SEQ ID NO:29, b

is an integer of 15 to 927, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:29, and where b is greater than or equal to a + 14.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 20

When tested against sensory neuron cell lines, supernatants removed from cells containing this gene activated the EGR1 assay. Thus, it is likely that this gene activates sensory neuron cells through a signal transduction pathway. Early growth response 1 (EGR1) is a promoter associated with certain genes that induces various
10 tissues and cell types upon activation, leading the cells to undergo differentiation and proliferation.

The computer algorithm BLASTX has been used to determine that the translation product of this gene shares sequence homology with, as a non-limiting example, the sequence accessible through the following database accession no.
15 gnl|PID|d1035475 (all information available through the recited accession number is incorporated herein by reference) which is described therein as "KIAA0774 protein [Homo sapiens]." A partial alignment demonstrating the observed homology is shown immediately below.

```
20  >gnl|PID|d1035475 (AB018317) KIAA0774 protein [Homo sapiens]
    >sp|D1035475|D1035475 KIAA0774 PROTEIN (FRAGMENT).
    Length = 1163

    Plus Strand HSPs:

25  Score = 371 (130.6 bits), Expect = 1.7e-29, P = 1.7e-29
    Identities = 82/201 (40%), Positives = 133/201 (66%), Frame = +1

30  Q:  667 EIKKGHEIEKKSLLEDLLSEKQESLEKQINDLKSENDALNEKLKSEEQ--KXXAREKANLK 840
      E+  HE+EKK LE+  + + SL+ Q++ L  ++ +L ++ + E+  +  E+  +
      S:  963 ELMSTHELEKKELEENFEKLRSLQDQVDTLTFQSQSLRDRARRFEEALRKNTEEQLEIA 1022

      Q:  841 NPQIMYLEQELESKAVLEIKNEKLHQDQDIKLMKMEKLVNNTALVDXLKRFQQENEELX 1020
      +LE++++SLK VLE+KN++++H+Q+ K++++EKL + N  L + ++ QQ+NE+L
```

S: 1023 LAPHQHLEEDMKSLKQVLEMKNQQIHEQEKKILELEKLAEKNIILEEKIQVLQQQONEDLK 1082
 Q: 1021 ARMDKHMAISRQLSTEQAVALQESLEKESKVNKRLSMENEELLWKLHNGDLCSK-KRSPTS 1197
 AR+D++ ++RQLS E A LQE +EKE++ KRLS NEELLWKL GD SP K SPTS
 5 S: 1083 ARIDQNTVVTRQLSEENANLQEYVEKETQEKRLSRTNEELLWKLQTDGPTSPIKLSPTS 1142
 Q: 1198 SAIPLOSPRNSG-SFPSP-SISPR 1263
 P+ +SG S P+ S +PR
 S: 1143 ---PVYRGSSSGPSSPARVSTTPR 1163

10

The segment of gnl|PID|d1035475 that is shown as "S" above is set out in the sequence listing as SEQ ID NO. 121.

Preferred polypeptides of the invention comprise a polypeptide having the amino acid sequence set out in the sequence listing as SEQ ID NO. 122 which
 15 corresponds to the "Q" sequence in the alignment shown above (gaps introduced in a sequence by the computer are, of course, removed).

Preferred polypeptides comprise the following amino acid

sequence:

MNKMLSFFKCFVQQRPCRCRNLFNLFLFLEESFGRRQKSSSRLPVSEAXIPPVV
 20 TLQLPTVITRVLIYLLCPRSSLGSLVLTQCIKMLSESLWTLGTCHLGEMGLGLGKE
 PEFLGDCKGMAEDVGDLLGLHRSPLCSFHRSSSFSIESRLLTFDSFSSDSCRTA
 CSVESCLEIAMCLSIRAXNSSFSCWKRFNXSTNAVLLSTSFSIFINLMSC (SEQ
 ID NO:). In this preferred sequence, "X" can represent any amino acid.

Polynucleotides encoding these polypeptides are also encompassed by the invention.

25 It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: Human fetal heart, Lambda ZAP Express and to a lesser extent in Soares_fetal_lung_NbHL19W; Human Umbilical Vein Endothelial Cells, uninduced; Human Placenta; Soares breast 3NbHBst; Endothelial cells-control;

- Stratagene endothelial cell 937223; Hepatocellular Tumor; Salivary Gland, Lib 2;
 Mo7e Cell Line GM-CSF treated (1ng/ml); human ovarian cancer;
 Soares_fetal_liver_spleen_1NFLS_S1; Human Hippocampus; Soares adult brain
 N2b5HB55Y; Stratagene lung (#937210); normalized infant brain cDNA; Soares
 5 melanocyte 2NbHM; Soares_multiple_sclerosis_2NbHMSP; Human Fetal Lung III;
 NCI_CGAP_GCB1; Colon Normal III; Soares_pregnant_uterus_NbHPU;
 Soares_total_fetus_Nb2HF8_9w; Soares placenta Nb2HP; Soares fetal liver spleen
 1NFLS; Soares infant brain 1NIB; Brain pons; Human Fetal Liver, mixed 10 & 14
 week; Human Prostate, subtracted; Weizmann Olfactory Epithelium; Soares retina
 10 N2b5HR; Human White Adipose; Human Lung; Human Quadriceps; Human adult
 small intestine, re-excision; Human Pineal Gland; Human Normal Breast; Apoptotic
 T-cell, re-excision; Human Hypothalamus, schizophrenia, re-excision; Human Colon,
 re-excision; Human Infant Brain; Fetal Liver, subtraction II; T-Cell PHA 16 hrs;
 Gessler Wilms tumor; Soares_fetal_heart_NbHH19W;
 15 Soares_multiple_sclerosis_2NbHMSP; Stromal cell TF274; Human
 Hypothalamus, Schizophrenia; Soares breast 2NbHBst; Human adult lung 3' directed
 Mbol cDNA; Soares_total_fetus_Nb2HF8_9w; Soares_parathyroid_tumor_NbHPA;
 Soares_senescent_fibroblasts_NbHSF; Stratagene liver (#937224); Macrophage-
 oxLDL, re-excision; Human Gall Bladder; Human Placenta; Endothelial-induced;
 20 Human Adult Pulmonary, re-excision; 22 week old human fetal liver cDNA library;
 Human adult (K.Okubo); Human heart cDNA (YNakamura); NCI_CGAP_Co3;
 NCI_CGAP_GC2; NCI_CGAP_GC4; NCI_CGAP_Lu5; NCI_CGAP_PNS1;
 NCI_CGAP_Pr22; Pancreatic Islet; Human Amygdala; Stratagene colon (#937204);
 Stratagene pancreas (#937208); Human Microvascular Endothelial Cells, fract. A;
 25 Nine Week Old Early Stage Human and Human Cerebellum.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 79 as residues: Gly-6 to Lys-12.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:30 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3273 of SEQ ID NO:30, b is an integer of 15 to 3287, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:30, and where b is greater than or equal to a + 14.

15 FEATURES OF PROTEIN ENCODED BY GENE NO: 21

The computer algorithm BLASTX has been used to determine that the translation product of this gene shares sequence homology with, as a non-limiting example, the sequence accessible through the following database accession no. gi|581505 (all information available through the recited accession number is incorporated herein by reference) which is described therein as "XYLA of Ruminococcus flavefaciens [Ruminococcus flavefaciens]." A partial alignment demonstrating the observed homology is shown immediately below.

```
25 >gi|581505 XYLA of Ruminococcus flavefaciens [Ruminococcus flavefaciens]
    >pir|S20907|S20907 endo-1,4-beta-xylanase (EC 3.2.1.8)
precursor,
    bifunctional - Ruminococcus flavefaciens
    Length = 954
```

Plus Strand HSPs:

Score = 168 (59.1 bits), Expect = 2.6e-10, Sum P(2) = 2.6e-10
 Identities = 57/285 (20%), Positives = 107/285 (37%), Frame = +1

5
 Q: 1699 KGASVQKSTGSKNDSWD--NNNRSTGGSWNFGPQDSND-NKW---GEGNKMTS--GVSQG 1854
 +G S +N+ W+ NNN+ WN Q +ND N+W G+ N + G
 S: 240 QGGSSDNGGQQQNNNDWNQQNNNQQQNNNDWNNWGQQNNNDWNQWNNQGGQQNNNDWNNWGQQNN 299

10
 Q: 1855 EWKQPTGSDELKIGEWSGPNQPNSSSTGAWDNQKGHPLPENQNAQAPCWGRSSSXTGSEV 2034
 +W Q + + +W+ Q N+ W+NQ G + N WG+ ++ ++
 S: 300 DWNQWNNQGGQQQNNNDWNNWGQQNNNDWNQWNNQ-GQQQNNNDWNN-----WGQQNNNDW-NQW 352

15
 Q: 2035 GGQSTGSNHXAGSSDSHNSGRRSYRPTHPCQAVLQTLRSRTDLDPRVLSNTGWGQTQIK 2214
 Q N+ + N+ + + + Q + + + W
 S: 353 NNQGGQQQNNNDWNNWGQQNNNDWNQWNNQNNNQQNAWNGWDNNNNWNNQNNQQQNNNDWNN-- 410

20
 Q: 2215 QDTVWDIEEVPRPEGKSDKGTGEGWESAATQTKNSGGWGDAPSQSNQMKSGWGELSASTEW 2394
 Q+ W+ + + W + Q + W + Q+N W + + W
 S: 411 QNN-WNNNQQQNNNDWNQWNNQNNNQQQNNNDWNQWNNQGGQQNNND---WNQWNNQNNW 465

25
 Q: 2395 KDPKNT-GGWN DYKNNNSSN-WGGGRP--DEKTPSSWNE NPSKDQGWGGGRQPNQGW 2553
 N WN + NNN+ N W +++ ++W+ N W +Q N W
 S: 466 NQNNNQQNAWNGWDNNNNWNNQWDQNNQWNNQQQNNNTWDWN--NQNNWNNNQQ--NNDW 519

The segment of gil581505 that is shown as "S" above is set out in the sequence listing as SEQ ID NO. 123.

Preferred polypeptides of the invention comprise a polypeptide having the amino acid sequence set out in the sequence listing as SEQ ID NO. 124 which
 30 corresponds to the "Q" sequence in the alignment shown above (gaps introduced in a sequence by the computer are, of course, removed).

It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: Human Whole Brain, re-excision; Human Osteoblasts II and to a lesser extent in Smooth Muscle- HASTE normalized; Synovial Fibroblasts
 35 (III/TNF), subt; Human Hypothalamus, Schizophrenia; Brain frontal cortex; Early Stage Human Brain; Dendritic cells, pooled; Bone marrow; human tonsils; Human Adult Pulmonary, re-excision and Primary Dendritic Cells, lib 1.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 80 as residues: Gly-4 to Gly-10.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:31 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically

5 excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 5069 of SEQ ID NO:31, b is an integer of 15 to 5083, where both a and b correspond to the positions of

10 nucleotide residues shown in SEQ ID NO:31, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 22

It has been discovered that this gene is expressed primarily in the following

15 tissues/cDNA libraries: Hepatocellular Tumor, re-excision; Stratagene ovarian cancer (#937219); Stratagene liver (#937224) and to a lesser extent in Human Liver, normal; NCI_CGAP_Kid5; Soares placenta Nb2HP; Human Gall Bladder, fraction II; Soares ovary tumor NbHOT; Soares retina N2b5HR; Temporal cortex-Alzheimer, subtracted; Human Bone Marrow, re-excision; Human Gall Bladder; Human

20 Osteoclastoma; Human Endometrial Tumor; Human 8 Week Whole Embryo; Soares infant brain INIB; Human Osteoarthritic Cartilage Fraction III; Liver Normal Met5No; HepG2 Cells, lambda library; Human Adult Spleen; Human Adult Pulmonary; Soares_NFL_T_GBC_S1; Hepatocellular Tumor, re-excision; Human Osteosarcoma; Fetal Liver, subtraction II; Soares_multiple_sclerosis_2NbHMSP; H.

25 Kidney Medulla, re-excision; Liver, Hepatoma; NTERA2, control; Human retina cDNA Tsp509I-cleaved sublibrary; NCI_CGAP_Li2; NCI_CGAP_Ov2;

NCI_CGAP_GCB1; NCI_CGAP_Br1.1; Stratagene HeLa cell s3 937216; Soares breast 3NbHBst; Adipocytes; Colon Normal III; Human B Cell Lymphoma and Soares fetal liver spleen INFLS.

Many polynucleotide sequences, such as EST sequences, are publicly
5 available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:32 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention
10 are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2094 of SEQ ID NO:32, b is an integer of 15 to 2108, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:32, and where b is greater than or equal to a + 14.

15

FEATURES OF PROTEIN ENCODED BY GENE NO: 23

It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: Human Osteoclastoma and to a lesser extent in Soares_NhHMPu_S1; Osteoclastoma-normalized B; 12 Week Old Early Stage
20 Human; H. Frontal cortex,epileptic,re-excision; NCI_CGAP_GCB1; Normalized infant brain, Bento Soares and Activated T-cell(12h)/Thiouridine-re-excision.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 82 as residues: His-35 to Gln-43.

Many polynucleotide sequences, such as EST sequences, are publicly
25 available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:33 and may have been publicly available prior to conception of

the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the

5 general formula of a-b, where a is any integer between 1 to 1234 of SEQ ID NO:33, b is an integer of 15 to 1248, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:33, and where b is greater than or equal to a + 14.

10 FEATURES OF PROTEIN ENCODED BY GENE NO: 24

The computer algorithm BLASTX has been used to determine that the translation product of this gene shares sequence homology with, as a non-limiting example, the sequence accessible through the following database accession no. gil1907327 (all information available through the recited accession number is

15 incorporated herein by reference) which is described therein as "angiopoietin-1 [Homo sapiens]." A partial alignment demonstrating the observed homology is shown immediately below.

20 >gi|1907327 angiopoietin-1 [Homo sapiens] >gnl|PID|d1003298 KIAA0003 [Homo sapiens] {SUB 307-498}
Length = 498

Plus Strand HSPs:

25 Score = 429 (151.0 bits), Expect = 6.5e-47, Sum P(3) = 6.5e-47
Identities = 95/215 (44%), Positives = 125/215 (58%), Frame = +2

30 Q: 722 RDCQELFQVGERQSGLEIQQGSP-PFLVNCKM-TSDGGWTVIQRHDGSDVFNRPWEA 895
RDC +++Q G +SG++ I P P V C M + GGWTVIQ R DGS+DF R W+

S: 284 RDCADVQAGFNKSGIYTYINNMPEPKKVFNCMDVNGGGWTVIQHREDGSLDFQRGWKE 343

Q: 896 YKAGFGDPHGEFWLGLKVSIMGDRNSRLAVQLRDWDGNAELLQFS-VHLGGEDTAYSL 1072
YK GFG+P GE+WLGE + +I R L ++L DW+GN Q+ H+G E Y L

35 S: 344 YKMGFGNPSGEYWLGNFIFAITSQRYMLRIELMDWEGNRAYSQYDRFHIGNEKQNYRL 403

Q: 1073 QLTAPVAGQLGATTVPSSGL---SVPFSTWDQDHLRRDKNCAKSLSGGWWFGTCSHSNL 1243
 L G G T S L FST D D+D K CA L+GGWWF C SNL
 S: 404 YLK----GHTG-TAGKQSSLILHGADFSTKDADNDNCMCK-CALMLTGGWWFDACGPSNL 457

5 Q: 1244 NGQYFRSIPQQRQKLKKGIFWKTWRGRYYPLQATTMLIQPM 1366
 NG ++ + Q KL GI W ++G Y L++TTM+I+P+
 S: 458 NGMFYTA-GQNHGKLN-GIKWHYFKGPSYSLRSTTMMIRPL 496

The segment of gil1907327 that is shown as "S" above is set out in the
 10 sequence listing as SEQ ID NO. 125. Based on the structural similarity these
 homologous polypeptides are expected to share at least some biological activities.
 Such activities are known in the art, some of which are described elsewhere herein.
 Assays for determining such activities are also known in the art, some of which have
 been described elsewhere herein.

15 Preferred polypeptides of the invention comprise a polypeptide having the
 amino acid sequence set out in the sequence listing as SEQ ID NO. 126 which
 corresponds to the "Q" sequence in the alignment shown above (gaps introduced in a
 sequence by the computer are, of course, removed).

It has been discovered that this gene is expressed primarily in the following
 20 tissues/cDNA libraries: Bone Marrow Stromal Cell, untreated and to a lesser extent in
 Stratagene placenta (#937225); Soares_pregnant_uterus_NbHPU; Human
 osteoarthritic,fraction II; Soares_senescent_fibroblasts_NbHSF; Human Adipose;
 Epithelial-TNF α and INF induced; Soares melanocyte 2NbHM; Soares infant brain
 1NIB; Soares ovary tumor NbHOT; Human osteoarthritis,fraction I; Human
 25 Synovium; Healing groin wound, 7.5 hours post incision; Synovial hypoxia; Human
 Infant Brain; Human Pancreas Tumor, Reexcision;
 Soares_placenta_8to9weeks_2NbHP8to9W; Human Activated T-Cells, re-excision;
 Adipocytes; NCI_CGAP_Kid5; Human Microvascular Endothelial Cells, fract. A;
 Human Hippocampus; H Kidney Cortex, subtracted III; Human Bone Marrow;

Larynx Carcinoma; HM3; Human adult (K.Okubo); NCI_CGAP_Pr22; Human Pre-Differentiated Adipocytes; Human epithelioid sarcoma; Smooth muscle, control, re-excision; H. Epididymus, caput & corpus; Human adult small intestine, re-excision; Human Lung Cancer, re-excision; Healing groin wound - zero hr post-incision

5 (control); Hepatocellular Tumor, re-excision; Synovial hypoxia-RSF subtracted; Human endometrial stromal cells-treated with progesterone; Soares_fetal_heart_NbHH19W; H. Kidney Medulla, re-excision; Human Brain, Striatum; Human Adult Testes, Large Inserts, Reexcision; Liver, Hepatoma; Soares_pineal_gland_N3HPG; Human Rhabdomyosarcoma; Soares_testis_NHT;

10 Human Thymus Stromal Cells; Rejected Kidney, lib 4; Human Liver, normal; Human Placenta; Human Fetal Lung III; Bone marrow; Endothelial-induced; Endothelial cells-control; NCI_CGAP_Co3; NCI_CGAP_Co9; NCI_CGAP_Lu1; NCI_CGAP_Brn23; Colon Normal III; Smooth muscle, control and Nine Week Old Early Stage Human.

15 Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 83 as residues: Pro-27 to Arg-34.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:34 and may have been publicly available prior to conception of

20 the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1897 of SEQ ID NO:34, b

25 is an integer of 15 to 1911, where both a and b correspond to the positions of

nucleotide residues shown in SEQ ID NO:34, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 25

5 It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: Human Pineal Gland and Human Testes.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:35 and may have been publicly available prior to conception of
10 the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 982 of SEQ ID NO:35, b
15 is an integer of 15 to 996, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:35, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 26

20 It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: prostate-edited; Human Bone Marrow, re-excision; and Primary Dendritic cells,frac 2.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are
25 related to SEQ ID NO:36 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically

excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1306 of SEQ ID NO:36, b is an integer of 15 to 1320, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:36, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 27

The computer algorithm BLASTX has been used to determine that the translation product of this gene shares sequence homology with, as a non-limiting example, the sequence accessible through the following database accession no. gnl|PID|d1016408 (all information available through the recited accession number is incorporated herein by reference) which is described therein as "Copper homeostasis protein CutC. [Escherichia coli]." A partial alignment demonstrating the observed homology is shown immediately below.

```

>gnl|PID|d1016408 Copper homeostasis protein CutC. [Escherichia coli]
>gnl|PID|d1016415 Copper homeostasis protein CutC.
[Escherichia coli]
Length = 248

Plus Strand HSPs:

Score = 494 (173.9 bits), Expect = 1.6e-46, P = 1.6e-46
Identities = 107/241 (44%), Positives = 141/241 (58%), Frame = +3

Q: 180 LMEVCVDSVESAVNAERGGADRIELCSGLSEGGTTPSMGVLQVVKQSVQIPVFVMIRPRG 359
L+E+C S+E A+ A++ GADR+ELC+ EGG TPS+GVL+ V+Q V IPV +IRPRG
S: 3 LLEICCYSMECALTAQQNGADRVLCAPKEGGLTPSLGVLKSVRQRTIPVHPPIRPRG 62

Q: 360 GDFLYSDREIEVMKADIRLAKLYGADGLVFGALTEDGHIDKELCMSLMAICRPLPVTFHR 539
GDF YSD E + D+R + G GLV G L DG++D +MA PL VTFHR
S: 63 GDFCYSDGEFAAILEDVRTVRELGFPLVTGVLDVDGNVDMRMEKIMAAAGPLAVTFHR 122

```

Q: 540 AFDMVHDPMAALETLLTLGFERVLTSGCDSSALEGLPLIKRLIEQAKGRIVVMPGGGITD 719
 AFDM +P+ L L LG RVLTS S AL+GL I LI I+ M G G+
 S: 123 AFDMCANPLYTLNNLAE LGIARVLTSGQKSDALQGLSKIMELIAHRDAPII-MAGAGVRA 181

5 Q: 720 RNLQRILEGSGATEFHCSARSTRDSGMKFRNSSVAMGASLSCSEYSLKVTDTVTKVRTLNA 899
 NL L+ +G E H SA + + S M++RN ++M + EYS + D V +
 S: 182 ENLHHFLD-AGVLEVHSSAGAWQASPMRYRNQGLSMSSDEHADEYSRYIVDGAAVAEMKG 240

10 Q: 900 I 902
 I
 S: 241 I 241

The segment of gnl|PID|d1016408 that is shown as "S" above is set out in the sequence listing as SEQ ID NO. 127.

15 Preferred polypeptides of the invention comprise a polypeptide having the amino acid sequence set out in the sequence listing as SEQ ID NO. 128 which corresponds to the "Q" sequence in the alignment shown above (gaps introduced in a sequence by the computer are, of course, removed).

It has been discovered that this gene is expressed primarily in the following

20 tissues/cDNA libraries: Soares fetal liver spleen 1NFLS and to a lesser extent in Human Prostate Cancer, Stage C fraction; Human Testes; Soares_pregnant_uterus_NbHPU; Soares_fetal_heart_NbHH19W; Human Eosinophils; Smooth muscle, serum treated; Stratagene muscle 937209; Hodgkin's Lymphoma II; Stratagene muscle 937209; T cell helper II; Soares placenta Nb2HP;

25 Testis, normal; Prostate; Activated T-cells; Human Soleus; Synovial IL-1/TNF stimulated; Human Ovary; Breast Cancer Cell line, angiogenic; NCI_CGAP_Br2; Human Umbilical Vein Endothelial Cells, uninduced; Human Hypothalamus, Schizophrenia; Human T-Cell Lymphoma; Soares_total_fetus_Nb2HF8_9w; Colon Tumor II; NCI_CGAP_AA1;

30 NCI_CGAP_GCB1 and T Cell helper I.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:37 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1362 of SEQ ID NO:37, b is an integer of 15 to 1376, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:37, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 28

The computer algorithm BLASTX has been used to determine that the translation product of this gene shares sequence homology with, as a non-limiting example, the sequence accessible through the following database accession no. gil2654161 (all information available through the recited accession number is incorporated herein by reference) which is described therein as "GPR39 [Homo sapiens]." A partial alignment demonstrating the observed homology is shown immediately below.

```
>gi|2654161 (AF034633) GPR39 [Homo sapiens] >sp|O43194|GP39_HUMAN PUTATIVE
G
      PROTEIN-COUPLED RECEPTOR GPR39.
      Length = 453

      Minus Strand HSPs:

      Score = 752 (264.7 bits), Expect = 7.1e-74, P = 7.1e-74
      Identities = 149/167 (89%), Positives = 149/167 (89%), Frame = -1
```

Q: 1626 LIVVTLAVCWMPNQIRIRIMAAAKPKHDWTRSYFRAYMILLPFSETFFYLSSVINPLLYTV 1447
 LIVVTLAVCWMPNQIRIRIMAAAKPKHDWTRSYFRAYMILLPFSETFFYLSSVINPLLYTV
 S: 287 LIVVTLAVCWMPNQIRIRIMAAAKPKHDWTRSYFRAYMILLPFSETFFYLSSVINPLLYTV 346
 5 Q: 1446 SSQQFRRVVFVQLCCRLSLQHANEKRLRVHAHSTDSARFVQRPLLFAARRQSSARRTE 1267
 SSQQFRRVVFVQLCCRLSLQHANEKRLRVHAHSTDSARFVQRPLLFAARRQSSARRTE
 S: 347 SSQQFRRVVFVQLCCRLSLQHANEKRLRVHAHSTDSARFVQRPLLFAARRQSSARRTE 406
 10 Q: 1266 KIFLSTFQSEAXXXXXXXXXXXXXXXXXXGAKPANSAAENGFOEHEV 1126
 KIFLSTFQSEA GAKPANSAAENGFOEHEV
 S: 407 KIFLSTFQSEAEPSKSKSLSELEPNSGAKPANSAAENGFOEHEV 453

The segment of gil2654161 that is shown as "S" above is set out in the
 sequence listing as SEQ ID NO. 129. Based on the structural similarity these
 15 homologous polypeptides are expected to share at least some biological activities.
 Such activities are known in the art, some of which are described elsewhere herein.
 Assays for determining such activities are also known in the art, some of which have
 been described elsewhere herein.

Preferred polypeptides of the invention comprise a polypeptide having the
 20 amino acid sequence set out in the sequence listing as SEQ ID NO. 130 which
 corresponds to the "Q" sequence in the alignment shown above (gaps introduced in a
 sequence by the computer are, of course, removed).

It has been discovered that this gene is expressed primarily in the following
 tissues/cDNA libraries: Soares infant brain 1NIB and to a lesser extent in Stratagene
 25 ovarian cancer (#937219); Soares ovary tumor NbHOT; H. Kidney Cortex,
 subtracted; Stratagene neuroepithelium NT2RAMI 937234; Human Cerebellum,
 subtracted; NTERA2 + retinoic acid, 14 days; Human Manic Depression Tissue;
 Human Infant Brain; H. Kidney Medulla, re-excision; 12 Week Old Early Stage
 Human, II; Human Ovarian Cancer Reexcision; Human Adrenal Gland Tumor;
 30 Stratagene pancreas (#937208); Stratagene endothelial cell 937223; Pancreas Islet

Cell Tumor; PC3 Prostate cell line; Endothelial-induced and Nine Week Old Early Stage Human.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are
5 related to SEQ ID NO:38 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the
10 general formula of a-b, where a is any integer between 1 to 1939 of SEQ ID NO:38, b is an integer of 15 to 1953, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:38, and where b is greater than or equal to a + 14.

15 FEATURES OF PROTEIN ENCODED BY GENE NO: 29

It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: Soares infant brain 1NIB and to a lesser extent in Soares melanocyte 2NbHM; Human Umbilical Vein, Endo. remake; Soares_pregnant_uterus_NbHPU; Soares_multiple_sclerosis_2NbHMSP; Human B
20 Cell Lymphoma; Soares_fetal_heart_NbHH19W; Kidney Pyramids; Stromal-Osteoclastoma; NTERA2 + retinoic acid, 14 days; LNCAP prostate cell line; Stratagene HeLa cell s3 937216; Synovial hypoxia; Human Adult Small Intestine; KMH2; T-Cell PHA 16 hrs; Human Brain, Striatum; human ovarian cancer; 12 Week Old Early Stage Human, II; Stratagene lung carcinoma 937218; Macrophage-oxLDL;
25 PC3 Prostate cell line; Human Placenta; Soares breast 3NbHBst; Adipocytes; Human Testes Tumor; Human Neutrophil, Activated; Endothelial cells-control; Spleen,

Chronic lymphocytic leukemia; Soares placenta Nb2HP; Human adult (K.Okubo); Human fetal heart, Lambda ZAP Express; NCI_CGAP_Co3 and Primary Dendritic Cells, lib 1.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO.

5 88 as residues: Arg-48 to Tyr-54.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:39 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically
10 excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2779 of SEQ ID NO:39, b is an integer of 15 to 2793, where both a and b correspond to the positions of
15 nucleotide residues shown in SEQ ID NO:39, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 30

It has been discovered that this gene is expressed primarily in the following
20 tissues/cDNA libraries: Soares infant brain 1N1B and to a lesser extent in Hepatocellular Tumor; Human Placenta; Palate normal; Human Thyroid; Human Hypothalamus, schizophrenia, re-excision; Human Adult Small Intestine; Hodgkin's Lymphoma II; Keratinocyte and Soares fetal liver spleen 1N1LS.

Many polynucleotide sequences, such as EST sequences, are publicly
25 available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:40 and may have been publicly available prior to conception of

the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the

5 general formula of a-b, where a is any integer between 1 to 1353 of SEQ ID NO:40, b is an integer of 15 to 1367, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:40, and where b is greater than or equal to a + 14.

10 FEATURES OF PROTEIN ENCODED BY GENE NO: 31

The computer algorithm BLASTX has been used to determine that the translation product of this gene shares sequence homology with, as a non-limiting example, the sequence accessible through the following database accession no. gnl|PID|e1254351 (all information available through the recited accession number is

15 incorporated herein by reference) which is described therein as "Exportin(tRNA) [Homo sapiens]." A partial alignment demonstrating the observed homology is shown immediately below.

20 >gnl|PID|e1254351 Exportin(tRNA) [Homo sapiens] >sp|O43784|O43784
EXPORTIN.
Length = 962
Minus Strand HSPs:

25 Score = 1607 (565.7 bits), Expect = 1.9e-164, P = 1.9e-164
Identities = 312/312 (100%), Positives = 312/312 (100%), Frame = -3

30 Q: 1724 LNHAVGFASRTSKAFSNKQTVKQCGCSEVYLDCLQTFPLALSCPLQKDILRSGVRTLHR 1545
LNHAVGFASRTSKAFSNKQTVKQCGCSEVYLDCLQTFPLALSCPLQKDILRSGVRTLHR
S: 651 LNHAVGFASRTSKAFSNKQTVKQCGCSEVYLDCLQTFPLALSCPLQKDILRSGVRTLHR 710

35 Q: 1544 MIICLEEEVLPFIPASAEHMLKDCEAKDLQEFIPLINQITAKFKIQVSPFLQQMFMPPLH 1365
MIICLEEEVLPFIPASAEHMLKDCEAKDLQEFIPLINQITAKFKIQVSPFLQQMFMPPLH
S: 711 MIICLEEEVLPFIPASAEHMLKDCEAKDLQEFIPLINQITAKFKIQVSPFLQQMFMPPLH 770

Q: 1364 AIFEVLLRPAEENDQSAALEKQMLRRSYFAFLQTVTGSGMSEVIANQGAENVERVLVTVI 1185
 AIFEVLLRPAEENDQSAALEKQMLRRSYFAFLQTVTGSGMSEVIANQGAENVERVLVTVI
 S: 771 AIFEVLLRPAEENDQSAALEKQMLRRSYFAFLQTVTGSGMSEVIANQGAENVERVLVTVI 830

5 Q: 1184 QGAVEYPDPIAQKTCFIILSKLVELWGGKDGPGFADFVYKHIVPACFLAPLKQTFDLAD 1005
 QGAVEYPDPIAQKTCFIILSKLVELWGGKDGPGFADFVYKHIVPACFLAPLKQTFDLAD
 S: 831 QGAVEYPDPIAQKTCFIILSKLVELWGGKDGPGFADFVYKHIVPACFLAPLKQTFDLAD 890

10 Q: 1004 AQTVLALSECAVTLKTIHLKRGPECVQYLQQEYLPQLQVAPEIIQEFCQALQQPDAKVFK 825
 AQTVLALSECAVTLKTIHLKRGPECVQYLQQEYLPQLQVAPEIIQEFCQALQQPDAKVFK
 S: 891 AQTVLALSECAVTLKTIHLKRGPECVQYLQQEYLPQLQVAPEIIQEFCQALQQPDAKVFK 950

Q: 824 NYLKVFFQRAKP 789
 NYLKVFFQRAKP
 15 S: 951 NYLKVFFQRAKP 962

The segment of gnlPIDle1254351 that is shown as "S" above is set out in the sequence listing as SEQ ID NO. 131. Based on the structural similarity these homologous polypeptides are expected to share at least some biological activities.

20 Such activities are known in the art, some of which are described elsewhere herein. Assays for determining such activities are also known in the art, some of which have been described elsewhere herein.

Preferred polypeptides of the invention comprise a polypeptide having the amino acid sequence set out in the sequence listing as SEQ ID NO. 132 which
 25 corresponds to the "Q" sequence in the alignment shown above (gaps introduced in a sequence by the computer are, of course, removed).

It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: Soares melanocyte 2NbHM and to a lesser extent in Synovial Fibroblasts (control); Soares_fetal_heart_NbHH19W; Soares placenta Nb2HP; Soares
 30 infant brain 1NIB; T cell helper II; NCI_CGAP_GCB1;
 Soares_fetal_liver_spleen_1NFLS_S1; Human Fetal Lung III; Human Placenta;
 Larynx Tumour; LNCAP + 30nM R1881; Human Prostate, subtracted; Human (Caco-2) cell line, adenocarcinoma, colon, remake; Morton Fetal Cochlea; Human Gall Bladder, fraction II; Human colon carcinoma (HCC) cell line, remake; Activated T-

cells; Stromal-Osteoclastoma; NTERA2 + retinoic acid, 14 days; Stratagene HeLa cell s3 937216; Synovial hypoxia; Spleen metastatic melanoma; Human Osteoblasts II; Human Jurkat Membrane Bound Polysomes; Stromal cell TF274; Macrophage-oxLDL; Bone Marrow Stromal Cell, untreated; NTERA2, control; Stratagene corneal stroma (#937222); Human Liver, normal; Human T-Cell Lymphoma; Stratagene NT2 neuronal precursor 937230; Human Placenta; Adipocytes; Colon Tumor II; Primary Dendritic cells, frac 2; Human Osteoclastoma; Smooth muscle, control; Human Bone Marrow, treated; Stratagene HeLa cell s3 937216; Stratagene hNT neuron (#937233); Keratinocyte; Human 8 Week Whole Embryo; Soares fetal liver spleen 1NFLS and
10 Primary Dendritic Cells, lib 1.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 90 as residues: Lys-24 to Tyr-40, Pro-42 to Ser-48.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are
15 related to SEQ ID NO:41 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the
20 general formula of a-b, where a is any integer between 1 to 1892 of SEQ ID NO:41, b is an integer of 15 to 1906, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:41, and where b is greater than or equal to a + 14.

25 FEATURES OF PROTEIN ENCODED BY GENE NO: 32

The computer algorithm BLASTX has been used to determine that the translation product of this gene shares sequence homology with, as a non-limiting example, the sequence accessible through the following database accession no. gnl|PID|e1340344 (all information available through the recited accession number is incorporated herein by reference) which is described therein as "NS1-binding protein [Homo sapiens]." A partial alignment demonstrating the observed homology is shown immediately below.

```
10 >gnl|PID|e1340344 (AJ012449) NS1-binding protein [Homo sapiens]
    >sp|E1340344|E1340344 NS1-BINDING PROTEIN.
    Length = 619

    Plus Strand HSPs:

15 Score = 2286 (804.7 bits), Expect = 1.7e-238, Sum P(2) = 1.7e-238
    Identities = 424/441 (96%), Positives = 425/441 (96%), Frame = +2

    Q:      2 LKLPRLKLEVMLEDNVCLPSNGKLYTKVINWVQRSIWENGDSLXXLMEEVQTLIYSADHK 181
        LKLPRLKLEVMLEDNVCLPSNGKLYTKVINWVQRSIWENGDSL LMEEVQTLIYSADHK
20 S:    171 LKLPRLKLEVMLEDNVCLPSNGKLYTKVINWVQRSIWENGDSL EELMEEVQTLIYSADHK 230

    Q:    182 LLDGNLLDGQAEVFGSDDDDHIQFVQKKPPRENGHKQISSSSTGCLSSPNATVQSPKHEWK 361
        LLDGNLLDGQAEVFGSDDDDHIQFVQKKPPRENGHKQISSSSTGCLSSPNATVQSPKHEWK
25 S:    231 LLDGNLLDGQAEVFGSDDDDHIQFVQKKPPRENGHKQISSSSTGCLSSPNATVQSPKHEWK 290

    Q:    362 IVASEKTSNNTYLCLAVLDGIFCVIFLHGRNSPQXXXXXXXXXXXXFEMQQDELIEKP 541
        IVASEKTSNNTYLCLAVLDGIFCVIFLHGRNSPQ FEMQQDELIEKP
30 S:    291 IVASEKTSNNTYLCLAVLDGIFCVIFLHGRNSPQSPTSTPKLSKLSFEMQQDELIEKP 350

    Q:    542 MSPMQYARSGLTAEENGKLIAGGYNREECLRTVECYNPHTDHSFLAPMRTTPRARFQM 721
        MSPMQYARSGLTAEENGKLIAGGYNREECLRTVECYNPHTDHSFLAPMRTTPRARFQM
35 S:    351 MSPMQYARSGLTAEENGKLIAGGYNREECLRTVECYNPHTDHSFLAPMRTTPRARFQM 410

    Q:    722 AVLMGQLYVVGGSNHSDDLSCGEMYDSNIDDWIPVPELRTNRCNAGVCALNGKLYIVGG 901
        AVLMGQLYVVGGSNHSDDLSCGEMYDSNIDDWIPVPELRTNRCNAGVCALNGKLYIVGG
40 S:    411 AVLMGQLYVVGGSNHSDDLSCGEMYDSNIDDWIPVPELRTNRCNAGVCALNGKLYIVGG 470

    Q:    902 SDPYGQKGLKNCDFDPVTKLWTSCAPLNIRRHQSAVCELGGYLYIIGGAESWNCNLNTE 1081
        SDPYGQKGLKNCDFDPVTKLWTSCAPLNIRRHQSAVCELGGYLYIIGGAESWNCNLNTE
45 S:    471 SDPYGQKGLKNCDFDPVTKLWTSCAPLNIRRHQSAVCELGGYLYIIGGAESWNCNLNTE 530

    Q:    1082 RYNPENNTWTLIAPMNVARRGAGVAVLNGKLFVCGGFDGSHAISCVEMYDPTRNEWKMMG 1261
        RYNPENNTWTLIAPMNVARRGAGVAVLNGKLFVCGGFDGSHAISCVEMYDPTRNEWKMMG
50 S:    531 RYNPENNTWTLIAPMNVARRGAGVAVLNGKLFVCGGFDGSHAISCVEMYDPTRNEWKMMG 590

    Q:    1262 NMTSPRSNAGIATVGNTIYAV 1324
        +MTSPRSNAGIATVGNTIYAV
```

S: 591 HMTSPRSNAGIATVGNTIYAV 611

Score = 360 (126.7 bits), Expect = 6.0e-30, P = 6.0e-30
Identities = 76/236 (32%), Positives = 124/236 (52%), Frame = +2

5 Q: 683 LAPMRTPRARFQMAVLMGQLYVVGSGNGHSDDLSCGEMYDSNIDDWIPVPELRTNRCNAG 862
++PM+ R+ A + G+L GG N + L E Y+ + D W + +RT R

S: 351 MSPMQYARSGLTAE MNGKLI AAGGYN-REECLRTVECYNPHTDHSFLAPMRTPRARFQ 409

10 Q: 863 VCALNGKLYIVGGSDPYGQKGLKNC-DVFDPVTKLWTSCAPLNIRRHQSAVCELGGYLYI 1039
+ L G+LY+VGGG+ G +C +++D W L R + VC L G LYI

S: 410 MAVLMGQLYVVGGSN--GHSDDLSCGEMYDSNIDDWIPVPELRTNRCNAGVCALNGKLYI 467

15 Q: 1040 IGGAESWNC--LNTVERYNPENNTWTLIAPMNVARRGAGVAVLNGKLFVCGGFDGSHAIS 1213
+GG++ + L + ++P WT AP+N+ R + V L G L++ GG + + ++

S: 468 VGGSDPYGQKGLKNCDFDPVTKLWTSCAPLNIRRHQSAVCELGGYLYIIGGAESWNCLN 527

Q: 1214 CVEMYDPTRNEWKMMGNMTSPRSNAGIATVGNTIYAVGGFDGNEFLNTVEVYNLESNEW 1390
VE Y+P N W ++ M R AG+A + ++ GGFDG+ ++ VE+Y+ NEW

20 S: 528 TVERYNPENNTWTLIAPMNVARRGAGVAVLNGKLFVCGGFDGSHAISCVEMYDPTRNEW 586

The segments of gnl|PID|e1340344 that are shown as "S" above are set out in the sequence listing as SEQ ID NO. 133 and SEQ ID NO. 135. Based on the structural similarity these homologous polypeptides are expected to share at least

25 some biological activities. Such activities are known in the art, some of which are described elsewhere herein. Assays for determining such activities are also known in the art, some of which have been described elsewhere herein.

Preferred polypeptides of the invention comprise a polypeptide having the amino acid sequence set out in the sequence listing as SEQ ID NO. 134 and/or SEQ

30 ID NO. 136 which correspond to the "Q" sequences in the alignment shown above (gaps introduced in a sequence by the computer are, of course, removed).

It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: Human Bone Marrow, treated and to a lesser extent in Human Endometrial Tumor; Colon Carcinoma; Early Stage Human Brain; Human Placenta;

35 Human Neutrophil, Activated; Human Ovary; Stratagene hNT neuron (#937233); Colon Normal III; Human Testes; Healing groin wound, 6.5 hours post incision;

- Soares_multiple_sclerosis_2NbHMSP; H. Kidney Medulla, re-excision; Mo7e Cell Line GM-CSF treated (1ng/ml); Stratagene Human skeletal muscle cDNA library, cat. #936215.; normalized infant brain cDNA; Human Pancreas Tumor; Synovial Fibroblasts (control); Stratagene lung (#937210); Human fetal heart, Lambda ZAP
- 5 Express; Soares_testis_NHT; Human Substantia Nigra; Human Testes, Reexcision; Bone marrow; Hodgkin's Lymphoma II; Soares fetal liver spleen 1NFLS; Human Fetal Brain, normalized 100024F; Human Fetal Brain, normalized AC5002; Thyroid Thyroiditis; Colon Tumor; Stomach Tumour; Tongue Tumour; Saos2 Cells, Vitamin D3 Treated; Saos2, Dexamethosome Treated; Dermatofibrosarcoma Protuberance;
- 10 Human (HCC) cell line liver (mouse) metastasis, remake; Human colon carcinoma (HCC) cell line, remake; Adipocytes, re-excision; Human Tonsils, Lib 2; HEL cell line; Hepatocellular Tumor; H. Kidney Cortex, subtracted; Salivary Gland, Lib 2; Stratagene HeLa cell s3 937216; Human Adipose Tissue, re-excision; Jurkat T-cell G1 phase; Soares_parathyroid_tumor_NbHPA; Prostate BPH; Soares_NbHMPu_S1;
- 15 TF-1 Cell Line GM-CSF Treated; T-Cell PHA 24 hrs; Human Ovarian Cancer Reexcision; Human umbilical vein endothelial cells, IL-4 induced; NCI_CGAP_Co3; NCI_CGAP_Ew1; NCI_CGAP_GC5; NCI_CGAP_Pr22; Ulcerative Colitis; Macrophage (GM-CSF treated); Soares_testis_NHT; Soares_fetal_liver_spleen_1NFLS_S1; Resting T-Cell Library, II; NCI_CGAP_Lu5;
- 20 Soares_multiple_sclerosis_2NbHMSP; Smooth muscle, serum treated; Colon Normal II; Soares_placenta_8to9weeks_2NbHP8to9W; H Macrophage (GM-CSF treated), re-excision; Normal colon; Soares melanocyte 2NbHM; 12 Week Early Stage Human II, Reexcision; Neutrophils control, re-excision; Human Fetal Heart; Endothelial-induced; Endothelial cells-control; Anergic T-cell; Human Osteoclastoma; Human B
- 25 Cell Lymphoma; NCI_CGAP_Br2; NCI_CGAP_Ew1; NCI_CGAP_Ov2; NCI_CGAP_Co10; NCI_CGAP_Co12; NCI_CGAP_Lip2; Spleen, Chronic

lymphocytic leukemia; Neutrophils IL-1 and LPS induced; Osteoblasts; Keratinocyte; Nine Week Old Early Stage Human; T cell helper II; Primary Dendritic Cells, lib 1 and Soares infant brain 1NIB.

Many polynucleotide sequences, such as EST sequences, are publicly
5 available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:42 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention
10 are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1709 of SEQ ID NO:42, b is an integer of 15 to 1723, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:42, and where b is greater than or equal to a + 14.

15

FEATURES OF PROTEIN ENCODED BY GENE NO: 33

The computer algorithm BLASTX has been used to determine that the translation product of this gene shares sequence homology with, as a non-limiting example, the sequence accessible through the following database accession no.
20 gil2197085 (all information available through the recited accession number is incorporated herein by reference) which is described therein as "ORF2-like protein [Homo sapiens]." A partial alignment demonstrating the observed homology is shown immediately below.

25

```
>gi|2197085 (AF003535) ORF2-like protein [Homo sapiens]
      Length = 573
```

Plus Strand HSPs:

Score = 185 (65.1 bits), Expect = 2.9e-10, P = 2.9e-10
 Identities = 40/72 (55%), Positives = 44/72 (61%), Frame = +2

5 Q: 1844 YKENLSLQXXXXXXXXXXXXNIPCSWVGRINIVKMAILPKVIYRFSAIPIKLPC-LSSQX 2020
 +KEN NIPCSWVGRINIVKMAILPKVIYRF+AIPIKLP ++
 S: 295 FKENYKPLLKEIKEDTNKWKNIIPCSWVGRINIVKMAILPKVIYRFNAIPIKLPMFTFTEL 354

10 Q: 2021 GKNYFKVXWXQK 2056
 K K W QK
 S: 355 EKTTLKFIWNQK 366

The segment of gil2197085 that is shown as "S" above is set out in the sequence listing as SEQ ID NO. 137.

15 Preferred polypeptides of the invention comprise a polypeptide having the amino acid sequence set out in the sequence listing as SEQ ID NO. 138 which corresponds to the "Q" sequence in the alignment shown above (gaps introduced in a sequence by the computer are, of course, removed).

It has been discovered that this gene is expressed primarily in the following
 20 tissues/cDNA libraries: Soares_fetal_heart_NbHH19W and to a lesser extent in pBMC stimulated w/ poly I/C; Human Neutrophil; Human Activated Monocytes; Neutrophils IL-1 and LPS induced; Human Placenta; Human Amygdala; NCI_CGAP_GCB1; Stratagene ovarian cancer (#937219); Monocyte activated; Nine Week Old Early Stage Human and Primary Dendritic Cells, lib 1.

25 Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:43 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence
 30 would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the

general formula of a-b, where a is any integer between 1 to 2060 of SEQ ID NO:43, b is an integer of 15 to 2074, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:43, and where b is greater than or equal to a + 14.

5

FEATURES OF PROTEIN ENCODED BY GENE NO: 34

When tested against K562 leukemia cell lines, supernatants removed from cells containing this gene activated the ISRE assay. Thus, it is likely that this gene activates leukemia cells through the Jak-STAT signal transduction pathway. The
10 interferon-sensitive response element is a promoter element found upstream of many genes which are involved in the Jak-STAT pathway. The Jak-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jak-STAT pathway, reflected by the binding of the ISRE element, can be used to indicate proteins involved in the proliferation and
15 differentiation of cells.

It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: PERM TF274.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 93 as residues: Gln-20 to Leu-25.

20 Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:44 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence
25 would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the

general formula of a-b, where a is any integer between 1 to 808 of SEQ ID NO:44, b is an integer of 15 to 822, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:44, and where b is greater than or equal to a + 14.

5

FEATURES OF PROTEIN ENCODED BY GENE NO: 35

It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: Soares fetal liver spleen 1NFLS and to a lesser extent in Soares adult brain N2b4HB55Y; Hippocampus, Alzheimer Subtracted; Human 8
 10 Week Whole Embryo; Stratagene HeLa cell s3 937216; Nine Week Old Early Stage Human; Jurkat T-Cell, S phase; H. Kidney Medulla, re-excision; Human T-Cell Lymphoma; Stratagene neuroepithelium (#937231); Soares infant brain 1NIB; Gessler Wilms tumor; Human Prostate Cancer, Stage C fraction; Soares_testis_NHT; Human Whole Brain #2 - Oligo dT > 1.5Kb; Human Rhabdomyosarcoma; Human
 15 Whole Six Week Old Embryo; Liver HepG2 cell line.; NCI_CGAP_Co10; NCI_CGAP_Kid6; Hepatocellular Tumor, re-excision; Human Substantia Nigra; Soares_fetal_heart_NbHH19W; Human Adult Pulmonary, re-excision; Human Amygdala; Human Microvascular Endothelial Cells, fract. A; Human Cerebellum; Soares placenta Nb2HP; Human Kidney Tumor; Human Amygdala Depression, re-
 20 excision; Human Whole 6 Week Old Embryo (II), subt; Human Tonsil, Lib 3; Whole 6 Week Old Embryo; Human Gall Bladder, fraction II; Human Fetal Spleen; Human Placenta; HSA 172 Cells; Soares_NFL_T_GBC_S1; Stratagene ovary (#937217); Human Tonsils, Lib 2; H. Whole Brain #2, re-excision; Apoptotic T-cell, re-excision; Healing groin wound - zero hr post-incision (control); Stomach cancer (human), re-
 25 excision; Alzheimers, spongy change; NTERA2 + retinoic acid, 14 days; Human Amygdala, re-excision; Human Osteosarcoma; Human Ovary; Prostate BPH; Human

Adult Small Intestine; Human Infant Brain; Soares_fetal_liver_spleen_1NFLS_S1;
 Human Prostate; T-Cell PHA 16 hrs; Human Jurkat Membrane Bound Polysomes;
 Human Ovarian Cancer Reexcision; Human Hippocampus; Human Thymus;
 NCI_CGAP_Br2; NCI_CGAP_Co11; NCI_CGAP_GCB1; NTERA2, control; Adult
 5 heart; Lambda gt11; Gessler Wilms tumor; Human fetal heart, Lambda ZAP Express;
 Human retina cDNA randomly primed sublibrary; NCI_CGAP_GC2;
 NCI_CGAP_Lu5; NCI_CGAP_Kid3; NCI_CGAP_Kid5; NCI_CGAP_PNS1;
 NCI_CGAP_Brn23; Soares_total_fetus_Nb2HF8_9w; Pancreas Islet Cell Tumor;
 Human Gall Bladder; Fetal Heart; Colon Carcinoma; Smooth muscle, serum treated;
 10 breast lymph node CDNA library; Adipocytes; Dendritic cells, pooled; H. Frontal
 cortex,epileptic,re-excision; Human Fetal Heart; human tonsils; Human Neutrophil,
 Activated; Human B Cell Lymphoma; Spleen, Chronic lymphocytic leukemia; Bone
 Marrow Cell Line (RS4,11) and Activated T-cell(12h)/Thiouridine-re-excision.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO.
 15 94 as residues: His-25 to Phe-30.

Many polynucleotide sequences, such as EST sequences, are publicly
 available and accessible through sequence databases. Some of these sequences are
 related to SEQ ID NO:45 and may have been publicly available prior to conception of
 the present invention. Preferably, such related polynucleotides are specifically
 20 excluded from the scope of the present invention. To list every related sequence
 would be cumbersome. Accordingly, preferably excluded from the present invention
 are one or more polynucleotides comprising a nucleotide sequence described by the
 general formula of a-b, where a is any integer between 1 to 2392 of SEQ ID NO:45, b
 is an integer of 15 to 2406, where both a and b correspond to the positions of
 25 nucleotide residues shown in SEQ ID NO:45, and where b is greater than or equal to a
 + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 36

- It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: Soares fetal liver spleen 1NFLS and to a lesser extent in
- 5 Soares placenta Nb2HP; Dendritic cells, pooled; Soares melanocyte 2NbHM; Early Stage Human Lung, subtracted; Soares retina N2b4HR; Stratagene ovarian cancer (#937219); human ovarian cancer; Stratagene fetal spleen (#937205); Soares_multiple_sclerosis_2NbHMSp; NTERA2, control; Soares_total_fetus_Nb2HF8_9w; Human Osteoclastoma; Human Cerebellum;
 - 10 Soares_fetal_heart_NbHH19W; Soares_senescent_fibroblasts_NbHSF; Soares infant brain 1NIB; Human Fetal Brain, normalized 100024F; Cheek Carcinoma; Human Normal Cartilage, Fraction I; Human Normal Cartilage Fraction II; Human Gall Bladder, fraction II; Human Cerebellum, subtracted; Human Skin Tumor; Human Synovium; Breast Cancer cell line, MDA 36; human corpus colosum; Human Whole
 - 15 Brain #2 - Oligo dT > 1.5Kb; Soares_pregnant_uterus_NbHPU; Human Osteoclastoma, re-excision; Synovial Fibroblasts (IL1/TNF), subt; Human Prostate; Human Fetal Dura Mater; T-Cell PHA 24 hrs; Human Hypothalamus, Schizophrenia; Human Activated Monocytes; Spinal cord; Ulcerative Colitis; Bone Marrow Stromal Cell, untreated; Hepatocellular Tumor, re-excision; Macrophage-oxLDL, re-excision;
 - 20 Pancreas Islet Cell Tumor; 12 Week Old Early Stage Human; breast lymph node CDNA library; Early Stage Human Brain; Human Fetal Lung III; Human Amygdala; T Cell helper I; Hodgkin's Lymphoma II; Soares_parathyroid_tumor_NbHPA; and Primary Dendritic Cells, lib 1.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO.

- 25 95 as residues: Arg-76 to Lys-91.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:46 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically
5 excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2441 of SEQ ID NO:46, b is an integer of 15 to 2455, where both a and b correspond to the positions of
10 nucleotide residues shown in SEQ ID NO:46, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 37

It has been discovered that this gene is expressed primarily in the following
15 tissues/cDNA libraries: Soares infant brain 1NIB and to a lesser extent in Soares placenta Nb2HP; Early Stage Human Brain; Nine Week Old Early Stage Human; Soares_pregnant_uterus_NbHPU; Morton Fetal Cochlea; Human Adult Small Intestine; NCI_CGAP_GCB1; Stromal cell TF274; Soares_fetal_heart_NbHH19W; Soares_senescent_fibroblasts_NbHSF; Human Chondrosarcoma; Stratagene lung
20 carcinoma 937218; 12 Week Old Early Stage Human; Soares fetal liver spleen 1NFLS; Messangial cell, frac 1; Human Prostate, subtracted; Human Adult Pulmonary; Human Stomach; NTERA2 teratocarcinoma cell line+retinoic acid (14 days); HEL cell line; Stomach cancer (human),re-excision; Morton Fetal; Human Ovary; Human Infant Brain; L428; Human Osteoblasts II;
25 Soares_placenta_8to9weeks_2NbHP8to9W; T-Cell PHA 24 hrs; Liver, Hepatoma; Human umbilical vein endothelial cells, IL-4 induced; Bone Marrow Stromal Cell,

untreated; Human Gall Bladder; PC3 Prostate cell line; Colon Tumor; Resting T-Cell Library,II; Colon Normal II; Human Testes Tumor; Dendritic cells, pooled; Human Placenta; Human Fetal Heart; Human Osteoclastoma; Human Endometrial Tumor and Human 8 Week Whole Embryo.

- 5 Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:47 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence
- 10 would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2560 of SEQ ID NO:47, b is an integer of 15 to 2574, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:47, and where b is greater than or equal to a
- 15 + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 38

- The computer algorithm BLASTX has been used to determine that the translation product of this gene shares sequence homology with, as a non-limiting
- 20 example, the sequence accessible through the following database accession no. gi1407655 (all information available through the recited accession number is incorporated herein by reference) which is described therein as "SH3P7 [Mus musculus]." A partial alignment demonstrating the observed homology is shown immediately below.

25

```
>gi1407655 SH3P7 [Mus musculus] >sp|Q62418|Q62418 DREBRIN-LIKE SH3  
DOMAIN-CONTAINING PROTEIN SH3P7.
```


Length = 433

Plus Strand HSPs:

5 Score = 748 (263.3 bits), Expect = 9.1e-106, Sum P(3) = 9.1e-106
 Identities = 149/201 (74%), Positives = 160/201 (79%), Frame = +2

10 Q: 344 SPQRTWEQQQEVVSRNRNEQESA----VHPREIFKQKERAMSTTSISSPQPGKLRSPFLQ 511
 +P RT E +QE VSR R E ESA HPREIFKQKERAMSTTS++S QPGKLRSPFLQ
 S: 233 APSRTGEPEQEAVSRTRQEWESAGQQAPHPREIFKQKERAMSTTSVTSSQPGKLRSPFLQ 292

15 Q: 512 KQLTQPETHFGREPAAISRPRADLPAEEPAPSTPPCLXXXXXXXXXXXXXXXXXTFYEQP 691
 KQLTQPET +GREP A +SRP A + EEPAPST T YE+P
 S: 293 KQLTQPETSYGREPTAPVSRPAAGV-CEEPAPSTLSS-AQTEEEPTYEVPPEQDTLYEEP 350

20 Q: 692 PLVQQQGAGSEHIDHHIQGQGLSGQGLCARALYDYQAADDTEISFDPENLITGIEVIDEG 871
 PLVQQQGAGSEHID+++Q QG SGQGLCARALYDYQAADDTEISFDPENLITGIEVIDEG
 S: 351 PLVQQQGAGSEHIDNYMQSGFSGQGLCARALYDYQAADDTEISFDPENLITGIEVIDEG 410

20 Q: 872 WWRGYGPDGHHFGMFPPANYVELIE 940
 WWRGYGPDGHHFGMFPPANYVELIE
 S: 411 WWRGYGPDGHHFGMFPPANYVELIE 433

The segment of gil1407655 that is shown as "S" above is set out in the
 25 sequence listing as SEQ ID NO. 139. Based on the structural similarity these
 homologous polypeptides are expected to share at least some biological activities.
 Such activities are known in the art, some of which are described elsewhere herein.
 Assays for determining such activities are also known in the art, some of which have
 been described elsewhere herein.

30 Preferred polypeptides of the invention comprise a polypeptide having the
 amino acid sequence set out in the sequence listing as SEQ ID NO. 140 which
 corresponds to the "Q" sequence in the alignment shown above (gaps introduced in a
 sequence by the computer are, of course, removed).

It has been discovered that this gene is expressed primarily in the following
 35 tissues/cDNA libraries: Primary Dendritic Cells, lib 1 and to a lesser extent in Human
 Rhabdomyosarcoma; Human Thymus; Soares placenta Nb2HP; Human Primary
 Breast Cancer Reexcision; Human Epididymus; Human Pituitary, subt IX; Merkel

- Cells; Soares breast 2NbHBst; Stratagene lung (#937210); Human Infant Adrenal Gland, subtracted; Colon, tumour; Larynx Tumour; Human Whole 6 Week Old Embryo (II), subt; Human Aortic Endothelium; Aorta endothelial cells + TNF-a; Activated T-cells; Breast Lymph node cDNA library; Synovial IL-1/TNF stimulated;
- 5 Breast Cancer cell line, MDA 36; H Female Bladder, Adult; NTERA2 + retinoic acid, 14 days; Synovial hypoxia-RSF subtracted; Human Whole Brain #2 - Oligo dT > 1.5Kb; Soares_NhHMPu_S1; Stratagene pancreas (#937208); Human endometrial stromal cells; Human Colon, re-excision; Jurkat T-cell G1 phase; Human Manic Depression Tissue; Human Chronic Synovitis; Fetal Liver, subtraction II; Human
- 10 Brain, Striatum; Human Activated Monocytes; Rejected Kidney, lib 4; Macrophage-oxLDL, re-excision; Human Gall Bladder; Colon Carcinoma; breast lymph node CDNA library; Soares breast 3NbHBst; Soares_total_fetus_Nb2HF8_9w; Normal colon; Stratagene corneal stroma (#937222); Human Neutrophil, Activated; Human Adult Pulmonary, re-excision; Activated T-Cell (12hs)/Thiouridine labelledEco;
- 15 Human Microvascular Endothelial Cells, fract. A; Monocyte activated; Human B Cell Lymphoma; Human Bone Marrow, treated; Hodgkin's Lymphoma II; Osteoblasts; T cell helper II; Human Cerebellum; Soares fetal liver spleen 1NFLS and Soares infant brain 1NIB.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO.

- 20 97 as residues: His-48 to Ser-61, Ala-66 to Val-72.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:48 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically

25 excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention

are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1746 of SEQ ID NO:48, b is an integer of 15 to 1760, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:48, and where b is greater than or equal to a

5 + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 39

The computer algorithm BLASTX has been used to determine that the translation product of this gene shares sequence homology with, as a non-limiting example, the sequence accessible through the following database accession no. gil425474 (all information available through the recited accession number is incorporated herein by reference) which is described therein as "SMDR1 [Schistosoma mansoni]." A partial alignment demonstrating the observed homology is shown immediately below.

15

```
>gi|425474 SMDR1 [Schistosoma mansoni] >sp|Q26598|Q26598 SMDR1.
      Length = 691
```

20

Plus Strand HSPs:

```
Score = 391 (137.6 bits), Expect = 6.2e-35, P = 6.2e-35
Identities = 89/221 (40%), Positives = 122/221 (55%), Frame = +3
```

25

```
Q:   3 EGLTFGYLVLLSHVGERMAVDMRRALFSSLLRQDITFFDANKTGQLVSRLTTDVQEFKS 182
      + L TF Y+ LL VGERMA MR LF L+ QD+ +FD + +G+LV + +DVQ FKS
S:  158 QSLSTFLYIGLLGSVGERMARRMRIQLFRKLVYQDVAYFDVHSSGKLVEIIGSDVQNFKS 217
```

30

```
Q:  183 SFKLVISQGLRSCQVAGCXXXXXXXXXXXXXXXXXATPALMGVGTLMGSLRKLRSRQCQ 362
      SFK ISQGLR+ QV G P + +G+LMG+ LR +SR+ Q
S:  218 SFKQCISQGLRNGIQVVGSVFALLSISPTLTAALIGCLPCVFLIGSLMGTELRLHISREVO 277
```

35

```
Q:  363 EQIARAMGVADEALGNVRTVRAFAMEQREEERYGXXXXXXXXXXXXXGRGIALFQGLSNI 542
      Q + + DEA ++RTV++ AME + GI FQGLSN+
S:  278 SQNSLFASLIDEAFSHIRTVKSLAMEDFLINKINYNVDAKMLSEKLSFGIGSFQGLSNL 337

Q:  543 AFNCMVLGTLFIGGSLVAGQQLTGGDLMSFLVASQTVQSFL 665
      N +VLG L++GG L++ +L G LMSFL +QT+Q L
S:  338 TLNGVVLGVLYVGGHLSRGELDAGHLSFLATTQTLQRSL 378
```

The segment of gil425474 that is shown as "S" above is set out in the sequence listing as SEQ ID NO. 141. Based on the structural similarity these homologous polypeptides are expected to share at least some biological activities. Such activities
5 are known in the art, some of which are described elsewhere herein. Assays for determining such activities are also known in the art, some of which have been described elsewhere herein.

Preferred polypeptides of the invention comprise a polypeptide having the amino acid sequence set out in the sequence listing as SEQ ID NO. 142 which
10 corresponds to the "Q" sequence in the alignment shown above (gaps introduced in a sequence by the computer are, of course, removed).

It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: Human Pituitary, subt IX and to a lesser extent in Stratagene pancreas (#937208); Soares adult brain N2b4HB55Y; Human Adult Testes, Large
15 Inserts, Reexcision; Spinal cord; Spleen, Chronic lymphocytic leukemia; Human Fetal Brain, normalized C500H; Crohn's Disease; Sinus piniformis Tumour; Brain Amygdala Depression; Weizmann Olfactory Epithelium; LNCAP untreated; Aorta endothelial cells + TNF-a; Human Stomach, re-excision; Human endometrial stromal cells-treated with progesterone; Human Frontal Cortex, Schizophrenia; Human Infant
20 Brain; Chromosome 7 Fetal Brain cDNA Library; Human; Human Rhabdomyosarcoma; Human Placenta; Nine Week Old Early Stage Human; Soares fetal liver spleen 1NFLS and Primary Dendritic Cells, lib 1.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 98 as residues: Lys-30 to Cys-35, Glu-62 to Tyr-69.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:49 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically

5 excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1009 of SEQ ID NO:49, b is an integer of 15 to 1023, where both a and b correspond to the positions of

10 nucleotide residues shown in SEQ ID NO:49, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 40

It has been discovered that this gene is expressed primarily in the following

15 tissues/cDNA libraries: Prostate BPH; T-Cell PHA 24 hrs and Human Hypothalamus, Schizophrenia.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:50 and may have been publicly available prior to conception of

20 the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 603 of SEQ ID NO:50, b

25 is an integer of 15 to 617, where both a and b correspond to the positions of

nucleotide residues shown in SEQ ID NO:50, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 41

- 5 It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: Soares breast 2NbHBst and to a lesser extent in Soares fetal liver spleen 1NFLS; Soares placenta Nb2HP; Soares_pregnant_uterus_NbHPU; Human Adipose; Soares_testis_NHT; NCI_CGAP_Pr1; Prostate BPH; Human Placenta; Human Adult Pulmonary, re-excision; Soares ovary tumor NbHOT; H
- 10 Female Bladder, Adult; NCI_CGAP_Pr2; NCI_CGAP_Kid5; Human Colon, re-excision; Stratagene fetal spleen (#937205); Soares breast 3NbHBst; Human Fetal Kidney, Reexcision; Human Synovial Sarcoma; Human Fetal Lung III; Smooth muscle, control; Nine Week Old Early Stage Human; Gessler Wilms tumor; Human Tongue, frac 1; Human osteoarthritic, fraction II; Human Uterus, normal; Human
- 15 Colon, subtraction; prostate-edited; Human Colon; Human Fetal Spleen; Smooth muscle-ILb induced; Human Thyroid; Human Prostate Cancer, Stage C fraction; Soares_NhHMPu_S1; Human Whole Brain #2 - Oligo dT > 1.5Kb; Stratagene muscle 937209; Human Adipose Tissue, re-excision; Human adult (K.Okubo); Human heart cDNA (YNakamura); Human fetal heart, Lambda ZAP Express; Human
- 20 retina cDNA Tsp509I-cleaved sublibrary; NCI_CGAP_Br3; NCI_CGAP_GC4; NCI_CGAP_Lu1; NCI_CGAP_Pr3; NCI_CGAP_Alv1; NCI_CGAP_Co10; NCI_CGAP_Pr11; WATM1; Soares_fetal_lung_NbHL19W; Human Ovary; wilm's tumor; Human Infant Brain; Human Chronic Synovitis; Human Uterine Cancer; Human Hypothalamus, Schizophrenia; Ulcerative Colitis; Bone Marrow Stromal Cell,
- 25 untreated; Fetal Heart; Smooth muscle, serum treated; HM3; Bone marrow; Human

Fetal Heart; Endothelial cells-control; Human Amygdala; Osteoblasts and Soares infant brain 1NIB.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:51 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 864 of SEQ ID NO:51, b is an integer of 15 to 878, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:51, and where b is greater than or equal to a + 14.

15 FEATURES OF PROTEIN ENCODED BY GENE NO: 42

The computer algorithm BLASTX has been used to determine that the translation product of this gene shares sequence homology with, as a non-limiting example, the sequence accessible through the following database accession no. gil2547132 (all information available through the recited accession number is incorporated herein by reference) which is described therein as "neuropilin-2(a17) [Homo sapiens]." A partial alignment demonstrating the observed homology is shown immediately below.

25 >gi|2547132 (AF022860) neuropilin-2(a17) [Homo sapiens] >sp|O14821|O14821
NEUROFILIN-2.
Length = 926

Minus Strand HSPs:

Score = 619 (217.9 bits), Expect = 8.9e-135, Sum P(5) = 8.9e-135
Identities = 121/152 (79%), Positives = 121/152 (79%), Frame = -1

5 Q: 3661 DQGGGEWKHGRIILPSYDMEYQIVFEGVIGKGRSGEIAIDDIRISTDVPLENCMEPISAF 3482
DQGGGEWKHGRIILPSYDMEYQIVFEGVIGKGRSGEIAIDDIRISTDVPLENCMEPISAF
S: 749 DQGGGEWKHGRIILPSYDMEYQIVFEGVIGKGRSGEIAIDDIRISTDVPLENCMEPISAF 808

10 Q: 3481 VDIPEIHXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXDKESWLYTLDPILITIIAMS 3302
VDIPEIH W DKEKSWLYTLDPILITIIAMS
S: 809 VDIPEIHEREGYEDEIDDEYEVDWSNSSSATS GSGAPSTDKEKSWLYTLDPILITIIAMS 868

15 Q: 3301 SLGVLLGATCAGLLLYCTCSYSGLSRSRCTTL 3206
SLGVLLGATCAGLLLYCTCSYSGLSRSRCTTL
S: 869 SLGVLLGATCAGLLLYCTCSYSGLSRSRCTTL 900

Score = 535 (188.3 bits), Expect = 8.9e-135, Sum P(5) = 8.9e-135
Identities = 96/100 (96%), Positives = 99/100 (99%), Frame = -3

20 Q: 3983 PSGFNCNFDLEPCGWMYDHAKWLRTTWASSSSPNDRTPDDRNLRLQSDSQREGQYA 3804
PSGFNCNFDLEPCGWMYDHAKWLRTTWASSSSPNDRTPDDRNLRLQSDSQREGQYA
S: 641 PSGFNCNFDLEPCGWMYDHAKWLRTTWASSSSPNDRTPDDRNLRLQSDSQREGQYA 700

25 Q: 3803 RLISPPVHLPRSPVCMEFQYQATGGRGVALQVVREAARRA 3684
RLISPPVHLPRSPVCMEFQYQATGGRGVALQVVREA++ +
S: 701 RLISPPVHLPRSPVCMEFQYQATGGRGVALQVVREASQES 740

Score = 168 (59.1 bits), Expect = 8.9e-135, Sum P(5) = 8.9e-135
Identities = 36/65 (55%), Positives = 40/65 (61%), Frame = -1

30 Q: 4177 PAGLQXRLLQHSLIFLCPYTD SKPTVETLGPTVKXXXXXXXXXXXXXXXXXCGENCSFEDD 3998
PAG+ RL + C +TDSKPTV+TLGPTVK S CGENCSFEDD
S: 580 PAGIGMRLE----VLGCDWTD SKPTVKTLGPTVKSEETTPYPTEEEATECGENCSFEDD 635

35 Q: 3997 KDLQL 3983
KDLQL
S: 636 KDLQL 640

The segments of gil2547132 that are shown as "S" above are set out in the sequence listing as SEQ ID NO. 143, SEQ ID NO. 145 and SEQ ID NO. 147. Based on the structural similarity these homologous polypeptides are expected to share at least some biological activities. Such activities are known in the art, some of which are described elsewhere herein. Assays for determining such activities are also known in the art, some of which have been described elsewhere herein.

Preferred polypeptides of the invention comprise a polypeptide having the amino acid sequence set out in the sequence listing as SEQ ID NO. 144, SEQ ID

NO. 146 and/or SEQ ID NO. 148 which correspond to the "Q" sequences in the alignment shown above (gaps introduced in a sequence by the computer are, of course, removed).

- It has been discovered that this gene is expressed primarily in the following
- 5 tissues/cDNA libraries: Soares melanocyte 2NbHM and to a lesser extent in Soares fetal liver spleen 1NFLS; Soares infant brain 1NIB; Soares_multiple_sclerosis_2NbHMSP; Soares placenta Nb2HP; Soares_NhHMPu_S1; Soares_pregnant_uterus_NbHPU; Human T-Cell Lymphoma; Stratagene corneal stroma (#937222); normalized infant brain cDNA; Human
 - 10 Pancreas Tumor, Reexcision; Soares_fetal_lung_NbHL19W; Macrophage-oxLDL, re-excision; Human Synovial Sarcoma; Smooth Muscle- HASTE normalized; Human Umbilical Vein, Reexcision; Soares_fetal_heart_NbHH19W; Soares_fetal_liver_spleen_1NFLS_S1; Stratagene endothelial cell 937223; Human Adipose; Hemangiopericytoma; Rejected Kidney, lib 4; Stratagene lung (#937210);
 - 15 Primary Dendritic cells,frac 2; Endothelial-induced; Human Microvascular Endothelial Cells, fract. A; Human 8 Week Whole Embryo; NCI_CGAP_GC4; Primary Dendritic Cells, lib 1; Human Microvascular Endothelial Cells, fract. B; H Umbilical Vein Endothelial Cells, frac A, re-excision; Hypothalamus; Human Placenta; Human Stomach; HSA 172 Cells; NTERA2 teratocarcinoma cell
 - 20 line+retinoic acid (14 days); Raji Cells, cyclohexamide treated; Soares adult brain N2b4HB55Y; Human Umbilical Vein, Endo. remake; Spinal Cord, re-excision; H. Kidney Medulla, re-excision; L428; Human Pancreas Tumor; Macrophage-oxLDL; Human Hypothalamus,Schizophrenia; Normalized infant brain, Bento Soares; Soares_NFL_T_GBC_S1; Human umbilical vein endothelial cells, IL-4 induced;
 - 25 Ulcerative Colitis; Jia bone marrow stroma; Soares_NbHFB; Soares_total_fetus_Nb2HF8_9w; Stratagene hNT neuron (#937233); Stratagene liver

(#937224); H Macrophage (GM-CSF treated), re-excision; Human fetal heart, Lambda ZAP Express; Human Fetal Kidney, Reexcision; 12 Week Early Stage Human II, Reexcision; Human Fetal Heart; Human Adult Pulmonary, re-excision; Endothelial cells-control; Nine Week Old Early Stage Human; T cell helper II;

5 NCI_CGAP_HN4; NCI_CGAP_Co10 and NCI_CGAP_Kid6.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 101 as residues: Pro-26 to Gly-34.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are

10 related to SEQ ID NO:52 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the

15 general formula of a-b, where a is any integer between 1 to 4547 of SEQ ID NO:52, b is an integer of 15 to 4561, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:52, and where b is greater than or equal to a + 14.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 43

The computer algorithm BLASTX has been used to determine that the translation product of this gene shares sequence homology with, as a non-limiting example, the sequence accessible through the following database accession no. gil1389766 (all information available through the recited accession number is

25 incorporated herein by reference) which is described therein as "unknown [Homo

sapiens]. A partial alignment demonstrating the observed homology is shown immediately below.

```

5      >gi|1389766 unknown [Homo sapiens] >sp|Q13629|Q13629 HYPOTHETICAL 13.3 KD
      PROTEIN.
      Length = 118

      Minus Strand HSPs:

10     Score = 137 (48.2 bits), Expect = 8.1e-08, P = 8.1e-08
      Identities = 32/64 (50%), Positives = 38/64 (59%), Frame = -2

      Q:  281 HVGRPR*VDLLSPRV*DQPGQHGMFPFLLLKIQKCS*MWWRMPVVLATQEAEVGGSSKPRK 102
          H GRPR D L V DQ GQ G+ P LLK K S WW +PV+ A +E E G S +P +
15     S:  56 HFGRPRRADYLRIGVPDQRGQGESPSLLKNTKISWAWW-VPVIPAIREFEAGESLEPGR 114

      Q:  101 LRLQ 90
          RLQ
      S:  115 QRLQ 118
20

```

The segment of gi1389766 that is shown as "S" above is set out in the sequence listing as SEQ ID NO. 149.

Preferred polypeptides of the invention comprise a polypeptide having the amino acid sequence set out in the sequence listing as SEQ ID NO. 150 which
 25 corresponds to the "Q" sequence in the alignment shown above (gaps introduced in a sequence by the computer are, of course, removed).

It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: Rejected Kidney, lib 4; human tonsils; Spleen, Chronic lymphocytic leukemia; and Soares fetal liver spleen 1NFLS.

30 Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:53 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence

would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1303 of SEQ ID NO:53, b is an integer of 15 to 1317, where both a and b correspond to the positions of
5 nucleotide residues shown in SEQ ID NO:53, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 44

The computer algorithm BLASTX has been used to determine that the
10 translation product of this gene shares sequence homology with, as a non-limiting example, the sequence accessible through the following database accession no. gi|3342794 (all information available through the recited accession number is incorporated herein by reference) which is described therein as "calcium binding protein [Homo sapiens]." A partial alignment demonstrating the observed homology
15 is shown immediately below.

```
>gi|3342794 (AF035606) calcium binding protein [Homo sapiens]
>sp|O75340|O75340
```

```
20      CALCIUM BINDING PROTEIN.
      Length = 191
```

Plus Strand HSPs:

```
25      Score = 349 (122.9 bits), Expect = 3.6e-31, P = 3.6e-31
      Identities = 77/180 (42%), Positives = 106/180 (58%), Frame = +1
```

```
Q:   319 PGLYGQGGAPPNVDPPE-AYSW--FQSVDSHSGYISMKELQALVNCNWSSFNDETCLMM 489
      PG  G G A      P+ ++ W  FQ VD D SG IS  EL+QAL N  W+ FN  T   +
S:   10  PGA-GPGPAAGAALPDQSFLWNVFRVDKDRSGVISDTTELQQALSNGTWTPTFPNVTVRSI 68

Q:   490 INMFDKTKSGRIDVYGFSALWKFIQQWKNLFQQYDRDRSGSISYTELQQALSQMGYNLSP 669
      I+MFD+      ++  F+ +WK+I  W+N+F+ YDRD SG I  EL+QALS  GY LS
S:   69  ISMFDRENKAGVNFSEFTGVWKYITDWQNVFRTYDRDNSGMIDKNELQALSGFGYRLSD 128

Q:   670 QFTQLLVSRYPERSANPAMQLDRFIQVCTQLQVLTEAFREKDTAVQGNIRLSFEDFVTMT 849
      QF  +L+ ++  R      +  D FIQ C  LQ LT+ FR  DT   G I++S+E +++M
S:   129 QFHDILIRKF-DRQGRGQIAFDDFIQGCIVLQRLTDIFRRYDTDQDGWIQVSYEQYLSMV 187
```

Q: 850 AS 855
 S
 S: 188 FS 189

5

The segment of gil3342794 that is shown as "S" above is set out in the sequence listing as SEQ ID NO. 151. Based on the structural similarity these

homologous polypeptides are expected to share at least some biological activities.

Such activities are known in the art, some of which are described elsewhere herein.

- 10 Assays for determining such activities are also known in the art, some of which have been described elsewhere herein.

Preferred polypeptides of the invention comprise a polypeptide having the amino acid sequence set out in the sequence listing as SEQ ID NO. 152 which corresponds to the "Q" sequence in the alignment shown above (gaps introduced in a
 15 sequence by the computer are, of course, removed).

It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: Soares fetal liver spleen 1NFLS and to a lesser extent in Soares_pregnant_uterus_NbHPU; Soares placenta Nb2HP; Activated T-Cell (12hs)/Thiouridine labelledEco; Activated T-cell(12h)/Thiouridine-re-excision;
 20 Human Jurkat Membrane Bound Polysomes; Human Adult Testes, Large Inserts, Reexcision; Soares_fetal_heart_NbHH19W; Keratinocyte; Human Cerebellum; Amniotic Cells - Primary Culture; Stratagene ovarian cancer (#937219); Human endometrial stromal cells-treated with progesterone; Human Pituitary, subt IX; Prostate BPH; H. Kidney Medulla, re-excision; Apoptotic T-cell; Human Pancreas
 25 Tumor; Human Rhabdomyosarcoma; Human Gall Bladder; Stratagene NT2 neuronal precursor 937230; Primary Dendritic cells,frac 2; Human Neutrophil, Activated; Endothelial-induced; Osteoblasts; Human Primary Breast Cancer; LNCAP + o.3nM R1881; Human Colon, subtraction; Human OB HOS treated (10 nM E2) fraction I;

Human Primary Breast Cancer, re-excision; Human Thyroid; Resting T-Cell, re-excision; Human Epididymus; Human Colon Cancer, re-excision; Soares_placenta_8to9weeks_2NbHP8to9W; Human Fetal Epithelium (Skin); Human Stomach, re-excision; Human Amygdala, re-excision; Jurkat T-cell G1 phase; Human

5 Manic Depression Tissue; Human Infant Brain; Breast Cancer Cell line, angiogenic; Human Fetal Kidney; Soares_fetal_lung_NbHL19W; Human Primary Breast Cancer Reexcision; Human Hypothalamus, Schizophrenia; Human Thymus; Bone Marrow Stromal Cell, untreated; Soares breast 2NbHBst; Human Adrenal Gland Tumor; Human adult testis, large inserts; NTERA2, control; Macrophage-oxLDL, re-

10 excision; Adipocytes; Human Testes Tumor; Normal colon; Soares melanocyte 2NbHM; Human Testes, Reexcision; Human Placenta; Human Fetal Heart; human tonsils; Human Adult Pulmonary, re-excision; Human Amygdala; Human Microvascular Endothelial Cells, fract. A; Monocyte activated; Human B Cell Lymphoma; Spleen, Chronic lymphocytic leukemia; Human Testes; Human

15 Endometrial Tumor; Hodgkin's Lymphoma II and Primary Dendritic Cells, lib 1.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:54 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically

20 excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1667 of SEQ ID NO:54, b is an integer of 15 to 1681, where both a and b correspond to the positions of

25 nucleotide residues shown in SEQ ID NO:54, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 45

The computer algorithm BLASTX has been used to determine that the translation product of this gene shares sequence homology with, as a non-limiting example, the sequence accessible through the following database accession no. gil2443886 (all information available through the recited accession number is incorporated herein by reference) which is described therein as "Unknown protein [Arabidopsis thaliana]." A partial alignment demonstrating the observed homology is shown immediately below.

10

```
>gi|2443886 (AC002294) Unknown protein [Arabidopsis thaliana]
      Length = 240
```

15

Plus Strand HSPs:

```
Score = 372 (131.0 bits), Expect = 9.4e-50, Sum P(2) = 9.4e-50
Identities = 68/129 (52%), Positives = 99/129 (76%), Frame = +3
```

20

```
Q: 168 ITKDEWMEKLNHLHVQRADNMNRLIMNYLVTEGFKEAAEKFRMESGIEPSVDLETDERIK 347
      IT++EW +KLN + +++ DMN L+MN+LVTEG+ EAAEK+ ESG +P +DL T+ +R+
S: 25 ITREEWEKKLNAVKLKEDMNTLVMNFLVTEGYVEAAEKFRMESGIEPSVDLETDERIK 84
```

25

```
Q: 348 IREMILKGQIQEAIALINSLHPELLDTNRYLYFHLQQQHLLIELIRQRETEAALEFAQTQL 527
      +++ + G +++AI +N L+PE+LDTN L+PHLQQQ LIELIRQ +TE ALEFAQ +L
S: 85 VKKAVQNGNVEDAIEKVNDLNPEILDTNPELFFHLQQQRLIELIRQKTEEALEFAQEEL 144
```

30

```
Q: 528 ADRARRAES 554
      A R ++
S: 145 APRGEENQA 153
```

```
Score = 169 (59.5 bits), Expect = 9.4e-50, Sum P(2) = 9.4e-50
Identities = 37/92 (40%), Positives = 51/92 (55%), Frame = +2
```

35

```
Q: 533 QGEESRECLTEMERTLALLAFDPSPEESPFGLLHTMQRQKVWSEVNQAVLDYENRESTPX 712
      +GEE++ L E+E+T+ALL FD P +LL R K SEVN A+L ++ E P
S: 147 RGEENQAFLEEELEKTVALLVFDDASTCPVKELLDLSHRLKTASEVNAAILTSQSHEKDPK 206
```

40

```
Q: 713 XXXXXXXXXWAQNELDQKKVKYPKMTDLSKGV 808
      WAQ +LD+K V YP + DLS +
S: 207 LPSLLKMLIWAQTQLDEKAV-YPHINDLSTAI 237
```

The segments of gil2443886 that are shown as "S" above are set out in the sequence listing as SEQ ID NO. 153 and SEQ ID NO. 155.

Preferred polypeptides of the invention comprise a polypeptide having the amino acid sequence set out in the sequence listing as SEQ ID NO. 154 and/or SEQ
5 ID NO. 156 which correspond to the "Q" sequences in the alignment shown above (gaps introduced in a sequence by the computer are, of course, removed).

It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: NCI_CGAP_GCB1 and to a lesser extent in
Soares_testis_NHT; Human Pancreas Tumor, Reexcision; Soares fetal liver spleen
10 INFLS; Soares_fetal_liver_spleen_INFLS_S1; Human Rhabdomyosarcoma; Human Prostate Cancer, Stage C fraction; Stratagene placenta (#937225); human corpus colosum; Apoptotic T-cell; Soares_pregnant_uterus_NbHPU; Stratagene colon (#937204); Human 8 Week Whole Embryo; Soares placenta Nb2HP; Soares_fetal_lung_NbHL19W; Soares_fetal_heart_NbHH19W; Human Pituitary, re-
15 excision; stomach cancer (human); Human Stomach; Aorta endothelial cells + TNF-a; Human Tonsils, Lib 2; Glioblastoma; CHME Cell Line,untreated; Human Primary Breast Cancer Reexcision; Human Hippocampus; HM1; Human adult (K.Okubo); NCI_CGAP_Co3; NCI_CGAP_Co9; Human umbilical vein endothelial cells, IL-4 induced; Human Adipose; Human Adrenal Gland Tumor; Human Whole Six Week
20 Old Embryo; Stratagene lung (#937210); Fetal Heart; Stratagene hNT neuron (#937233); Resting T-Cell Library,II; Human T-Cell Lymphoma; Colon Tumor II; Human Placenta; human tonsils; Human B Cell Lymphoma; Human Bone Marrow, treated; T cell helper II and Soares infant brain INIB.

Many polynucleotide sequences, such as EST sequences, are publicly
25 available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:55 and may have been publicly available prior to conception of

the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the
5 general formula of a-b, where a is any integer between 1 to 1581 of SEQ ID NO:55, b is an integer of 15 to 1595, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:55, and where b is greater than or equal to a + 14.

10 **FEATURES OF PROTEIN ENCODED BY GENE NO: 46**

It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: Human Rhabdomyosarcoma.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are
15 related to SEQ ID NO:56 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the
20 general formula of a-b, where a is any integer between 1 to 939 of SEQ ID NO:56, b is an integer of 15 to 953, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:56, and where b is greater than or equal to a + 14.

25 **FEATURES OF PROTEIN ENCODED BY GENE NO: 47**

It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: Glioblastoma; NCI_CGAP_Co3; Human Ovarian Cancer Reexcision; Anergic T-cell; and Human B Cell Lymphoma.

Many polynucleotide sequences, such as EST sequences, are publicly
5 available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:57 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would be cumbersome. Accordingly, preferably excluded from the present invention
10 are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1238 of SEQ ID NO:57, b is an integer of 15 to 1252, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:57, and where b is greater than or equal to a + 14.

15

FEATURES OF PROTEIN ENCODED BY GENE NO: 48

It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: Soares infant brain 1NIB and to a lesser extent in Soares retina N2b4HR; Soares melanocyte 2NbHM; Soares placenta Nb2HP; Healing groin
20 wound, 6.5 hours post incision; Human Prostate; Macrophage-oxLDL; Human Hypothalamus, Schizophrenia; NCI_CGAP_GCB1; Anergic T-cell; Human Whole 6 Week Old Embryo (II), sub; Bone Cancer; Hypothalamus; Human (Caco-2) cell line, adenocarcinoma, colon, remake; H. cerebellum, Enzyme subtracted; Salivary Gland; Human Frontal Cortex, Schizophrenia; Human Ovary; wilm's tumor; Human Adult
25 Small Intestine; L428; Human Hippocampus; Synovial Fibroblasts (control); Human Gall Bladder; Human Testes Tumor; Stratagene colon (#937204); Stratagene fetal

retina 937202; Stratagene endothelial cell 937223; H. Frontal cortex, epileptic, re-excision; Soares_fetal_lung_NbHL19W; Human Synovial Sarcoma; Bone marrow; human tonsils; Human Osteoclastoma; Spleen, Chronic lymphocytic leukemia; T cell helper II; Soares fetal liver spleen 1NFLS and Primary Dendritic Cells, lib 1.

5 Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:58 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence
10 would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1035 of SEQ ID NO:58, b is an integer of 15 to 1049, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:58, and where b is greater than or equal to a
15 + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 49

It has been discovered that this gene is expressed primarily in the following tissues/cDNA libraries: Brain frontal cortex and Anergic T-cell.

20 Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:59 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence
25 would be cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the

general formula of a-b, where a is any integer between 1 to 1609 of SEQ ID NO:59, b is an integer of 15 to 1623, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:59, and where b is greater than or equal to a + 14.

Table 1

Gene No.	cDNA Clone ID	ATCC Deposit No.:Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
1	HTXOL30	203959 4/26/99	Uni-ZAP XR	11	840	1	840	272	272	60	1			14
2	HTXOW27	203959 4/26/99	Uni-ZAP XR	12	2387	627	2372	1070	1070	61	1	16	17	26
3	HTXPD86	203959 4/26/99	Uni-ZAP XR	13	2064	559	1458	900	900	62	1	21	22	47
4	HWLGP26	203959 4/26/99	pSport1	14	1898	1007	1835	1091	1091	63	1	23	24	71
5	HWLHO31	203959 4/26/99	pSport1	15	1701	1	1701	183	183	64	1			10

Gene No.	cDNA Clone ID	ATCC Deposit No:Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
6	HOGAR36	203959 4/26/99	pCMVSPORT 2.0	16	1175	1	1175	205	205	65	1	25	26	26
7	HOGCC26	203959 4/26/99	pCMVSPORT 2.0	17	1827	566	1816	713	713	66	1			19
8	HAJAY92	203959 4/26/99	pCMVSPORT 3.0	18	2345	1	2345	12	12	67	1	20	21	94
9	HTJMJ72	203959 4/26/99	pCMVSPORT 2.0	19	854	1	854	263	263	68	1	26	27	27
10	HOUEJ43	203959 4/26/99	Uni-ZAP XR	20	1450	1	1450	157	157	69	1			14
11	HSVCF53	203959 4/26/99	Uni-ZAP XR	21	1248	1	1248	259	259	70	1	23	24	23

Gene No.	cDNA Clone ID	ATCC Deposit No:Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
12	HSYBZ94	203959 4/26/99	pCMVSPORT 3.0	22	3268	1	3268	52	52	71	1	35	36	79
13	HPRBH85	203959 4/26/99	Uni-ZAP XR	23	1673	558	1648	684	684	72	1	18	19	134
14	HTECE87	203959 4/26/99	Uni-ZAP XR	24	946	1	946	157	157	73	1	34	35	41
15	HNHCT47	203959 4/26/99	Uni-ZAP XR	25	621	12	621	73	73	74	1	20	21	39
16	HNHFJ49	203959 4/26/99	Uni-ZAP XR	26	1736	1	1736	26	26	75	1	26	27	28
17	HNKAA76	203959 4/26/99	pSport1	27	1803	1	1803	384	384	76	1	23	24	47

Gene No.	cDNA Clone ID	ATCC Deposit No:Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
18	HNTSQ23	203959 4/26/99	pSport1	28	2287	231	2287	1255	1255	77	1	28	29	38
19	HOABP31	203959 4/26/99	Uni-ZAP XR	29	927	1	890		148	78	1	19	20	123
20	HODAW64	203959 4/26/99	Uni-ZAP XR	30	3287	1	828		3184	79	1	8	9	33
21	HOHBC57	203959 4/26/99	pCMVSPORT 2.0	31	5083	699	5083	891	891	80	1	28	29	51
22	HLQBX64	203959 4/26/99	Lambda ZAP II	32	2108	762	1349	810	810	81	1			15
23	HOSCZ41	203959 4/26/99	Uni-ZAP XR	33	1248	127	1246	188	188	82	1	20	21	50

Gene No.	cDNA Clone ID	ATCC Deposit No:Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of 5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
24	HOUDR07	203959 4/26/99	Uni-ZAP XR	34	1911	1	1911	170	170	83	1	27	28	65
25	HPBCT11	203959 4/26/99	pBluescript SK-	35	996	1	996	149	149	84	1	27	28	38
26	HPCAG17	203959 4/26/99	Uni-ZAP XR	36	1320	1	1320		214	85	1	29	30	31
27	HPFDB66	203959 4/26/99	Uni-ZAP XR	37	1376	741	1376		973	86	1			9
28	HPJAN76	203959 4/26/99	Uni-ZAP XR	38	1953	70	1953	275	275	87	1	18	19	18
29	HPJBJ51	203959 4/26/99	Uni-ZAP XR	39	2793	522	2421	715	715	88	1	14	15	69

Gene No.	cDNA Clone ID	ATCC Deposit No:Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
30	HPMBW95	203959 4/26/99	Uni-ZAP XR	40	1367	418	1355	523	523	89	1			3
31	HGBBR29	203959 4/26/99	Uni-ZAP XR	41	1906	1	1693	251	251	90	1	16	17	61
32	HPMDD27	203959 4/26/99	Uni-ZAP XR	42	1723	230	1720	327	327	91	1	43	44	54
33	HPMEG72	203959 4/26/99	Uni-ZAP XR	43	2074	91	1727	172	172	92	1	19	20	31
34	HPQBI48	203959 4/26/99	Lambda ZAP II	44	822	1	822	251	251	93	1	19	20	36
35	HBXAT27	203959 4/26/99	ZAP Express	45	2406	958	2385		1097	94	1	18	19	40

Gene No.	cDNA Clone ID	ATCC Deposit No:Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
36	HPRCM72	203959 4/26/99	Uni-ZAP XR	46	2455	26	1572		281	95	1	36	37	108
37	HOHCH71	203959 4/26/99	pCMVSPORT 2.0	47	2574	166	2574	333	333	96	1	24	25	38
38	HPTRM02	203959 4/26/99	pBluescript	48	1760	658	1680	885	885	97	1	16	17	80
39	HPTRW28	203959 4/26/99	pBluescript	49	1023	1	1023	255	255	98	1	18	19	160
40	HPWAT86	203959 4/26/99	Uni-ZAP XR	50	617	1	617	83	83	99	1	32	33	59
41	HPWDK06	203959 4/26/99	Uni-ZAP XR	51	878	240	854	405	405	100	1			26

Gene No.	cDNA Clone ID	ATCC Deposit No.:Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
42	HRAAZ12	203959 4/26/99	pCMVSPORT 3.0	52	4561	3116	4561	3201	3201	101	1	21	22	39
43	HRABP28	203959 4/26/99	pCMVSPORT 3.0	53	1317	1	1317	224	224	102	1	23	24	35
44	HRDEX93	203959 4/26/99	Uni-ZAP XR	54	1681	711	1638	649	649	103	1	21	22	72
45	HRDFE30	203959 4/26/99	Uni-ZAP XR	55	1595	821	1595	1193	1193	104	1	34	35	41
46	HRDFT83	203959 4/26/99	Uni-ZAP XR	56	953	8	953	51	51	105	1	27	28	34
47	HBJHT01	203959 4/26/99	Uni-ZAP XR	57	1252	1	1252	193	193	106	1	22	23	47

Gene No.	cDNA Clone ID	ATCC Deposit No.:Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
48	HHSB106	203959 4/26/99	Uni-ZAP XR	58	1049	27	803		690	107	1			5
49	HSAVO11	203959 4/26/99	Uni-ZAP XR	59	1623	1	1623	208	208	108	1	19	20	22

Table 1 summarizes the information corresponding to each "Gene No." described above. The nucleotide sequence identified as "NT SEQ ID NO:X" was assembled from partially homologous ("overlapping") sequences obtained from the "cDNA clone ID" identified in Table 1 and, in some cases, from additional related DNA clones. The overlapping sequences were assembled into a single contiguous sequence of high redundancy (usually three to five overlapping sequences at each nucleotide position), resulting in a final sequence identified as SEQ ID NO:X.

The cDNA Clone ID was deposited on the date and given the corresponding deposit number listed in "ATCC Deposit No:Z and Date." Some of the deposits contain multiple different clones corresponding to the same gene. "Vector" refers to the type of vector contained in the cDNA Clone ID.

"Total NT Seq." refers to the total number of nucleotides in the contig identified by "Gene No." The deposited clone may contain all or most of these sequences, reflected by the nucleotide position indicated as "5' NT of Clone Seq." and the "3' NT of Clone Seq." of SEQ ID NO:X. The nucleotide position of SEQ ID NO:X of the putative start codon (methionine) is identified as "5' NT of Start Codon." Similarly, the nucleotide position of SEQ ID NO:X of the predicted signal sequence is identified as "5' NT of First AA of Signal Pep."

The translated amino acid sequence, beginning with the methionine, is identified as "AA SEQ ID NO:Y," although other reading frames can also be easily translated using known molecular biology techniques. The polypeptides produced by these alternative open reading frames are specifically contemplated by the present invention.

The first and last amino acid position of SEQ ID NO:Y of the predicted signal peptide is identified as "First AA of Sig Pep" and "Last AA of Sig Pep." The predicted first amino acid position of SEQ ID NO:Y of the secreted portion is

identified as "Predicted First AA of Secreted Portion." Finally, the amino acid position of SEQ ID NO:Y of the last amino acid in the open reading frame is identified as "Last AA of ORF."

SEQ ID NO:X (where X may be any of the polynucleotide sequences disclosed in the sequence listing) and the translated SEQ ID NO:Y (where Y may be any of the polypeptide sequences disclosed in the sequence listing) are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and described further below. For instance, SEQ ID NO:X is useful for designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the cDNA contained in the deposited clone. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y may be used, for example, to generate antibodies which bind specifically to proteins containing the polypeptides and the secreted proteins encoded by the cDNA clones identified in Table 1.

Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).

Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X and the predicted

translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing a human cDNA of the invention deposited with the ATCC, as set forth in Table 1. The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods.

- 5 The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

- 10 The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, or the deposited clone. The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include preparing probes or primers from the disclosed sequence and identifying or amplifying the corresponding gene from appropriate
15 sources of genomic material.

- Also provided in the present invention are allelic variants, orthologs, and/or species homologs. Procedures known in the art can be used to obtain full-length genes, allelic variants, splice variants, full-length coding portions, orthologs, and/or species homologs of genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, or a
20 deposited clone, using information from the sequences disclosed herein or the clones deposited with the ATCC. For example, allelic variants and/or species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for allelic variants and/or the desired homologue.

- 25 The polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly

produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below). It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.

10 The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified using techniques described herein or otherwise known in the art, such as, for example, by the one-step method described in Smith and Johnson, Gene 67:31-40
15 (1988). Polypeptides of the invention also can be purified from natural, synthetic or recombinant sources using techniques described herein or otherwise known in the art, such as, for example, antibodies of the invention raised against the secreted protein.

The present invention provides a polynucleotide comprising, or alternatively consisting of, the nucleic acid sequence of SEQ ID NO:X, and/or a cDNA contained
20 in ATCC deposit Z. The present invention also provides a polypeptide comprising, or alternatively, consisting of, the polypeptide sequence of SEQ ID NO:Y and/or a polypeptide encoded by the cDNA contained in ATCC deposit Z. Polynucleotides encoding a polypeptide comprising, or alternatively consisting of the polypeptide sequence of SEQ ID NO:Y and/or a polypeptide sequence encoded by the cDNA
25 contained in ATCC deposit Z are also encompassed by the invention.

Signal Sequences

The present invention also encompasses mature forms of the polypeptide having the polypeptide sequence of SEQ ID NO:Y and/or the polypeptide sequence encoded by the cDNA in a deposited clone. Polynucleotides encoding the mature forms (such as, for example, the polynucleotide sequence in SEQ ID NO:X and/or the polynucleotide sequence contained in the cDNA of a deposited clone) are also encompassed by the invention. According to the signal hypothesis, proteins secreted by mammalian cells have a signal or secretary leader sequence which is cleaved from the mature protein once export of the growing protein chain across the rough endoplasmic reticulum has been initiated. Most mammalian cells and even insect cells cleave secreted proteins with the same specificity. However, in some cases, cleavage of a secreted protein is not entirely uniform, which results in two or more mature species of the protein. Further, it has long been known that cleavage specificity of a secreted protein is ultimately determined by the primary structure of the complete protein, that is, it is inherent in the amino acid sequence of the polypeptide.

Methods for predicting whether a protein has a signal sequence, as well as the cleavage point for that sequence, are available. For instance, the method of McGeoch, *Virus Res.* 3:271-286 (1985), uses the information from a short N-terminal charged region and a subsequent uncharged region of the complete (uncleaved) protein. The method of von Heinje, *Nucleic Acids Res.* 14:4683-4690 (1986) uses the information from the residues surrounding the cleavage site, typically residues -13 to +2, where +1 indicates the amino terminus of the secreted protein. The accuracy of predicting the cleavage points of known mammalian secretory proteins for each of these methods is in the range of 75-80%. (von Heinje, *supra*.) However, the two methods do not always produce the same predicted cleavage point(s) for a given protein.

In the present case, the deduced amino acid sequence of the secreted polypeptide was analyzed by a computer program called SignalP (Henrik Nielsen et al., Protein Engineering 10:1-6 (1997)), which predicts the cellular location of a protein based on the amino acid sequence. As part of this computational prediction of localization, the methods of McGeoch and von Heinje are incorporated. The analysis of the amino acid sequences of the secreted proteins described herein by this program provided the results shown in Table 1.

As one of ordinary skill would appreciate, however, cleavage sites sometimes vary from organism to organism and cannot be predicted with absolute certainty. Accordingly, the present invention provides secreted polypeptides having a sequence shown in SEQ ID NO:Y which have an N-terminus beginning within 5 residues (i.e., + or - 5 residues) of the predicted cleavage point. Similarly, it is also recognized that in some cases, cleavage of the signal sequence from a secreted protein is not entirely uniform, resulting in more than one secreted species. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

Moreover, the signal sequence identified by the above analysis may not necessarily predict the naturally occurring signal sequence. For example, the naturally occurring signal sequence may be further upstream from the predicted signal sequence. However, it is likely that the predicted signal sequence will be capable of directing the secreted protein to the ER. Nonetheless, the present invention provides the mature protein produced by expression of the polynucleotide sequence of SEQ ID NO:X and/or the polynucleotide sequence contained in the cDNA of a deposited clone, in a mammalian cell (e.g., COS cells, as described below). These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

Polynucleotide and Polypeptide Variants

The present invention is directed to variants of the polynucleotide sequence disclosed in SEQ ID NO:X, the complementary strand thereto, and/or the cDNA
5 sequence contained in a deposited clone.

The present invention also encompasses variants of the polypeptide sequence disclosed in SEQ ID NO:Y and/or encoded by a deposited clone.

"Variant" refers to a polynucleotide or polypeptide differing from the polynucleotide or polypeptide of the present invention, but retaining essential
10 properties thereof. Generally, variants are overall closely similar, and, in many regions, identical to the polynucleotide or polypeptide of the present invention.

The present invention is also directed to nucleic acid molecules which comprise, or alternatively consist of, a nucleotide sequence which is at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to, for example, the nucleotide
15 coding sequence in SEQ ID NO:X or the complementary strand thereto, the nucleotide coding sequence contained in a deposited cDNA clone or the complementary strand thereto, a nucleotide sequence encoding the polypeptide of SEQ ID NO:Y, a nucleotide sequence encoding the polypeptide encoded by the cDNA contained in a deposited clone, and/or polynucleotide fragments of any of
20 these nucleic acid molecules (e.g., those fragments described herein).

Polynucleotides which hybridize to these nucleic acid molecules under stringent hybridization conditions or lower stringency conditions are also encompassed by the invention, as are polypeptides encoded by these polynucleotides.

The present invention is also directed to polypeptides which comprise, or
25 alternatively consist of, an amino acid sequence which is at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% identical to, for example, the polypeptide sequence

shown in SEQ ID NO:Y, the polypeptide sequence encoded by the cDNA contained in a deposited clone, and/or polypeptide fragments of any of these polypeptides (e.g., those fragments described herein).

By a nucleic acid having a nucleotide sequence at least, for example, 95%
5 "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the nucleic acid is identical to the reference sequence except that the nucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the polypeptide. In other words, to obtain a nucleic acid having a nucleotide sequence at least 95%
10 identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. The query sequence may be an entire sequence shown in Table 1, the ORF (open reading frame), or any fragment specified
15 as described herein.

As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the present invention can be determined conventionally using known computer programs. A preferred method for determining the best
20 overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. 6:237-245(1990)). In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be compared by
25 converting U's to T's. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to

calculate percent identity are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, Window Size=500 or the length of the subject nucleotide sequence, whichever is shorter.

5 If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for 5' and 3' truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the query sequence, the percent
10 identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using
15 the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only bases outside the 5' and 3' bases of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

20 For example, a 90 base subject sequence is aligned to a 100 base query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignment of the first 10 bases at 5' end. The 10 unpaired bases represent
25 10% of the sequence (number of bases at the 5' and 3' ends not matched/total number of bases in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 bases were perfectly

matched the final percent identity would be 90%. In another example, a 90 base subject sequence is compared with a 100 base query sequence. This time the deletions are internal deletions so that there are no bases on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only bases 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to made for the purposes of the present invention.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that the subject polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query amino acid sequence, up to 5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, an amino acid sequences shown in Table 1 (SEQ ID NO:Y) or to the amino acid sequence encoded by cDNA contained in a deposited clone can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject

sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. 6:237-245(1990)). In a sequence alignment the query and subject sequences are either both nucleotide sequences or both amino acid sequences. The result of said

5 global sequence alignment is in percent identity. Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the subject amino acid sequence, whichever is shorter.

10 If the subject sequence is shorter than the query sequence due to N- or C-terminal deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity. For subject sequences truncated at the N- and C-termini, relative to the
15 query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from
20 the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are considered for the purposes of manually adjusting the percent identity
25 score. That is, only query residue positions outside the farthest N- and C-terminal residues of the subject sequence.

For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-terminus of the subject sequence and therefore, the FASTDB alignment does not show a matching/alignment of the first 10 residues at the N-terminus. The 10
5 unpaired residues represent 10% of the sequence (number of residues at the N- and C-termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100
10 residue query sequence. This time the deletions are internal deletions so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not
15 matched/aligned with the query sequence are manually corrected for. No other manual corrections are to be made for the purposes of the present invention.

The variants may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce silent substitutions, additions, or deletions, but do not alter
20 the properties or activities of the encoded polypeptide. Nucleotide variants produced by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, variants in which 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also preferred. Polynucleotide variants can be produced for a variety of reasons, e.g., to optimize codon expression for a particular host
25 (change codons in the human mRNA to those preferred by a bacterial host such as *E. coli*).

Naturally occurring variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. (Genes II, Lewin, B., ed., John Wiley & Sons, New York (1985).) These allelic variants can vary at either the polynucleotide and/or polypeptide level and are
5 included in the present invention. Alternatively, non-naturally occurring variants may be produced by mutagenesis techniques or by direct synthesis.

Using known methods of protein engineering and recombinant DNA technology, variants may be generated to improve or alter the characteristics of the polypeptides of the present invention. For instance, one or more amino acids can be
10 deleted from the N-terminus or C-terminus of the secreted protein without substantial loss of biological function. The authors of Ron et al., J. Biol. Chem. 268: 2984-2988 (1993), reported variant KGF proteins having heparin binding activity even after deleting 3, 8, or 27 amino-terminal amino acid residues. Similarly, Interferon gamma exhibited up to ten times higher activity after deleting 8-10 amino acid residues from
15 the carboxy terminus of this protein. (Dobeli et al., J. Biotechnology 7:199-216 (1988).)

Moreover, ample evidence demonstrates that variants often retain a biological activity similar to that of the naturally occurring protein. For example, Gayle and coworkers (J. Biol. Chem 268:22105-22111 (1993)) conducted extensive mutational
20 analysis of human cytokine IL-1a. They used random mutagenesis to generate over 3,500 individual IL-1a mutants that averaged 2.5 amino acid changes per variant over the entire length of the molecule. Multiple mutations were examined at every possible amino acid position. The investigators found that "[m]ost of the molecule could be altered with little effect on either [binding or biological activity]." (See,
25 Abstract.) In fact, only 23 unique amino acid sequences, out of more than 3,500

nucleotide sequences examined, produced a protein that significantly differed in activity from wild-type.

Furthermore, even if deleting one or more amino acids from the N-terminus or C-terminus of a polypeptide results in modification or loss of one or more biological functions, other biological activities may still be retained. For example, the ability of a deletion variant to induce and/or to bind antibodies which recognize the secreted form will likely be retained when less than the majority of the residues of the secreted form are removed from the N-terminus or C-terminus. Whether a particular polypeptide lacking N- or C-terminal residues of a protein retains such immunogenic activities can readily be determined by routine methods described herein and otherwise known in the art.

Thus, the invention further includes polypeptide variants which show substantial biological activity. Such variants include deletions, insertions, inversions, repeats, and substitutions selected according to general rules known in the art so as have little effect on activity. For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie et al., Science 247:1306-1310 (1990), wherein the authors indicate that there are two main strategies for studying the tolerance of an amino acid sequence to change.

The first strategy exploits the tolerance of amino acid substitutions by natural selection during the process of evolution. By comparing amino acid sequences in different species, conserved amino acids can be identified. These conserved amino acids are likely important for protein function. In contrast, the amino acid positions where substitutions have been tolerated by natural selection indicates that these positions are not critical for protein function. Thus, positions tolerating amino acid substitution could be modified while still maintaining biological activity of the protein.

The second strategy uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene to identify regions critical for protein function. For example, site directed mutagenesis or alanine-scanning mutagenesis (introduction of single alanine mutations at every residue in the molecule) can be used.

- 5 (Cunningham and Wells, Science 244:1081-1085 (1989).) The resulting mutant molecules can then be tested for biological activity.

As the authors state, these two strategies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at certain amino acid positions in the protein. For example, most buried (within the tertiary structure of the protein) amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Moreover, tolerated conservative amino acid substitutions involve replacement of the aliphatic or hydrophobic amino acids Ala, Val, Leu and Ile; replacement of the hydroxyl residues Ser and Thr; replacement of the acidic residues Asp and Glu; replacement of the amide residues Asn and Gln, replacement of the basic residues Lys, Arg, and His; replacement of the aromatic residues Phe, Tyr, and Trp, and replacement of the small-sized amino acids Ala, Ser, Thr, Met, and Gly.

Besides conservative amino acid substitution, variants of the present invention include (i) substitutions with one or more of the non-conserved amino acid residues, where the substituted amino acid residues may or may not be one encoded by the genetic code, or (ii) substitution with one or more of amino acid residues having a substituent group, or (iii) fusion of the mature polypeptide with another compound, such as a compound to increase the stability and/or solubility of the polypeptide (for example, polyethylene glycol), or (iv) fusion of the polypeptide with additional amino acids, such as, for example, an IgG Fc fusion region peptide, or leader or secretory

sequence, or a sequence facilitating purification. Such variant polypeptides are deemed to be within the scope of those skilled in the art from the teachings herein.

For example, polypeptide variants containing amino acid substitutions of charged amino acids with other charged or neutral amino acids may produce proteins with improved characteristics, such as less aggregation. Aggregation of pharmaceutical formulations both reduces activity and increases clearance due to the aggregate's immunogenic activity. (Pinckard et al., Clin. Exp. Immunol. 2:331-340 (1967); Robbins et al., Diabetes 36: 838-845 (1987); Cleland et al., Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377 (1993).)

10 A further embodiment of the invention relates to a polypeptide which comprises the amino acid sequence of the present invention having an amino acid sequence which contains at least one amino acid substitution, but not more than 50 amino acid substitutions, even more preferably, not more than 40 amino acid substitutions, still more preferably, not more than 30 amino acid substitutions, and
15 still even more preferably, not more than 20 amino acid substitutions. Of course, in order of ever-increasing preference, it is highly preferable for a peptide or polypeptide to have an amino acid sequence which comprises the amino acid sequence of the present invention, which contains at least one, but not more than 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 amino acid substitutions. In specific embodiments, the number of additions,
20 substitutions, and/or deletions in the amino acid sequence of the present invention or fragments thereof (e.g., the mature form and/or other fragments described herein), is 1-5, 5-10, 5-25, 5-50, 10-50 or 50-150, conservative amino acid substitutions are preferable.

25 Polynucleotide and Polypeptide Fragments

The present invention is also directed to polynucleotide fragments of the polynucleotides of the invention.

In the present invention, a "polynucleotide fragment" refers to a short polynucleotide having a nucleic acid sequence which: is a portion of that contained in
5 a deposited clone, or encoding the polypeptide encoded by the cDNA in a deposited clone; is a portion of that shown in SEQ ID NO:X or the complementary strand thereto, or is a portion of a polynucleotide sequence encoding the polypeptide of SEQ ID NO:Y. The nucleotide fragments of the invention are preferably at least about 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt,
10 and even more preferably, at least about 40 nt, at least about 50 nt, at least about 75 nt, or at least about 150 nt in length. A fragment "at least 20 nt in length," for example, is intended to include 20 or more contiguous bases from the cDNA sequence contained in a deposited clone or the nucleotide sequence shown in SEQ ID NO:X. In this context "about" includes the particularly recited value, a value larger
15 or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. These nucleotide fragments have uses that include, but are not limited to, as diagnostic probes and primers as discussed herein. Of course, larger fragments (e.g., 50, 150, 500, 600, 2000 nucleotides) are preferred.

Moreover, representative examples of polynucleotide fragments of the
20 invention, include, for example, fragments comprising, or alternatively consisting of, a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 651-700, 701-750, 751-800, 800-850, 851-900, 901-950, 951-1000, 1001-1050, 1051-1100, 1101-1150, 1151-1200, 1201-1250, 1251-1300, 1301-1350, 1351-1400, 1401-1450, 1451-1500,
25 1501-1550, 1551-1600, 1601-1650, 1651-1700, 1701-1750, 1751-1800, 1801-1850, 1851-1900, 1901-1950, 1951-2000, or 2001 to the end of SEQ ID NO:X, or the

complementary strand thereto, or the cDNA contained in a deposited clone. In this context "about" includes the particularly recited ranges, and ranges larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini.

Preferably, these fragments encode a polypeptide which has biological activity. More

5 preferably, these polynucleotides can be used as probes or primers as discussed herein. Polynucleotides which hybridize to these nucleic acid molecules under stringent hybridization conditions or lower stringency conditions are also encompassed by the invention, as are polypeptides encoded by these polynucleotides.

In the present invention, a "polypeptide fragment" refers to an amino acid
10 sequence which is a portion of that contained in SEQ ID NO:Y or encoded by the cDNA contained in a deposited clone. Protein (polypeptide) fragments may be "free-standing," or comprised within a larger polypeptide of which the fragment forms a part or region, most preferably as a single continuous region. Representative examples of polypeptide fragments of the invention, include, for example, fragments
15 comprising, or alternatively consisting of, from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, 102-120, 121-140, 141-160, or 161 to the end of the coding region. Moreover, polypeptide fragments can be about 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, or 150 amino acids in length. In this context "about" includes the particularly recited ranges or values, and ranges or values larger or
20 smaller by several (5, 4, 3, 2, or 1) amino acids, at either extreme or at both extremes. Polynucleotides encoding these polypeptides are also encompassed by the invention.

Preferred polypeptide fragments include the secreted protein as well as the mature form. Further preferred polypeptide fragments include the secreted protein or the mature form having a continuous series of deleted residues from the amino or the
25 carboxy terminus, or both. For example, any number of amino acids, ranging from 1-60, can be deleted from the amino terminus of either the secreted polypeptide or the

mature form. Similarly, any number of amino acids, ranging from 1-30, can be deleted from the carboxy terminus of the secreted protein or mature form.

Furthermore, any combination of the above amino and carboxy terminus deletions are preferred. Similarly, polynucleotides encoding these polypeptide fragments are also
5 preferred.

Also preferred are polypeptide and polynucleotide fragments characterized by structural or functional domains, such as fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet-forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic
10 regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions, substrate binding region, and high antigenic index regions. Polypeptide fragments of SEQ ID NO:Y falling within conserved domains are specifically contemplated by the present invention. Moreover, polynucleotides encoding these domains are also contemplated.

15 Other preferred polypeptide fragments are biologically active fragments. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide of the present invention. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity. Polynucleotides encoding these polypeptide fragments are also
20 encompassed by the invention.

Preferably, the polynucleotide fragments of the invention encode a polypeptide which demonstrates a functional activity. By a polypeptide demonstrating a "functional activity" is meant, a polypeptide capable of displaying one or more known functional activities associated with a full-length (complete)
25 polypeptide of invention protein. Such functional activities include, but are not limited to, biological activity, antigenicity [ability to bind (or compete with a

polypeptide of the invention for binding) to an antibody to the polypeptide of the invention], immunogenicity (ability to generate antibody which binds to a polypeptide of the invention), ability to form multimers with polypeptides of the invention, and ability to bind to a receptor or ligand for a polypeptide of the invention.

5 The functional activity of polypeptides of the invention, and fragments, variants derivatives, and analogs thereof, can be assayed by various methods.

For example, in one embodiment where one is assaying for the ability to bind or compete with full-length polypeptide of the invention for binding to an antibody of the polypeptide of the invention, various immunoassays known in the art can be used, including but not limited to, competitive and non-competitive assay systems using techniques such as radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoradiometric assays, gel diffusion precipitation reactions, immunodiffusion assays, in situ immunoassays (using colloidal gold, enzyme or radioisotope labels, for example), western blots, precipitation reactions, agglutination assays (e.g., gel agglutination assays, hemagglutination assays), complement fixation assays, immunofluorescence assays, protein A assays, and immunoelectrophoresis assays, etc. In one embodiment, antibody binding is detected by detecting a label on the primary antibody. In another embodiment, the primary antibody is detected by detecting binding of a secondary antibody or reagent to the primary antibody. In a further embodiment, the secondary antibody is labeled. Many means are known in the art for detecting binding in an immunoassay and are within the scope of the present invention.

In another embodiment, where a ligand for a polypeptide of the invention identified, or the ability of a polypeptide fragment, variant or derivative of the invention to multimerize is being evaluated, binding can be assayed, e.g., by means well-known in the art, such as, for example, reducing and non-reducing gel

chromatography, protein affinity chromatography, and affinity blotting. See generally, Phizicky, E., et al., 1995, Microbiol. Rev. 59:94-123. In another embodiment, physiological correlates of binding of a polypeptide of the invention to its substrates (signal transduction) can be assayed.

5 In addition, assays described herein (see Examples) and otherwise known in the art may routinely be applied to measure the ability of polypeptides of the invention and fragments, variants derivatives and analogs thereof to elicit related biological activity related to that of the polypeptide of the invention (either in vitro or in vivo). Other methods will be known to the skilled artisan and are within the scope
10 of the invention.

Epitopes and Antibodies

The present invention encompasses polypeptides comprising, or alternatively consisting of, an epitope of the polypeptide having an amino acid sequence of SEQ ID
15 NO:Y, or an epitope of the polypeptide sequence encoded by a polynucleotide sequence contained in ATCC deposit No. Z or encoded by a polynucleotide that hybridizes to the complement of the sequence of SEQ ID NO:X or contained in ATCC deposit No. Z under stringent hybridization conditions or lower stringency hybridization conditions as defined supra. The present invention further encompasses
20 polynucleotide sequences encoding an epitope of a polypeptide sequence of the invention (such as, for example, the sequence disclosed in SEQ ID NO:X), polynucleotide sequences of the complementary strand of a polynucleotide sequence encoding an epitope of the invention, and polynucleotide sequences which hybridize to the complementary strand under stringent hybridization conditions or lower
25 stringency hybridization conditions defined supra.

The term "epitopes," as used herein, refers to portions of a polypeptide having antigenic or immunogenic activity in an animal, preferably a mammal, and most preferably in a human. In a preferred embodiment, the present invention encompasses a polypeptide comprising an epitope, as well as the polynucleotide encoding this polypeptide. An "immunogenic epitope," as used herein, is defined as a portion of a protein that elicits an antibody response in an animal, as determined by any method known in the art, for example, by the methods for generating antibodies described infra. (See, for example, Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998-4002 (1983)). The term "antigenic epitope," as used herein, is defined as a portion of a protein to which an antibody can immunospecifically bind its antigen as determined by any method well known in the art, for example, by the immunoassays described herein. Immunospecific binding excludes non-specific binding but does not necessarily exclude cross-reactivity with other antigens. Antigenic epitopes need not necessarily be immunogenic.

Fragments which function as epitopes may be produced by any conventional means. (See, e.g., Houghten, Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985), further described in U.S. Patent No. 4,631,211).

In the present invention, antigenic epitopes preferably contain a sequence of at least 4, at least 5, at least 6, at least 7, more preferably at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 20, at least 25, at least 30, at least 40, at least 50, and, most preferably, between about 15 to about 30 amino acids. Preferred polypeptides comprising immunogenic or antigenic epitopes are at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 amino acid residues in length. Additional non-exclusive preferred antigenic epitopes include the antigenic epitopes disclosed herein, as well as portions thereof. Antigenic epitopes are useful, for example, to raise antibodies, including monoclonal antibodies,

that specifically bind the epitope. Preferred antigenic epitopes include the antigenic epitopes disclosed herein, as well as any combination of two, three, four, five or more of these antigenic epitopes. Antigenic epitopes can be used as the target molecules in immunoassays. (See, for instance, Wilson et al., *Cell* 37:767-778 (1984); Sutcliffe et al., *Science* 219:660-666 (1983)).

Similarly, immunogenic epitopes can be used, for example, to induce antibodies according to methods well known in the art. (See, for instance, Sutcliffe et al., *supra*; Wilson et al., *supra*; Chow et al., *Proc. Natl. Acad. Sci. USA* 82:910-914; and Bittle et al., *J. Gen. Virol.* 66:2347-2354 (1985)). Preferred immunogenic epitopes include the immunogenic epitopes disclosed herein, as well as any combination of two, three, four, five or more of these immunogenic epitopes. The polypeptides comprising one or more immunogenic epitopes may be presented for eliciting an antibody response together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse), or, if the polypeptide is of sufficient length (at least about 25 amino acids), the polypeptide may be presented without a carrier. However, immunogenic epitopes comprising as few as 8 to 10 amino acids have been shown to be sufficient to raise antibodies capable of binding to, at the very least, linear epitopes in a denatured polypeptide (e.g., in Western blotting).

Epitope-bearing polypeptides of the present invention may be used to induce antibodies according to methods well known in the art including, but not limited to, in vivo immunization, in vitro immunization, and phage display methods. See, e.g., Sutcliffe et al., *supra*; Wilson et al., *supra*, and Bittle et al., *J. Gen. Virol.*, 66:2347-2354 (1985). If in vivo immunization is used, animals may be immunized with free peptide; however, anti-peptide antibody titer may be boosted by coupling the peptide to a macromolecular carrier, such as keyhole limpet hemacyanin (KLH) or tetanus toxoid. For instance, peptides containing cysteine residues may be coupled to a

carrier using a linker such as maleimidobenzoyl- N-hydroxysuccinimide ester (MBS), while other peptides may be coupled to carriers using a more general linking agent such as glutaraldehyde. Animals such as rabbits, rats and mice are immunized with either free or carrier- coupled peptides, for instance, by intraperitoneal and/or

5 intradermal-injection of emulsions containing about 100 μ g of peptide or carrier protein and Freund's adjuvant or any other adjuvant known for stimulating an immune response. Several booster injections may be needed, for instance, at intervals of about two weeks, to provide a useful titer of anti-peptide antibody which can be detected, for example, by ELISA assay using free peptide adsorbed to a solid

10 surface. The titer of anti-peptide antibodies in serum from an immunized animal may be increased by selection of anti-peptide antibodies, for instance, by adsorption to the peptide on a solid support and elution of the selected antibodies according to methods well known in the art.

As one of skill in the art will appreciate, and as discussed above, the

15 polypeptides of the present invention comprising an immunogenic or antigenic epitope can be fused to other polypeptide sequences. For example, the polypeptides of the present invention may be fused with the constant domain of immunoglobulins (IgA, IgE, IgG, IgM), or portions thereof (CH1, CH2, CH3, or any combination thereof and portions thereof) resulting in chimeric polypeptides. Such fusion proteins

20 may facilitate purification and may increase half-life in vivo. This has been shown for chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. See, e.g., EP 394,827; Traunecker et al., Nature, 331:84-86 (1988). Enhanced delivery of an antigen across the epithelial barrier to the

25 immune system has been demonstrated for antigens (e.g., insulin) conjugated to an FcRn binding partner such as IgG or Fc fragments (see, e.g., PCT Publications WO

96/22024 and WO 99/04813). IgG Fusion proteins that have a disulfide-linked dimeric structure due to the IgG portion desulfide bonds have also been found to be more efficient in binding and neutralizing other molecules than monomeric polypeptides or fragments thereof alone. See, e.g., Fountoulakis et al., J. Biochem., 5 270:3958-3964 (1995). Nucleic acids encoding the above epitopes can also be recombined with a gene of interest as an epitope tag (e.g., the hemagglutinin ("HA") tag or flag tag) to aid in detection and purification of the expressed polypeptide. For example, a system described by Janknecht et al. allows for the ready purification of non-denatured fusion proteins expressed in human cell lines (Janknecht et al., 1991, 10 Proc. Natl. Acad. Sci. USA 88:8972- 897). In this system, the gene of interest is subcloned into a vaccinia recombination plasmid such that the open reading frame of the gene is translationally fused to an amino-terminal tag consisting of six histidine residues. The tag serves as a matrix binding domain for the fusion protein. Extracts from cells infected with the recombinant vaccinia virus are loaded onto Ni²⁺ 15 nitriloacetic acid-agarose column and histidine-tagged proteins can be selectively eluted with imidazole-containing buffers.

Additional fusion proteins of the invention may be generated through the techniques of gene-shuffling, motif-shuffling, exon-shuffling, and/or codon-shuffling (collectively referred to as "DNA shuffling"). DNA shuffling may be employed to 20 modulate the activities of polypeptides of the invention, such methods can be used to generate polypeptides with altered activity, as well as agonists and antagonists of the polypeptides. See, generally, U.S. Patent Nos. 5,605,793; 5,811,238; 5,830,721; 5,834,252; and 5,837,458, and Patten et al., Curr. Opinion Biotechnol. 8:724-33 (1997); Harayama, Trends Biotechnol. 16(2):76-82 (1998); Hansson, et al., J. Mol. 25 Biol. 287:265-76 (1999); and Lorenzo and Blasco, Biotechniques 24(2):308- 13 (1998) (each of these patents and publications are hereby incorporated by reference in

its entirety). In one embodiment, alteration of polynucleotides corresponding to SEQ ID NO:X and the polypeptides encoded by these polynucleotides may be achieved by DNA shuffling. DNA shuffling involves the assembly of two or more DNA segments by homologous or site-specific recombination to generate variation in the polynucleotide sequence. In another embodiment, polynucleotides of the invention, or the encoded polypeptides, may be altered by being subjected to random mutagenesis by error-prone PCR, random nucleotide insertion or other methods prior to recombination. In another embodiment, one or more components, motifs, sections, parts, domains, fragments, etc., of a polynucleotide encoding a polypeptide of the invention may be recombined with one or more components, motifs, sections, parts, domains, fragments, etc. of one or more heterologous molecules.

Antibodies

Further polypeptides of the invention relate to antibodies and T-cell antigen receptors (TCR) which immunospecifically bind a polypeptide, polypeptide fragment, or variant of SEQ ID NO:Y, and/or an epitope, of the present invention (as determined by immunoassays well known in the art for assaying specific antibody-antigen binding). Antibodies of the invention include, but are not limited to, polyclonal, monoclonal, multispecific, human, humanized or chimeric antibodies, single chain antibodies, Fab fragments, F(ab') fragments, fragments produced by a Fab expression library, anti-idiotypic (anti-Id) antibodies (including, e.g., anti-Id antibodies to antibodies of the invention), and epitope-binding fragments of any of the above. The term "antibody," as used herein, refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, i.e., molecules that contain an antigen binding site that immunospecifically binds an antigen. The immunoglobulin molecules of the invention can be of any type (e.g., IgG, IgE, IgM,

IgD, IgA and IgY), class (e.g., IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2) or subclass of immunoglobulin molecule.

Most preferably the antibodies are human antigen-binding antibody fragments of the present invention and include, but are not limited to, Fab, Fab' and F(ab')₂, Fd, 5 single-chain Fvs (scFv), single-chain antibodies, disulfide-linked Fvs (sdFv) and fragments comprising either a VL or VH domain. Antigen-binding antibody fragments, including single-chain antibodies, may comprise the variable region(s) alone or in combination with the entirety or a portion of the following: hinge region, CH1, CH2, and CH3 domains. Also included in the invention are antigen-binding 10 fragments also comprising any combination of variable region(s) with a hinge region, CH1, CH2, and CH3 domains. The antibodies of the invention may be from any animal origin including birds and mammals. Preferably, the antibodies are human, murine (e.g., mouse and rat), donkey, ship rabbit, goat, guinea pig, camel, horse, or chicken. As used herein, "human" antibodies include antibodies having the amino 15 acid sequence of a human immunoglobulin and include antibodies isolated from human immunoglobulin libraries or from animals transgenic for one or more human immunoglobulin and that do not express endogenous immunoglobulins, as described infra and, for example in, U.S. Patent No. 5,939,598 by Kucherlapati et al.

The antibodies of the present invention may be monospecific, bispecific, 20 trispecific or of greater multispecificity. Multispecific antibodies may be specific for different epitopes of a polypeptide of the present invention or may be specific for both a polypeptide of the present invention as well as for a heterologous epitope, such as a heterologous polypeptide or solid support material. See, e.g., PCT publications WO 93/17715; WO 92/08802; WO 91/00360; WO 92/05793; Tutt, et al., J. Immunol. 25 147:60-69 (1991); U.S. Patent Nos. 4,474,893; 4,714,681; 4,925,648; 5,573,920; 5,601,819; Kostelny et al., J. Immunol. 148:1547-1553 (1992).

Antibodies of the present invention may be described or specified in terms of the epitope(s) or portion(s) of a polypeptide of the present invention which they recognize or specifically bind. The epitope(s) or polypeptide portion(s) may be specified as described herein, e.g., by N-terminal and C-terminal positions, by size in contiguous amino acid residues, or listed in the Tables and Figures. Antibodies which specifically bind any epitope or polypeptide of the present invention may also be excluded. Therefore, the present invention includes antibodies that specifically bind polypeptides of the present invention, and allows for the exclusion of the same.

Antibodies of the present invention may also be described or specified in terms of their cross-reactivity. Antibodies that do not bind any other analog, ortholog, or homolog of a polypeptide of the present invention are included. Antibodies that bind polypeptides with at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 65%, at least 60%, at least 55%, and at least 50% identity (as calculated using methods known in the art and described herein) to a polypeptide of the present invention are also included in the present invention. In specific embodiments, antibodies of the present invention cross-react with murine, rat and/or rabbit homologs of human proteins and the corresponding epitopes thereof. Antibodies that do not bind polypeptides with less than 95%, less than 90%, less than 85%, less than 80%, less than 75%, less than 70%, less than 65%, less than 60%, less than 55%, and less than 50% identity (as calculated using methods known in the art and described herein) to a polypeptide of the present invention are also included in the present invention. In a specific embodiment, the above-described cross-reactivity is with respect to any single specific antigenic or immunogenic polypeptide, or combination(s) of 2, 3, 4, 5, or more of the specific antigenic and/or immunogenic polypeptides disclosed herein. Further included in the present invention are antibodies which bind polypeptides encoded by polynucleotides

which hybridize to a polynucleotide of the present invention under stringent hybridization conditions (as described herein). Antibodies of the present invention may also be described or specified in terms of their binding affinity to a polypeptide of the invention. Preferred binding affinities include those with a dissociation constant or K_d less than 5×10^{-2} M, 10^{-2} M, 5×10^{-3} M, 10^{-3} M, 5×10^{-4} M, 10^{-4} M, 5×10^{-5} M, 10^{-5} M, 5×10^{-6} M, 10^{-6} M, 5×10^{-7} M, 10^{-7} M, 5×10^{-8} M, 10^{-8} M, 5×10^{-9} M, 10^{-9} M, 5×10^{-10} M, 10^{-10} M, 5×10^{-11} M, 10^{-11} M, 5×10^{-12} M, 10^{-12} M, 5×10^{-13} M, 10^{-13} M, 5×10^{-14} M, 10^{-14} M, 5×10^{-15} M, or 10^{-15} M.

The invention also provides antibodies that competitively inhibit binding of an antibody to an epitope of the invention as determined by any method known in the art for determining competitive binding, for example, the immunoassays described herein. In preferred embodiments, the antibody competitively inhibits binding to the epitope by at least 95%, at least 90%, at least 85 %, at least 80%, at least 75%, at least 70%, at least 60%, or at least 50%.

Antibodies of the present invention may act as agonists or antagonists of the polypeptides of the present invention. For example, the present invention includes antibodies which disrupt the receptor/ligand interactions with the polypeptides of the invention either partially or fully. Preferably, antibodies of the present invention bind an antigenic epitope disclosed herein, or a portion thereof. The invention features both receptor-specific antibodies and ligand-specific antibodies. The invention also features receptor-specific antibodies which do not prevent ligand binding but prevent receptor activation. Receptor activation (i.e., signaling) may be determined by techniques described herein or otherwise known in the art. For example, receptor activation can be determined by detecting the phosphorylation (e.g., tyrosine or serine/threonine) of the receptor or its substrate by immunoprecipitation followed by western blot analysis (for example, as described

supra). In specific embodiments, antibodies are provided that inhibit ligand activity or receptor activity by at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 60%, or at least 50% of the activity in absence of the antibody.

5 ----- The invention also features receptor-specific antibodies which both prevent ligand binding and receptor activation as well as antibodies that recognize the receptor-ligand complex, and, preferably, do not specifically recognize the unbound receptor or the unbound ligand. Likewise, included in the invention are neutralizing antibodies which bind the ligand and prevent binding of the ligand to the receptor, as
10 well as antibodies which bind the ligand, thereby preventing receptor activation, but do not prevent the ligand from binding the receptor. Further included in the invention are antibodies which activate the receptor. These antibodies may act as receptor agonists, i.e., potentiate or activate either all or a subset of the biological activities of the ligand-mediated receptor activation, for example, by inducing dimerization of the
15 receptor. The antibodies may be specified as agonists, antagonists or inverse agonists for biological activities comprising the specific biological activities of the peptides of the invention disclosed herein. The above antibody agonists can be made using methods known in the art. See, e.g., PCT publication WO 96/40281; U.S. Patent No. 5,811,097; Deng et al., Blood 92(6):1981-1988 (1998); Chen et al., Cancer Res.
20 58(16):3668-3678 (1998); Harrop et al., J. Immunol. 161(4):1786-1794 (1998); Zhu et al., Cancer Res. 58(15):3209-3214 (1998); Yoon et al., J. Immunol. 160(7):3170-3179 (1998); Prat et al., J. Cell. Sci. 111(Pt2):237-247 (1998); Pitard et al., J. Immunol. Methods 205(2):177-190 (1997); Liautard et al., Cytokine 9(4):233-241 (1997); Carlson et al., J. Biol. Chem. 272(17):11295-11301 (1997); Taryman et al.,
25 Neuron 14(4):755-762 (1995); Muller et al., Structure 6(9):1153-1167 (1998);

Bartunek et al., Cytokine 8(1):14-20 (1996) (which are all incorporated by reference herein in their entireties).

Antibodies of the present invention may be used, for example, but not limited to, to purify, detect, and target the polypeptides of the present invention, including
5 both in vitro and in vivo diagnostic and therapeutic methods. For example, the antibodies have use in immunoassays for qualitatively and quantitatively measuring levels of the polypeptides of the present invention in biological samples. See, e.g., Harlow et al., Antibodies: A Laboratory Manual, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988) (incorporated by reference herein in its entirety).

10 As discussed in more detail below, the antibodies of the present invention may be used either alone or in combination with other compositions. The antibodies may further be recombinantly fused to a heterologous polypeptide at the N- or C-terminus or chemically conjugated (including covalently and non-covalently conjugations) to polypeptides or other compositions. For example, antibodies of the present invention
15 may be recombinantly fused or conjugated to molecules useful as labels in detection assays and effector molecules such as heterologous polypeptides, drugs, radionuclides, or toxins. See, e.g., PCT publications WO 92/08495; WO 91/14438; WO 89/12624; U.S. Patent No. 5,314,995; and EP 396,387.

The antibodies of the invention include derivatives that are modified, i.e., by
20 the covalent attachment of any type of molecule to the antibody such that covalent attachment does not prevent the antibody from generating an anti-idiotypic response. For example, but not by way of limitation, the antibody derivatives include antibodies that have been modified, e.g., by glycosylation, acetylation, pegylation, phosphorylation, amidation, derivatization by known protecting/blocking groups,
25 proteolytic cleavage, linkage to a cellular ligand or other protein, etc. Any of numerous chemical modifications may be carried out by known techniques,

including, but not limited to specific chemical cleavage, acetylation, formylation, metabolic synthesis of tunicamycin, etc. Additionally, the derivative may contain one or more non-classical amino acids.

The antibodies of the present invention may be generated by any suitable method known in the art. Polyclonal antibodies to an antigen-of-interest can be produced by various procedures well known in the art. For example, a polypeptide of the invention can be administered to various host animals including, but not limited to, rabbits, mice, rats, etc. to induce the production of sera containing polyclonal antibodies specific for the antigen. Various adjuvants may be used to increase the immunological response, depending on the host species, and include but are not limited to, Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, and potentially useful human adjuvants such as BCG (bacille Calmette-Guerin) and corynebacterium parvum. Such adjuvants are also well known in the art.

Monoclonal antibodies can be prepared using a wide variety of techniques known in the art including the use of hybridoma, recombinant, and phage display technologies, or a combination thereof. For example, monoclonal antibodies can be produced using hybridoma techniques including those known in the art and taught, for example, in Harlow et al., *Antibodies: A Laboratory Manual*, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988); Hammerling, et al., in: *Monoclonal Antibodies and T-Cell Hybridomas* 563-681 (Elsevier, N.Y., 1981) (said references incorporated by reference in their entireties). The term "monoclonal antibody" as used herein is not limited to antibodies produced through hybridoma technology. The term "monoclonal antibody" refers to an antibody that is derived from a single clone,

including any eukaryotic, prokaryotic, or phage clone, and not the method by which it is produced.

Methods for producing and screening for specific antibodies using hybridoma technology are routine and well known in the art and are discussed in detail in the

5 Examples (e.g., Example 16). In a non-limiting example, mice can be immunized with a polypeptide of the invention or a cell expressing such peptide. Once an immune response is detected, e.g., antibodies specific for the antigen are detected in the mouse serum, the mouse spleen is harvested and splenocytes isolated. The splenocytes are then fused by well known techniques to any suitable myeloma cells,

10 for example cells from cell line SP20 available from the ATCC. Hybridomas are selected and cloned by limited dilution. The hybridoma clones are then assayed by methods known in the art for cells that secrete antibodies capable of binding a polypeptide of the invention. Ascites fluid, which generally contains high levels of antibodies, can be generated by immunizing mice with positive hybridoma clones.

15 Accordingly, the present invention provides methods of generating monoclonal antibodies as well as antibodies produced by the method comprising culturing a hybridoma cell secreting an antibody of the invention wherein, preferably, the hybridoma is generated by fusing splenocytes isolated from a mouse immunized with an antigen of the invention with myeloma cells and then screening the

20 hybridomas resulting from the fusion for hybridoma clones that secrete an antibody able to bind a polypeptide of the invention.

Antibody fragments which recognize specific epitopes may be generated by known techniques. For example, Fab and F(ab')₂ fragments of the invention may be produced by proteolytic cleavage of immunoglobulin molecules, using enzymes such

25 as papain (to produce Fab fragments) or pepsin (to produce F(ab')₂ fragments).

F(ab')₂ fragments contain the variable region, the light chain constant region and the CH1 domain of the heavy chain.

For example, the antibodies of the present invention can also be generated using various phage display methods known in the art. In phage display methods, functional antibody domains are displayed on the surface of phage particles which carry the polynucleotide sequences encoding them. In a particular embodiment, such phage can be utilized to display antigen binding domains expressed from a repertoire or combinatorial antibody library (e.g., human or murine). Phage expressing an antigen binding domain that binds the antigen of interest can be selected or identified with antigen, e.g., using labeled antigen or antigen bound or captured to a solid surface or bead. Phage used in these methods are typically filamentous phage including fd and M13 binding domains expressed from phage with Fab, Fv or disulfide stabilized Fv antibody domains recombinantly fused to either the phage gene III or gene VIII protein. Examples of phage display methods that can be used to make the antibodies of the present invention include those disclosed in Brinkman et al., *J. Immunol. Methods* 182:41-50 (1995); Ames et al., *J. Immunol. Methods* 184:177-186 (1995); Kettleborough et al., *Eur. J. Immunol.* 24:952-958 (1994); Persic et al., *Gene* 187 9-18 (1997); Burton et al., *Advances in Immunology* 57:191-280 (1994); PCT application No. PCT/GB91/01134; PCT publications WO 90/02809; WO 91/10737; WO 92/01047; WO 92/18619; WO 93/11236; WO 95/15982; WO 95/20401; and U.S. Patent Nos. 5,698,426; 5,223,409; 5,403,484; 5,580,717; 5,427,908; 5,750,753; 5,821,047; 5,571,698; 5,427,908; 5,516,637; 5,780,225; 5,658,727; 5,733,743 and 5,969,108; each of which is incorporated herein by reference in its entirety.

As described in the above references, after phage selection, the antibody coding regions from the phage can be isolated and used to generate whole antibodies,

including human antibodies, or any other desired antigen binding fragment, and expressed in any desired host, including mammalian cells, insect cells, plant cells, yeast, and bacteria, e.g., as described in detail below. For example, techniques to recombinantly produce Fab, Fab' and F(ab')₂ fragments can also be employed using
5 methods known in the art such as those disclosed in PCT publication WO 92/22324; Mullinax et al., *BioTechniques* 12(6):864-869 (1992); and Sawai et al., *AJRI* 34:26-34 (1995); and Better et al., *Science* 240:1041-1043 (1988) (said references incorporated by reference in their entirety).

Examples of techniques which can be used to produce single-chain Fvs and
10 antibodies include those described in U.S. Patents 4,946,778 and 5,258,498; Huston et al., *Methods in Enzymology* 203:46-88 (1991); Shu et al., *PNAS* 90:7995-7999 (1993); and Skerra et al., *Science* 240:1038-1040 (1988). For some uses, including in vivo use of antibodies in humans and in vitro detection assays, it may be preferable to use chimeric, humanized, or human antibodies. A chimeric antibody is a molecule
15 in which different portions of the antibody are derived from different animal species, such as antibodies having a variable region derived from a murine monoclonal antibody and a human immunoglobulin constant region. Methods for producing chimeric antibodies are known in the art. See e.g., Morrison, *Science* 229:1202 (1985); Oi et al., *BioTechniques* 4:214 (1986); Gillies et al., (1989) *J. Immunol.*
20 *Methods* 125:191-202; U.S. Patent Nos. 5,807,715; 4,816,567; and 4,816,397, which are incorporated herein by reference in their entirety. Humanized antibodies are antibody molecules from non-human species antibody that binds the desired antigen having one or more complementarity determining regions (CDRs) from the non-human species and a framework regions from a human immunoglobulin molecule.
25 Often, framework residues in the human framework regions will be substituted with the corresponding residue from the CDR donor antibody to alter, preferably improve,

antigen binding. These framework substitutions are identified by methods well known in the art, e.g., by modeling of the interactions of the CDR and framework residues to identify framework residues important for antigen binding and sequence comparison to identify unusual framework residues at particular positions. (See, e.g.,

5 Queen et al., U.S. Patent No. 5,585,089; Riechmann et al., Nature 332:323 (1988), which are incorporated herein by reference in their entireties.) Antibodies can be humanized using a variety of techniques known in the art including, for example, CDR-grafting (EP 239,400; PCT publication WO 91/09967; U.S. Patent Nos. 5,225,539; 5,530,101; and 5,585,089), veneering or resurfacing (EP 592,106; EP

10 519,596; Padlan, Molecular Immunology 28(4/5):489-498 (1991); Studnicka et al., Protein Engineering 7(6):805-814 (1994); Roguska. et al., PNAS 91:969-973 (1994)), and chain shuffling (U.S. Patent No. 5,565,332).

Completely human antibodies are particularly desirable for therapeutic treatment of human patients. Human antibodies can be made by a variety of methods

15 known in the art including phage display methods described above using antibody libraries derived from human immunoglobulin sequences. See also, U.S. Patent Nos. 4,444,887 and 4,716,111; and PCT publications WO 98/46645, WO 98/50433, WO 98/24893, WO 98/16654, WO 96/34096, WO 96/33735, and WO 91/10741; each of which is incorporated herein by reference in its entirety.

20 Human antibodies can also be produced using transgenic mice which are incapable of expressing functional endogenous immunoglobulins, but which can express human immunoglobulin genes. For example, the human heavy and light chain immunoglobulin gene complexes may be introduced randomly or by homologous recombination into mouse embryonic stem cells. Alternatively, the

25 human variable region, constant region, and diversity region may be introduced into mouse embryonic stem cells in addition to the human heavy and light chain genes.

The mouse heavy and light chain immunoglobulin genes may be rendered non-functional separately or simultaneously with the introduction of human immunoglobulin loci by homologous recombination. In particular, homozygous deletion of the JH region prevents endogenous antibody production. The modified
5 embryonic stem cells are expanded and microinjected into blastocysts to produce chimeric mice. The chimeric mice are then bred to produce homozygous offspring which express human antibodies. The transgenic mice are immunized in the normal fashion with a selected antigen, e.g., all or a portion of a polypeptide of the invention. Monoclonal antibodies directed against the antigen can be obtained from the
10 immunized, transgenic mice using conventional hybridoma technology. The human immunoglobulin transgenes harbored by the transgenic mice rearrange during B cell differentiation, and subsequently undergo class switching and somatic mutation. Thus, using such a technique, it is possible to produce therapeutically useful IgG, IgA, IgM and IgE antibodies. For an overview of this technology for producing human
15 antibodies, see Lonberg and Huszar, *Int. Rev. Immunol.* 13:65-93 (1995). For a detailed discussion of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, see, e.g., PCT publications WO 98/24893; WO 92/01047; WO 96/34096; WO 96/33735; European Patent No. 0 598 877; U.S. Patent Nos. 5,413,923; 5,625,126; 5,633,425; 5,569,825;
20 5,661,016; 5,545,806; 5,814,318; 5,885,793; 5,916,771; and 5,939,598, which are incorporated by reference herein in their entirety. In addition, companies such as Abgenix, Inc. (Freemont, CA) and Genpharm (San Jose, CA) can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above.

25 Completely human antibodies which recognize a selected epitope can be generated using a technique referred to as "guided selection." In this approach a

selected non-human monoclonal antibody, e.g., a mouse antibody, is used to guide the selection of a completely human antibody recognizing the same epitope. (Jespers et al., Bio/technology 12:899-903 (1988)).

Further, antibodies to the polypeptides of the invention can, in turn, be utilized to generate anti-idiotypic antibodies that "mimic" polypeptides of the invention using techniques well known to those skilled in the art. (See, e.g., Greenspan & Bona, FASEB J. 7(5):437-444; (1989) and Nissinoff, J. Immunol. 147(8):2429-2438 (1991)). For example, antibodies which bind to and competitively inhibit polypeptide multimerization and/or binding of a polypeptide of the invention to a ligand can be used to generate anti-idiotypes that "mimic" the polypeptide multimerization and/or binding domain and, as a consequence, bind to and neutralize polypeptide and/or its ligand. Such neutralizing anti-idiotypes or Fab fragments of such anti-idiotypes can be used in therapeutic regimens to neutralize polypeptide ligand. For example, such anti-idiotypic antibodies can be used to bind a polypeptide of the invention and/or to bind its ligands/receptors, and thereby block its biological activity.

Polynucleotides Encoding Antibodies

The invention further provides polynucleotides comprising a nucleotide sequence encoding an antibody of the invention and fragments thereof. The invention also encompasses polynucleotides that hybridize under stringent or lower stringency hybridization conditions, e.g., as defined supra, to polynucleotides that encode an antibody, preferably, that specifically binds to a polypeptide of the invention, preferably, an antibody that binds to a polypeptide having the amino acid sequence of SEQ ID NO:Y.

The polynucleotides may be obtained, and the nucleotide sequence of the polynucleotides determined, by any method known in the art. For example, if the

nucleotide sequence of the antibody is known, a polynucleotide encoding the antibody may be assembled from chemically synthesized oligonucleotides (e.g., as described in Kutmeier et al., *BioTechniques* 17:242 (1994)), which, briefly, involves the synthesis of overlapping oligonucleotides containing portions of the sequence
5 encoding the antibody, annealing and ligating of those oligonucleotides, and then amplification of the ligated oligonucleotides by PCR.

Alternatively, a polynucleotide encoding an antibody may be generated from nucleic acid from a suitable source. If a clone containing a nucleic acid encoding a particular antibody is not available, but the sequence of the antibody molecule is
10 known, a nucleic acid encoding the immunoglobulin may be chemically synthesized or obtained from a suitable source (e.g., an antibody cDNA library, or a cDNA library generated from, or nucleic acid, preferably poly A+ RNA, isolated from, any tissue or cells expressing the antibody, such as hybridoma cells selected to express an antibody of the invention) by PCR amplification using synthetic primers hybridizable
15 to the 3' and 5' ends of the sequence or by cloning using an oligonucleotide probe specific for the particular gene sequence to identify, e.g., a cDNA clone from a cDNA library that encodes the antibody. Amplified nucleic acids generated by PCR may then be cloned into replicable cloning vectors using any method well known in the art.

20 . Once the nucleotide sequence and corresponding amino acid sequence of the antibody is determined, the nucleotide sequence of the antibody may be manipulated using methods well known in the art for the manipulation of nucleotide sequences, e.g., recombinant DNA techniques, site directed mutagenesis, PCR, etc. (see, for example, the techniques described in Sambrook et al., 1990, *Molecular Cloning, A Laboratory Manual*, 2d Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, NY and Ausubel et al., eds., 1998, *Current Protocols in Molecular Biology*, John
25

Wiley & Sons, NY, which are both incorporated by reference herein in their entireties), to generate antibodies having a different amino acid sequence, for example to create amino acid substitutions, deletions, and/or insertions.

In a specific embodiment, the amino acid sequence of the heavy and/or light chain variable domains may be inspected to identify the sequences of the complementarity determining regions (CDRs) by methods that are well known in the art, e.g., by comparison to known amino acid sequences of other heavy and light chain variable regions to determine the regions of sequence hypervariability. Using routine recombinant DNA techniques, one or more of the CDRs may be inserted within framework regions, e.g., into human framework regions to humanize a non-human antibody, as described supra. The framework regions may be naturally occurring or consensus framework regions, and preferably human framework regions (see, e.g., Chothia et al., J. Mol. Biol. 278: 457-479 (1998) for a listing of human framework regions). Preferably, the polynucleotide generated by the combination of the framework regions and CDRs encodes an antibody that specifically binds a polypeptide of the invention. Preferably, as discussed supra, one or more amino acid substitutions may be made within the framework regions, and, preferably, the amino acid substitutions improve binding of the antibody to its antigen. Additionally, such methods may be used to make amino acid substitutions or deletions of one or more variable region cysteine residues participating in an intrachain disulfide bond to generate antibody molecules lacking one or more intrachain disulfide bonds. Other alterations to the polynucleotide are encompassed by the present invention and within the skill of the art.

In addition, techniques developed for the production of "chimeric antibodies" (Morrison et al., Proc. Natl. Acad. Sci. 81:851-855 (1984); Neuberger et al., Nature 312:604-608 (1984); Takeda et al., Nature 314:452-454 (1985)) by splicing genes

from a mouse antibody molecule of appropriate antigen specificity together with genes from a human antibody molecule of appropriate biological activity can be used. As described supra, a chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived
5 from a murine mAb and a human immunoglobulin constant region, e.g., humanized antibodies.

Alternatively, techniques described for the production of single chain antibodies (U.S. Patent No. 4,946,778; Bird, Science 242:423- 42 (1988); Huston et al., Proc. Natl. Acad. Sci. USA 85:5879-5883 (1988); and Ward et al., Nature
10 334:544-54 (1989)) can be adapted to produce single chain antibodies. Single chain antibodies are formed by linking the heavy and light chain fragments of the Fv region via an amino acid bridge, resulting in a single chain polypeptide. Techniques for the assembly of functional Fv fragments in E. coli may also be used (Skerra et al., Science 242:1038- 1041 (1988)).

15

Methods of Producing Antibodies

The antibodies of the invention can be produced by any method known in the art for the synthesis of antibodies, in particular, by chemical synthesis or preferably, by recombinant expression techniques.

20 Recombinant expression of an antibody of the invention, or fragment, derivative or analog thereof, (e.g., a heavy or light chain of an antibody of the invention or a single chain antibody of the invention), requires construction of an expression vector containing a polynucleotide that encodes the antibody. Once a polynucleotide encoding an antibody molecule or a heavy or light chain of an
25 antibody, or portion thereof (preferably containing the heavy or light chain variable domain), of the invention has been obtained, the vector for the production of the

antibody molecule may be produced by recombinant DNA technology using techniques well known in the art. Thus, methods for preparing a protein by expressing a polynucleotide containing an antibody encoding nucleotide sequence are described herein. Methods which are well known to those skilled in the art can be

5 used to construct expression vectors containing antibody coding sequences and appropriate transcriptional and translational control signals. These methods include, for example, in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. The invention, thus, provides replicable vectors comprising a nucleotide sequence encoding an antibody molecule of the invention, or a heavy or

10 light chain thereof, or a heavy or light chain variable domain, operably linked to a promoter. Such vectors may include the nucleotide sequence encoding the constant region of the antibody molecule (see, e.g., PCT Publication WO 86/05807; PCT Publication WO 89/01036; and U.S. Patent No. 5,122,464) and the variable domain of the antibody may be cloned into such a vector for expression of the entire heavy or

15 light chain.

The expression vector is transferred to a host cell by conventional techniques and the transfected cells are then cultured by conventional techniques to produce an antibody of the invention. Thus, the invention includes host cells containing a polynucleotide encoding an antibody of the invention; or a heavy or light chain

20 thereof, or a single chain antibody of the invention, operably linked to a heterologous promoter. In preferred embodiments for the expression of double-chained antibodies, vectors encoding both the heavy and light chains may be co-expressed in the host cell for expression of the entire immunoglobulin molecule, as detailed below.

A variety of host-expression vector systems may be utilized to express the

25 antibody molecules of the invention. Such host-expression systems represent vehicles by which the coding sequences of interest may be produced and subsequently

purified, but also represent cells which may, when transformed or transfected with the appropriate nucleotide coding sequences, express an antibody molecule of the invention in situ. These include but are not limited to microorganisms such as bacteria (e.g., *E. coli*, *B. subtilis*) transformed with recombinant bacteriophage DNA, 5 plasmid DNA or cosmid DNA expression vectors containing antibody coding sequences; yeast (e.g., *Saccharomyces*, *Pichia*) transformed with recombinant yeast expression vectors containing antibody coding sequences; insect cell systems infected with recombinant virus expression vectors (e.g., baculovirus) containing antibody coding sequences; plant cell systems infected with recombinant virus 10 expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expression vectors (e.g., Ti plasmid) containing antibody coding sequences; or mammalian cell systems (e.g., COS, CHO, BHK, 293, 3T3 cells) harboring recombinant expression constructs containing promoters derived from the genome of mammalian cells (e.g., metallothionein 15 promoter) or from mammalian viruses (e.g., the adenovirus late promoter; the vaccinia virus 7.5K promoter). Preferably, bacterial cells such as *Escherichia coli*, and more preferably, eukaryotic cells, especially for the expression of whole recombinant antibody molecule, are used for the expression of a recombinant antibody molecule. For example, mammalian cells such as Chinese hamster ovary 20 cells (CHO), in conjunction with a vector such as the major intermediate early gene promoter element from human cytomegalovirus is an effective expression system for antibodies (Foecking et al., *Gene* 45:101 (1986); Cockett et al., *Bio/Technology* 8:2 (1990)).

In bacterial systems, a number of expression vectors may be advantageously 25 selected depending upon the use intended for the antibody molecule being expressed. For example, when a large quantity of such a protein is to be produced, for the

generation of pharmaceutical compositions of an antibody molecule, vectors which direct the expression of high levels of fusion protein products that are readily purified may be desirable. Such vectors include, but are not limited, to the *E. coli* expression vector pUR278 (Ruther et al., EMBO J. 2:1791 (1983)), in which the antibody coding sequence may be ligated individually into the vector in frame with the lac Z coding region so that a fusion protein is produced; pIN vectors (Inouye & Inouye, Nucleic Acids Res. 13:3101-3109 (1985); Van Heeke & Schuster, J. Biol. Chem. 24:5503-5509 (1989)); and the like. pGEX vectors may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption and binding to matrix glutathione-agarose beads followed by elution in the presence of free glutathione. The pGEX vectors are designed to include thrombin or factor Xa protease cleavage sites so that the cloned target gene product can be released from the GST moiety.

In an insect system, *Autographa californica* nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes. The virus grows in *Spodoptera frugiperda* cells. The antibody coding sequence may be cloned individually into non-essential regions (for example the polyhedrin gene) of the virus and placed under control of an AcNPV promoter (for example the polyhedrin promoter).

In mammalian host cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, the antibody coding sequence of interest may be ligated to an adenovirus transcription/translation control complex, e.g., the late promoter and tripartite leader sequence. This chimeric gene may then be inserted in the adenovirus genome by in vitro or in vivo recombination. Insertion in a non-essential region of the viral genome (e.g., region

E1 or E3) will result in a recombinant virus that is viable and capable of expressing the antibody molecule in infected hosts. (e.g., see Logan & Shenk, Proc. Natl. Acad. Sci. USA 81:355-359 (1984)). Specific initiation signals may also be required for efficient translation of inserted antibody coding sequences. These signals include the

5 ATG initiation codon and adjacent sequences. Furthermore, the initiation codon must be in phase with the reading frame of the desired coding sequence to ensure translation of the entire insert. These exogenous translational control signals and initiation codons can be of a variety of origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of appropriate

10 transcription enhancer elements, transcription terminators, etc. (see Bittner et al., Methods in Enzymol. 153:51-544 (1987)).

In addition, a host cell strain may be chosen which modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Such modifications (e.g., glycosylation) and processing (e.g.,

15 cleavage) of protein products may be important for the function of the protein. Different host cells have characteristic and specific mechanisms for the post-translational processing and modification of proteins and gene products. Appropriate cell lines or host systems can be chosen to ensure the correct modification and processing of the foreign protein expressed. To this end, eukaryotic host cells which

20 possess the cellular machinery for proper processing of the primary transcript, glycosylation, and phosphorylation of the gene product may be used. Such mammalian host cells include but are not limited to CHO, VERO, BHK, HeLa, COS, MDCK, 293, 3T3, WI38, and in particular, breast cancer cell lines such as, for example, BT483, Hs578T, HTB2, BT20 and T47D, and normal mammary gland cell

25 line such as, for example, CRL7030 and Hs578Bst.

For long-term, high-yield production of recombinant proteins, stable expression is preferred. For example, cell lines which stably express the antibody molecule may be engineered. Rather than using expression vectors which contain viral origins of replication, host cells can be transformed with DNA controlled by appropriate expression control elements (e.g., promoter, enhancer, sequences, transcription terminators, polyadenylation sites, etc.), and a selectable marker. Following the introduction of the foreign DNA, engineered cells may be allowed to grow for 1-2 days in an enriched media, and then are switched to a selective media. The selectable marker in the recombinant plasmid confers resistance to the selection and allows cells to stably integrate the plasmid into their chromosomes and grow to form foci which in turn can be cloned and expanded into cell lines. This method may advantageously be used to engineer cell lines which express the antibody molecule. Such engineered cell lines may be particularly useful in screening and evaluation of compounds that interact directly or indirectly with the antibody molecule.

15 A number of selection systems may be used, including but not limited to the herpes simplex virus thymidine kinase (Wigler et al., Cell 11:223 (1977)), hypoxanthine-guanine phosphoribosyltransferase (Szybalska & Szybalski, Proc. Natl. Acad. Sci. USA 48:202 (1992)), and adenine phosphoribosyltransferase (Lowy et al., Cell 22:817 (1980)) genes can be employed in tk-, hgp^rt- or ap^rt- cells, respectively.

20 Also, antimetabolite resistance can be used as the basis of selection for the following genes: dhfr, which confers resistance to methotrexate (Wigler et al., Natl. Acad. Sci. USA 77:357 (1980); O'Hare et al., Proc. Natl. Acad. Sci. USA 78:1527 (1981)); gpt, which confers resistance to mycophenolic acid (Mulligan & Berg, Proc. Natl. Acad. Sci. USA 78:2072 (1981)); neo, which confers resistance to the aminoglycoside G-

25 418 Clinical Pharmacy 12:488-505; Wu and Wu, Biotherapy 3:87-95 (1991); Tolstoshev, Ann. Rev. Pharmacol. Toxicol. 32:573-596 (1993); Mulligan, Science

260:926-932 (1993); and Morgan and Anderson, *Ann. Rev. Biochem.* 62:191-217 (1993); May, 1993, *TIB TECH* 11(5):155-215); and hyg^r, which confers resistance to hygromycin (Santerre et al., *Gene* 30:147 (1984)). Methods commonly known in the art of recombinant DNA technology may be routinely applied to select the desired recombinant clone, and such methods are described, for example, in Ausubel et al. (eds.), *Current Protocols in Molecular Biology*, John Wiley & Sons, NY (1993); Kriegler, *Gene Transfer and Expression, A Laboratory Manual*, Stockton Press, NY (1990); and in Chapters 12 and 13, Dracopoli et al. (eds), *Current Protocols in Human Genetics*, John Wiley & Sons, NY (1994); Colberre-Garapin et al., *J. Mol. Biol.* 150:1 (1981), which are incorporated by reference herein in their entireties.

The expression levels of an antibody molecule can be increased by vector amplification (for a review, see Bebbington and Hentschel, *The use of vectors based on gene amplification for the expression of cloned genes in mammalian cells in DNA cloning*, Vol.3. (Academic Press, New York, 1987)). When a marker in the vector system expressing antibody is amplifiable, increase in the level of inhibitor present in culture of host cell will increase the number of copies of the marker gene. Since the amplified region is associated with the antibody gene, production of the antibody will also increase (Crouse et al., *Mol. Cell. Biol.* 3:257 (1983)).

The host cell may be co-transfected with two expression vectors of the invention, the first vector encoding a heavy chain derived polypeptide and the second vector encoding a light chain derived polypeptide. The two vectors may contain identical selectable markers which enable equal expression of heavy and light chain polypeptides. Alternatively, a single vector may be used which encodes, and is capable of expressing, both heavy and light chain polypeptides. In such situations, the light chain should be placed before the heavy chain to avoid an excess of toxic free heavy chain (Proudfoot, *Nature* 322:52 (1986); Kohler, *Proc. Natl. Acad. Sci.*

USA 77:2197 (1980)). The coding sequences for the heavy and light chains may comprise cDNA or genomic DNA.

Once an antibody molecule of the invention has been produced by an animal, chemically synthesized, or recombinantly expressed, it may be purified by any method known in the art for purification of an immunoglobulin molecule, for example, by chromatography (e.g., ion exchange, affinity, particularly by affinity for the specific antigen after Protein A, and sizing column chromatography), centrifugation, differential solubility, or by any other standard technique for the purification of proteins. In addition, the antibodies of the present invention or fragments thereof can be fused to heterologous polypeptide sequences described herein or otherwise known in the art, to facilitate purification.

The present invention encompasses antibodies recombinantly fused or chemically conjugated (including both covalently and non-covalently conjugations) to a polypeptide (or portion thereof, preferably at least 10, 20, 30, 40, 50, 60, 70, 80, 90 or 100 amino acids of the polypeptide) of the present invention to generate fusion proteins. The fusion does not necessarily need to be direct, but may occur through linker sequences. The antibodies may be specific for antigens other than polypeptides (or portion thereof, preferably at least 10, 20, 30, 40, 50, 60, 70, 80, 90 or 100 amino acids of the polypeptide) of the present invention. For example, antibodies may be used to target the polypeptides of the present invention to particular cell types, either in vitro or in vivo, by fusing or conjugating the polypeptides of the present invention to antibodies specific for particular cell surface receptors. Antibodies fused or conjugated to the polypeptides of the present invention may also be used in in vitro immunoassays and purification methods using methods known in the art. See e.g., Harbor et al., supra, and PCT publication WO 93/21232; EP 439,095; Naramura et al., Immunol. Lett. 39:91-99 (1994); U.S. Patent 5,474,981; Gillies et al., PNAS

89:1428-1432 (1992); Fell et al., J. Immunol. 146:2446-2452(1991), which are incorporated by reference in their entirety.

The present invention further includes compositions comprising the polypeptides of the present invention fused or conjugated to antibody domains other than the variable regions. For example, the polypeptides of the present invention may be fused or conjugated to an antibody Fc region, or portion thereof. The antibody portion fused to a polypeptide of the present invention may comprise the constant region, hinge region, CH1 domain, CH2 domain, and CH3 domain or any combination of whole domains or portions thereof. The polypeptides may also be fused or conjugated to the above antibody portions to form multimers. For example, Fc portions fused to the polypeptides of the present invention can form dimers through disulfide bonding between the Fc portions. Higher multimeric forms can be made by fusing the polypeptides to portions of IgA and IgM. Methods for fusing or conjugating the polypeptides of the present invention to antibody portions are known in the art. See, e.g., U.S. Patent Nos. 5,336,603; 5,622,929; 5,359,046; 5,349,053; 5,447,851; 5,112,946; EP 307,434; EP 367,166; PCT publications WO 96/04388; WO 91/06570; Ashkenazi et al., Proc. Natl. Acad. Sci. USA 88:10535-10539 (1991); Zheng et al., J. Immunol. 154:5590-5600 (1995); and Vil et al., Proc. Natl. Acad. Sci. USA 89:11337-11341(1992) (said references incorporated by reference in their entirety).

As discussed, supra, the polypeptides corresponding to a polypeptide, polypeptide fragment, or a variant of SEQ ID NO:Y may be fused or conjugated to the above antibody portions to increase the in vivo half life of the polypeptides or for use in immunoassays using methods known in the art. Further, the polypeptides corresponding to SEQ ID NO:Y may be fused or conjugated to the above antibody portions to facilitate purification. One reported example describes chimeric proteins

consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. (EP 394,827; Traunecker et al., *Nature* 331:84-86 (1988)). The polypeptides of the present invention fused or conjugated to an antibody having

5 disulfide- linked dimeric structures (due to the IgG) may also be more efficient in binding and neutralizing other molecules, than the monomeric secreted protein or protein fragment alone. (Fountoulakis et al., *J. Biochem.* 270:3958-3964 (1995)). In many cases, the Fc part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties. (EP A

10 232,262). Alternatively, deleting the Fc part after the fusion protein has been expressed, detected, and purified, would be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for immunizations. In drug discovery, for example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to

15 identify antagonists of hIL-5. (See, Bennett et al., *J. Molecular Recognition* 8:52-58 (1995); Johanson et al., *J. Biol. Chem.* 270:9459-9471 (1995)).

Moreover, the antibodies or fragments thereof of the present invention can be fused to marker sequences, such as a peptide to facilitate purification. In preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the

20 tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., *Proc. Natl. Acad. Sci. USA* 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein. Other peptide tags useful for purification include, but are not limited to, the "HA" tag, which

25 corresponds to an epitope derived from the influenza hemagglutinin protein (Wilson et al., *Cell* 37:767 (1984)) and the "flag" tag.

The present invention further encompasses antibodies or fragments thereof conjugated to a diagnostic or therapeutic agent. The antibodies can be used diagnostically to, for example, monitor the development or progression of a tumor as part of a clinical testing procedure to, e.g., determine the efficacy of a given

5 treatment regimen. Detection can be facilitated by coupling the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, radioactive materials, positron emitting metals using various positron emission tomographies, and nonradioactive paramagnetic metal ions. The detectable

10 substance may be coupled or conjugated either directly to the antibody (or fragment thereof) or indirectly, through an intermediate (such as, for example, a linker known in the art) using techniques known in the art. See, for example, U.S. Patent No. 4,741,900 for metal ions which can be conjugated to antibodies for use as diagnostics according to the present invention. Examples of suitable enzymes include horseradish

15 peroxidase, alkaline phosphatase, beta-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material

20 includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin; and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{111}In or ^{99}Tc .

Further, an antibody or fragment thereof may be conjugated to a therapeutic moiety such as a cytotoxin, e.g., a cytostatic or cytotoxic agent, a therapeutic agent or

25 a radioactive metal ion, e.g., alpha-emitters such as, for example, ^{213}Bi . A cytotoxin or cytotoxic agent includes any agent that is detrimental to cells. Examples include

paclitaxol, cytochalasin B, gramicidin D, ethidium bromide, emetine, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin, dihydroxy anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and

5 puromycin and analogs or homologs thereof. Therapeutic agents include, but are not limited to, antimetabolites (e.g., methotrexate, 6-mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil decarbazine), alkylating agents (e.g., mechlorethamine, thioepa chlorambucil, melphalan, carmustine (BSNU) and lomustine (CCNU), cyclophosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C, and cis-

10 dichlorodiamine platinum (II) (DDP) cisplatin), anthracyclines (e.g., daunorubicin (formerly daunomycin) and doxorubicin), antibiotics (e.g., dactinomycin (formerly actinomycin), bleomycin, mithramycin, and anthramycin (AMC)), and anti-mitotic agents (e.g., vincristine and vinblastine).

The conjugates of the invention can be used for modifying a given biological

15 response, the therapeutic agent or drug moiety is not to be construed as limited to classical chemical therapeutic agents. For example, the drug moiety may be a protein or polypeptide possessing a desired biological activity. Such proteins may include, for example, a toxin such as abrin, ricin A, pseudomonas exotoxin, or diphtheria toxin; a protein such as tumor necrosis factor, α -interferon, β -interferon, nerve growth

20 factor, platelet derived growth factor, tissue plasminogen activator, an apoptotic agent, e.g., TNF-alpha, TNF-beta, AIM I (See, International Publication No. WO 97/33899), AIM II (See, International Publication No. WO 97/34911), Fas Ligand (Takahashi *et al.*, *Int. Immunol.*, 6:1567-1574 (1994)), VEGF (See, International Publication No. WO 99/23105), a thrombotic agent or an anti-angiogenic agent, e.g.,

25 angiostatin or endostatin; or, biological response modifiers such as, for example, lymphokines, interleukin-1 ("IL-1"), interleukin-2 ("IL-2"), interleukin-6 ("IL-6"),

granulocyte macrophage colony stimulating factor ("GM-CSF"), granulocyte colony stimulating factor ("G-CSF"), or other growth factors.

Antibodies may also be attached to solid supports, which are particularly useful for immunoassays or purification of the target antigen. Such solid supports
5 include, but are not limited to, glass, cellulose, polyacrylamide, nylon, polystyrene, polyvinyl chloride or polypropylene.

Techniques for conjugating such therapeutic moiety to antibodies are well known, see, e.g., Arnon et al., "Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy", in *Monoclonal Antibodies And Cancer Therapy*, Reisfeld et al. (eds.), pp. 243-56 (Alan R. Liss, Inc. 1985); Hellstrom et al., "Antibodies For
10 Drug Delivery", in *Controlled Drug Delivery* (2nd Ed.), Robinson et al. (eds.), pp. 623-53 (Marcel Dekker, Inc. 1987); Thorpe, "Antibody Carriers Of Cytotoxic Agents In Cancer Therapy: A Review", in *Monoclonal Antibodies '84: Biological And Clinical Applications*, Pinchera et al. (eds.), pp. 475-506 (1985); "Analysis, Results,
15 And Future Prospective Of The Therapeutic Use Of Radiolabeled Antibody In Cancer Therapy", in *Monoclonal Antibodies For Cancer Detection And Therapy*, Baldwin et al. (eds.), pp. 303-16 (Academic Press 1985), and Thorpe et al., "The Preparation And Cytotoxic Properties Of Antibody-Toxin Conjugates", *Immunol. Rev.* 62:119-58 (1982).

20 Alternatively, an antibody can be conjugated to a second antibody to form an antibody heteroconjugate as described by Segal in U.S. Patent No. 4,676,980, which is incorporated herein by reference in its entirety.

An antibody, with or without a therapeutic moiety conjugated to it, administered alone or in combination with cytotoxic factor(s) and/or cytokine(s) can
25 be used as a therapeutic.

Immunophenotyping

The antibodies of the invention may be utilized for immunophenotyping of cell lines and biological samples. The translation product of the gene of the present invention may be useful as a cell specific marker, or more specifically as a cellular marker that is differentially expressed at various stages of differentiation and/or maturation of particular cell types. Monoclonal antibodies directed against a specific epitope, or combination of epitopes, will allow for the screening of cellular populations expressing the marker. Various techniques can be utilized using monoclonal antibodies to screen for cellular populations expressing the marker(s), and include magnetic separation using antibody-coated magnetic beads, "panning" with antibody attached to a solid matrix (i.e., plate), and flow cytometry (See, e.g., U.S. Patent 5,985,660; and Morrison *et al.*, *Cell*, 96:737-49 (1999)).

These techniques allow for the screening of particular populations of cells, such as might be found with hematological malignancies (i.e. minimal residual disease (MRD) in acute leukemic patients) and "non-self" cells in transplantations to prevent Graft-versus-Host Disease (GVHD). Alternatively, these techniques allow for the screening of hematopoietic stem and progenitor cells capable of undergoing proliferation and/or differentiation, as might be found in human umbilical cord blood.

Assays For Antibody Binding

The antibodies of the invention may be assayed for immunospecific binding by any method known in the art. The immunoassays which can be used include but are not limited to competitive and non-competitive assay systems using techniques such as western blots, radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoprecipitation assays, precipitin reactions, gel diffusion precipitin reactions, immunodiffusion assays, agglutination assays,

complement-fixation assays, immunoradiometric assays, fluorescent immunoassays, protein A immunoassays, to name but a few. Such assays are routine and well known in the art (see, e.g., Ausubel et al, eds, 1994, Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York, which is incorporated by
5 reference herein in its entirety). Exemplary immunoassays are described briefly below (but are not intended by way of limitation).

Immunoprecipitation protocols generally comprise lysing a population of cells in a lysis buffer such as RIPA buffer (1% NP-40 or Triton X- 100, 1% sodium deoxycholate, 0.1% SDS, 0.15 M NaCl, 0.01 M sodium phosphate at pH 7.2, 1%
10 Trasylol) supplemented with protein phosphatase and/or protease inhibitors (e.g., EDTA, PMSF, aprotinin, sodium vanadate), adding the antibody of interest to the cell lysate, incubating for a period of time (e.g., 1-4 hours) at 4° C, adding protein A and/or protein G sepharose beads to the cell lysate, incubating for about an hour or more at 4° C, washing the beads in lysis buffer and resuspending the beads in
15 SDS/sample buffer. The ability of the antibody of interest to immunoprecipitate a particular antigen can be assessed by, e.g., western blot analysis. One of skill in the art would be knowledgeable as to the parameters that can be modified to increase the binding of the antibody to an antigen and decrease the background (e.g., pre-clearing the cell lysate with sepharose beads). For further discussion regarding
20 immunoprecipitation protocols see, e.g., Ausubel et al, eds, 1994, Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York at 10.16.1.

Western blot analysis generally comprises preparing protein samples, electrophoresis of the protein samples in a polyacrylamide gel (e.g., 8%- 20% SDS-PAGE depending on the molecular weight of the antigen), transferring the protein
25 sample from the polyacrylamide gel to a membrane such as nitrocellulose, PVDF or nylon, blocking the membrane in blocking solution (e.g., PBS with 3% BSA or non-

fat milk), washing the membrane in washing buffer (e.g., PBS-Tween 20), blocking the membrane with primary antibody (the antibody of interest) diluted in blocking buffer, washing the membrane in washing buffer, blocking the membrane with a secondary antibody (which recognizes the primary antibody, e.g., an anti-human antibody) conjugated to an enzymatic substrate (e.g., horseradish peroxidase or alkaline phosphatase) or radioactive molecule (e.g., ^{32}P or ^{125}I) diluted in blocking buffer, washing the membrane in wash buffer, and detecting the presence of the antigen. One of skill in the art would be knowledgeable as to the parameters that can be modified to increase the signal detected and to reduce the background noise. For further discussion regarding western blot protocols see, e.g., Ausubel et al, eds, 1994, Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York at 10.8.1.

ELISAs comprise preparing antigen, coating the well of a 96 well microtiter plate with the antigen, adding the antibody of interest conjugated to a detectable compound such as an enzymatic substrate (e.g., horseradish peroxidase or alkaline phosphatase) to the well and incubating for a period of time, and detecting the presence of the antigen. In ELISAs the antibody of interest does not have to be conjugated to a detectable compound; instead, a second antibody (which recognizes the antibody of interest) conjugated to a detectable compound may be added to the well. Further, instead of coating the well with the antigen, the antibody may be coated to the well. In this case, a second antibody conjugated to a detectable compound may be added following the addition of the antigen of interest to the coated well. One of skill in the art would be knowledgeable as to the parameters that can be modified to increase the signal detected as well as other variations of ELISAs known in the art. For further discussion regarding ELISAs see, e.g., Ausubel et al,

eds, 1994, Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York at 11.2.1.

The binding affinity of an antibody to an antigen and the off-rate of an antibody-antigen interaction can be determined by competitive binding assays. One
5 example of a competitive binding assay is a radioimmunoassay comprising the incubation of labeled antigen (e.g., ³H or ¹²⁵I) with the antibody of interest in the presence of increasing amounts of unlabeled antigen, and the detection of the antibody bound to the labeled antigen. The affinity of the antibody of interest for a particular antigen and the binding off-rates can be determined from the data by
10 scatchard plot analysis. Competition with a second antibody can also be determined using radioimmunoassays. In this case, the antigen is incubated with antibody of interest conjugated to a labeled compound (e.g., ³H or ¹²⁵I) in the presence of increasing amounts of an unlabeled second antibody.

15 Therapeutic Uses

The present invention is further directed to antibody-based therapies which involve administering antibodies of the invention to an animal, preferably a mammal, and most preferably a human, patient for treating one or more of the disclosed diseases, disorders, or conditions. Therapeutic compounds of the invention include,
20 but are not limited to, antibodies of the invention (including fragments, analogs and derivatives thereof as described herein) and nucleic acids encoding antibodies of the invention (including fragments, analogs and derivatives thereof and anti-idiotypic antibodies as described herein). The antibodies of the invention can be used to treat, inhibit or prevent diseases, disorders or conditions associated with aberrant expression
25 and/or activity of a polypeptide of the invention, including, but not limited to, any one or more of the diseases, disorders, or conditions described herein. The treatment

and/or prevention of diseases, disorders, or conditions associated with aberrant expression and/or activity of a polypeptide of the invention includes, but is not limited to, alleviating symptoms associated with those diseases, disorders or conditions. Antibodies of the invention may be provided in pharmaceutically acceptable compositions as known in the art or as described herein.

A summary of the ways in which the antibodies of the present invention may be used therapeutically includes binding polynucleotides or polypeptides of the present invention locally or systemically in the body or by direct cytotoxicity of the antibody, e.g. as mediated by complement (CDC) or by effector cells (ADCC).

Some of these approaches are described in more detail below. Armed with the teachings provided herein, one of ordinary skill in the art will know how to use the antibodies of the present invention for diagnostic, monitoring or therapeutic purposes without undue experimentation.

The antibodies of this invention may be advantageously utilized in combination with other monoclonal or chimeric antibodies, or with lymphokines or hematopoietic growth factors (such as, e.g., IL-2, IL-3 and IL-7), for example, which serve to increase the number or activity of effector cells which interact with the antibodies.

The antibodies of the invention may be administered alone or in combination with other types of treatments (e.g., radiation therapy, chemotherapy, hormonal therapy, immunotherapy and anti-tumor agents). Generally, administration of products of a species origin or species reactivity (in the case of antibodies) that is the same species as that of the patient is preferred. Thus, in a preferred embodiment, human antibodies, fragments derivatives, analogs, or nucleic acids, are administered to a human patient for therapy or prophylaxis.

It is preferred to use high affinity and/or potent in vivo inhibiting and/or neutralizing antibodies against polypeptides or polynucleotides of the present invention, fragments or regions thereof, for both immunoassays directed to and therapy of disorders related to polynucleotides or polypeptides, including fragments thereof, of the present invention. Such antibodies, fragments, or regions, will preferably have an affinity for polynucleotides or polypeptides of the invention, including fragments thereof. Preferred binding affinities include those with a dissociation constant or K_d less than 5×10^{-2} M, 10^{-2} M, 5×10^{-3} M, 10^{-3} M, 5×10^{-4} M, 10^{-4} M, 5×10^{-5} M, 10^{-5} M, 5×10^{-6} M, 10^{-6} M, 5×10^{-7} M, 10^{-7} M, 5×10^{-8} M, 10^{-8} M, 5×10^{-9} M, 10^{-9} M, 5×10^{-10} M, 10^{-10} M, 5×10^{-11} M, 10^{-11} M, 5×10^{-12} M, 10^{-12} M, 5×10^{-13} M, 10^{-13} M, 5×10^{-14} M, 10^{-14} M, 5×10^{-15} M, and 10^{-15} M.

Gene Therapy

In a specific embodiment, nucleic acids comprising sequences encoding antibodies or functional derivatives thereof, are administered to treat, inhibit or prevent a disease or disorder associated with aberrant expression and/or activity of a polypeptide of the invention, by way of gene therapy. Gene therapy refers to therapy performed by the administration to a subject of an expressed or expressible nucleic acid. In this embodiment of the invention, the nucleic acids produce their encoded protein that mediates a therapeutic effect.

Any of the methods for gene therapy available in the art can be used according to the present invention. Exemplary methods are described below.

For general reviews of the methods of gene therapy, see Goldspiel et al., Clinical Pharmacy 12:488-505 (1993); Wu and Wu, Biotherapy 3:87-95 (1991); Tolstoshev, Ann. Rev. Pharmacol. Toxicol. 32:573-596 (1993); Mulligan, Science 260:926-932 (1993); and Morgan and Anderson, Ann. Rev. Biochem. 62:191-217

(1993); May, TIBTECH 11(5):155-215 (1993). Methods commonly known in the art of recombinant DNA technology which can be used are described in Ausubel et al. (eds.), Current Protocols in Molecular Biology, John Wiley & Sons, NY (1993); and Kriegler, Gene Transfer and Expression, A Laboratory Manual, Stockton Press, NY (1990).

In a preferred aspect, the compound comprises nucleic acid sequences encoding an antibody, said nucleic acid sequences being part of expression vectors that express the antibody or fragments or chimeric proteins or heavy or light chains thereof in a suitable host. In particular, such nucleic acid sequences have promoters operably linked to the antibody coding region, said promoter being inducible or constitutive, and, optionally, tissue-specific. In another particular embodiment, nucleic acid molecules are used in which the antibody coding sequences and any other desired sequences are flanked by regions that promote homologous recombination at a desired site in the genome, thus providing for intrachromosomal expression of the antibody encoding nucleic acids (Koller and Smithies, Proc. Natl. Acad. Sci. USA 86:8932-8935 (1989); Zijlstra et al., Nature 342:435-438 (1989). In specific embodiments, the expressed antibody molecule is a single chain antibody; alternatively, the nucleic acid sequences include sequences encoding both the heavy and light chains, or fragments thereof, of the antibody.

Delivery of the nucleic acids into a patient may be either direct, in which case the patient is directly exposed to the nucleic acid or nucleic acid-carrying vectors, or indirect, in which case, cells are first transformed with the nucleic acids in vitro, then transplanted into the patient. These two approaches are known, respectively, as in vivo or ex vivo gene therapy.

In a specific embodiment, the nucleic acid sequences are directly administered in vivo, where it is expressed to produce the encoded product. This can be

accomplished by any of numerous methods known in the art, e.g., by constructing them as part of an appropriate nucleic acid expression vector and administering it so that they become intracellular, e.g., by infection using defective or attenuated retrovirals or other viral vectors (see U.S. Patent No. 4,980,286), or by direct
5 injection of naked DNA, or by use of microparticle bombardment (e.g., a gene gun; Biolistic, Dupont), or coating with lipids or cell-surface receptors or transfecting agents, encapsulation in liposomes, microparticles, or microcapsules, or by administering them in linkage to a peptide which is known to enter the nucleus, by administering it in linkage to a ligand subject to receptor-mediated endocytosis (see,
10 e.g., Wu and Wu, J. Biol. Chem. 262:4429-4432 (1987)) (which can be used to target cell types specifically expressing the receptors), etc. In another embodiment, nucleic acid-ligand complexes can be formed in which the ligand comprises a fusogenic viral peptide to disrupt endosomes, allowing the nucleic acid to avoid lysosomal degradation. In yet another embodiment, the nucleic acid can be targeted in vivo for
15 cell specific uptake and expression, by targeting a specific receptor (see, e.g., PCT Publications WO 92/06180; WO 92/22635; WO92/20316; WO93/14188, WO 93/20221). Alternatively, the nucleic acid can be introduced intracellularly and incorporated within host cell DNA for expression, by homologous recombination (Koller and Smithies, Proc. Natl. Acad. Sci. USA 86:8932-8935 (1989); Zijlstra et al.,
20 Nature 342:435-438 (1989)).

In a specific embodiment, viral vectors that contains nucleic acid sequences encoding an antibody of the invention are used. For example, a retroviral vector can be used (see Miller et al., Meth. Enzymol. 217:581-599 (1993)). These retroviral vectors contain the components necessary for the correct packaging of the viral
25 genome and integration into the host cell DNA. The nucleic acid sequences encoding the antibody to be used in gene therapy are cloned into one or more vectors, which

facilitates delivery of the gene into a patient. More detail about retroviral vectors can be found in Boesen et al., *Biotherapy* 6:291-302 (1994), which describes the use of a retroviral vector to deliver the *mdr1* gene to hematopoietic stem cells in order to make the stem cells more resistant to chemotherapy. Other references illustrating the use of retroviral vectors in gene therapy are: Clowes et al., *J. Clin. Invest.* 93:644-651 (1994); Kiem et al., *Blood* 83:1467-1473 (1994); Salmons and Gunzberg, *Human Gene Therapy* 4:129-141 (1993); and Grossman and Wilson, *Curr. Opin. in Genetics and Devel.* 3:110-114 (1993).

Adenoviruses are other viral vectors that can be used in gene therapy.

Adenoviruses are especially attractive vehicles for delivering genes to respiratory epithelia. Adenoviruses naturally infect respiratory epithelia where they cause a mild disease. Other targets for adenovirus-based delivery systems are liver, the central nervous system, endothelial cells, and muscle. Adenoviruses have the advantage of being capable of infecting non-dividing cells. Kozarsky and Wilson, *Current Opinion in Genetics and Development* 3:499-503 (1993) present a review of adenovirus-based gene therapy. Bout et al., *Human Gene Therapy* 5:3-10 (1994) demonstrated the use of adenovirus vectors to transfer genes to the respiratory epithelia of rhesus monkeys. Other instances of the use of adenoviruses in gene therapy can be found in Rosenfeld et al., *Science* 252:431-434 (1991); Rosenfeld et al., *Cell* 68:143-155 (1992); Mastrangeli et al., *J. Clin. Invest.* 91:225-234 (1993); PCT Publication WO94/12649; and Wang, et al., *Gene Therapy* 2:775-783 (1995). In a preferred embodiment, adenovirus vectors are used.

Adeno-associated virus (AAV) has also been proposed for use in gene therapy (Walsh et al., *Proc. Soc. Exp. Biol. Med.* 204:289-300 (1993); U.S. Patent No.

5,436,146).

Another approach to gene therapy involves transferring a gene to cells in tissue culture by such methods as electroporation, lipofection, calcium phosphate mediated transfection, or viral infection. Usually, the method of transfer includes the transfer of a selectable marker to the cells. The cells are then placed under selection
5 to isolate those cells that have taken up and are expressing the transferred gene. Those cells are then delivered to a patient.

In this embodiment, the nucleic acid is introduced into a cell prior to administration in vivo of the resulting recombinant cell. Such introduction can be carried out by any method known in the art, including but not limited to transfection,
10 electroporation, microinjection, infection with a viral or bacteriophage vector containing the nucleic acid sequences, cell fusion, chromosome-mediated gene transfer, microcell-mediated gene transfer, spheroplast fusion, etc. Numerous techniques are known in the art for the introduction of foreign genes into cells (see, e.g., Loeffler and Behr, Meth. Enzymol. 217:599-618 (1993); Cohen et al., Meth.
15 Enzymol. 217:618-644 (1993); Cline, Pharmac. Ther. 29:69-92m (1985) and may be used in accordance with the present invention, provided that the necessary developmental and physiological functions of the recipient cells are not disrupted. The technique should provide for the stable transfer of the nucleic acid to the cell, so that the nucleic acid is expressible by the cell and preferably heritable and
20 expressible by its cell progeny.

The resulting recombinant cells can be delivered to a patient by various methods known in the art. Recombinant blood cells (e.g., hematopoietic stem or progenitor cells) are preferably administered intravenously. The amount of cells envisioned for use depends on the desired effect, patient state, etc., and can be
25 determined by one skilled in the art.

Cells into which a nucleic acid can be introduced for purposes of gene therapy encompass any desired, available cell type, and include but are not limited to epithelial cells, endothelial cells, keratinocytes, fibroblasts, muscle cells, hepatocytes; blood cells such as Tlymphocytes, Blymphocytes, monocytes, macrophages, 5 neutrophils, eosinophils, megakaryocytes, granulocytes; various stem or progenitor cells, in particular hematopoietic stem or progenitor cells, e.g., as obtained from bone marrow, umbilical cord blood, peripheral blood, fetal liver, etc.

In a preferred embodiment, the cell used for gene therapy is autologous to the patient.

10 In an embodiment in which recombinant cells are used in gene therapy, nucleic acid sequences encoding an antibody are introduced into the cells such that they are expressible by the cells or their progeny, and the recombinant cells are then administered in vivo for therapeutic effect. In a specific embodiment, stem or progenitor cells are used. Any stem and/or progenitor cells which can be isolated and 15 maintained in vitro can potentially be used in accordance with this embodiment of the present invention (see e.g. PCT Publication WO 94/08598; Stemple and Anderson, Cell 71:973-985 (1992); Rheinwald, Meth. Cell Bio. 21A:229 (1980); and Pittelkow and Scott, Mayo Clinic Proc. 61:771 (1986)).

In a specific embodiment, the nucleic acid to be introduced for purposes of 20 gene therapy comprises an inducible promoter operably linked to the coding region, such that expression of the nucleic acid is controllable by controlling the presence or absence of the appropriate inducer of transcription. Demonstration of Therapeutic or Prophylactic Activity

The compounds or pharmaceutical compositions of the invention are 25 preferably tested in vitro, and then in vivo for the desired therapeutic or prophylactic activity, prior to use in humans. For example, in vitro assays to demonstrate the

therapeutic or prophylactic utility of a compound or pharmaceutical composition include, the effect of a compound on a cell line or a patient tissue sample. The effect of the compound or composition on the cell line and/or tissue sample can be determined utilizing techniques known to those of skill in the art including, but not
5 limited to, rosette formation assays and cell lysis assays. In accordance with the invention, in vitro assays which can be used to determine whether administration of a specific compound is indicated, include in vitro cell culture assays in which a patient tissue sample is grown in culture, and exposed to or otherwise administered a compound, and the effect of such compound upon the tissue sample is observed.

10

Therapeutic/Prophylactic Administration and Composition

The invention provides methods of treatment, inhibition and prophylaxis by administration to a subject of an effective amount of a compound or pharmaceutical composition of the invention, preferably an antibody of the invention. In a preferred
15 aspect, the compound is substantially purified (e.g., substantially free from substances that limit its effect or produce undesired side-effects). The subject is preferably an animal, including but not limited to animals such as cows, pigs, horses, chickens, cats, dogs, etc., and is preferably a mammal, and most preferably human.

Formulations and methods of administration that can be employed when the
20 compound comprises a nucleic acid or an immunoglobulin are described above; additional appropriate formulations and routes of administration can be selected from among those described herein below.

Various delivery systems are known and can be used to administer a compound of the invention, e.g., encapsulation in liposomes, microparticles,
25 microcapsules, recombinant cells capable of expressing the compound, receptor-mediated endocytosis (see, e.g., Wu and Wu, J. Biol. Chem. 262:4429-4432 (1987)),

construction of a nucleic acid as part of a retroviral or other vector, etc. Methods of introduction include but are not limited to intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, epidural, and oral routes. The compounds or compositions may be administered by any convenient route, for example by infusion or bolus injection, by absorption through epithelial or mucocutaneous linings (e.g., oral mucosa, rectal and intestinal mucosa, etc.) and may be administered together with other biologically active agents. Administration can be systemic or local. In addition, it may be desirable to introduce the pharmaceutical compounds or compositions of the invention into the central nervous system by any suitable route, including intraventricular and intrathecal injection; intraventricular injection may be facilitated by an intraventricular catheter, for example, attached to a reservoir, such as an Ommaya reservoir. Pulmonary administration can also be employed, e.g., by use of an inhaler or nebulizer, and formulation with an aerosolizing agent.

In a specific embodiment, it may be desirable to administer the pharmaceutical compounds or compositions of the invention locally to the area in need of treatment; this may be achieved by, for example, and not by way of limitation, local infusion during surgery, topical application, e.g., in conjunction with a wound dressing after surgery, by injection, by means of a catheter, by means of a suppository, or by means of an implant, said implant being of a porous, non-porous, or gelatinous material, including membranes, such as sialastic membranes, or fibers. Preferably, when administering a protein, including an antibody, of the invention, care must be taken to use materials to which the protein does not absorb.

In another embodiment, the compound or composition can be delivered in a vesicle, in particular a liposome (see Langer, Science 249:1527-1533 (1990); Treat et al., in Liposomes in the Therapy of Infectious Disease and Cancer, Lopez-Berestein

and Fidler (eds.), Liss, New York, pp. 353- 365 (1989); Lopez-Berestein, *ibid.*, pp. 317-327; see generally *ibid.*)

In yet another embodiment, the compound or composition can be delivered in a controlled release system. In one embodiment, a pump may be used (see Langer, *supra*; Sefton, *CRC Crit. Ref. Biomed. Eng.* 14:201 (1987); Buchwald et al., *Surgery* 88:507 (1980); Saudek et al., *N. Engl. J. Med.* 321:574 (1989)). In another embodiment, polymeric materials can be used (see *Medical Applications of Controlled Release*, Langer and Wise (eds.), CRC Pres., Boca Raton, Florida (1974); *Controlled Drug Bioavailability, Drug Product Design and Performance*, Smolen and Ball (eds.), Wiley, New York (1984); Ranger and Peppas, J., *Macromol. Sci. Rev. Macromol. Chem.* 23:61 (1983); see also Levy et al., *Science* 228:190 (1985); During et al., *Ann. Neurol.* 25:351 (1989); Howard et al., *J. Neurosurg.* 71:105 (1989)). In yet another embodiment, a controlled release system can be placed in proximity of the therapeutic target, i.e., the brain, thus requiring only a fraction of the systemic dose (see, e.g., Goodson, in *Medical Applications of Controlled Release*, *supra*, vol. 2, pp. 115-138 (1984)).

Other controlled release systems are discussed in the review by Langer (*Science* 249:1527-1533 (1990)).

In a specific embodiment where the compound of the invention is a nucleic acid encoding a protein, the nucleic acid can be administered *in vivo* to promote expression of its encoded protein, by constructing it as part of an appropriate nucleic acid expression vector and administering it so that it becomes intracellular, e.g., by use of a retroviral vector (see U.S. Patent No. 4,980,286), or by direct injection, or by use of microparticle bombardment (e.g., a gene gun; Biolistic, Dupont), or coating with lipids or cell-surface receptors or transfecting agents, or by administering it in linkage to a homeobox- like peptide which is known to enter the nucleus (see e.g.,

Joliot et al., Proc. Natl. Acad. Sci. USA 88:1864-1868 (1991)), etc. Alternatively, a nucleic acid can be introduced intracellularly and incorporated within host cell DNA for expression, by homologous recombination.

The present invention also provides pharmaceutical compositions. Such

5 compositions comprise a therapeutically effective amount of a compound, and a pharmaceutically acceptable carrier. In a specific embodiment, the term "pharmaceutically acceptable" means approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, and more particularly in humans. The term

10 "carrier" refers to a diluent, adjuvant, excipient, or vehicle with which the therapeutic is administered. Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. Water is a preferred carrier when the pharmaceutical composition is administered intravenously. Saline

15 solutions and aqueous dextrose and glycerol solutions can also be employed as liquid carriers, particularly for injectable solutions. Suitable pharmaceutical excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. The composition, if desired,

20 can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. These compositions can take the form of solutions, suspensions, emulsion, tablets, pills, capsules, powders, sustained-release formulations and the like. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as

25 pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, etc. Examples of suitable

pharmaceutical carriers are described in "Remington's Pharmaceutical Sciences" by E.W. Martin. Such compositions will contain a therapeutically effective amount of the compound, preferably in purified form, together with a suitable amount of carrier so as to provide the form for proper administration to the patient. The formulation
5 should suit the mode of administration.

In a preferred embodiment, the composition is formulated in accordance with routine procedures as a pharmaceutical composition adapted for intravenous administration to human beings. Typically, compositions for intravenous administration are solutions in sterile isotonic aqueous buffer. Where necessary, the
10 composition may also include a solubilizing agent and a local anesthetic such as lignocaine to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent. Where the
15 composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the composition is administered by injection, an ampoule of sterile water for injection or saline can be provided so that the ingredients may be mixed prior to administration.

The compounds of the invention can be formulated as neutral or salt forms.
20 Pharmaceutically acceptable salts include those formed with anions such as those derived from hydrochloric, phosphoric, acetic, oxalic, tartaric acids, etc., and those formed with cations such as those derived from sodium, potassium, ammonium, calcium, ferric hydroxides, isopropylamine, triethylamine, 2-ethylamino ethanol, histidine, procaine, etc.

25 The amount of the compound of the invention which will be effective in the treatment, inhibition and prevention of a disease or disorder associated with aberrant

expression and/or activity of a polypeptide of the invention can be determined by standard clinical techniques. In addition, in vitro assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of the practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from in vitro or animal model test systems.

For antibodies, the dosage administered to a patient is typically 0.1 mg/kg to 100 mg/kg of the patient's body weight. Preferably, the dosage administered to a patient is between 0.1 mg/kg and 20 mg/kg of the patient's body weight, more preferably 1 mg/kg to 10 mg/kg of the patient's body weight. Generally, human antibodies have a longer half-life within the human body than antibodies from other species due to the immune response to the foreign polypeptides. Thus, lower dosages of human antibodies and less frequent administration is often possible. Further, the dosage and frequency of administration of antibodies of the invention may be reduced by enhancing uptake and tissue penetration (e.g., into the brain) of the antibodies by modifications such as, for example, lipidation.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. **Diagnosis and Imaging**

Labeled antibodies, and derivatives and analogs thereof, which specifically bind to a polypeptide of interest can be used for diagnostic purposes to detect,

diagnose, or monitor diseases, disorders, and/or conditions associated with the aberrant expression and/or activity of a polypeptide of the invention. The invention provides for the detection of aberrant expression of a polypeptide of interest, comprising (a) assaying the expression of the polypeptide of interest in cells or body fluid of an individual using one or more antibodies specific to the polypeptide interest and (b) comparing the level of gene expression with a standard gene expression level, whereby an increase or decrease in the assayed polypeptide gene expression level compared to the standard expression level is indicative of aberrant expression.

The invention provides a diagnostic assay for diagnosing a disorder, comprising (a) assaying the expression of the polypeptide of interest in cells or body fluid of an individual using one or more antibodies specific to the polypeptide interest and (b) comparing the level of gene expression with a standard gene expression level, whereby an increase or decrease in the assayed polypeptide gene expression level compared to the standard expression level is indicative of a particular disorder. With respect to cancer, the presence of a relatively high amount of transcript in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

Antibodies of the invention can be used to assay protein levels in a biological sample using classical immunohistological methods known to those of skill in the art (e.g., see Jalkanen, et al., J. Cell. Biol. 101:976-985 (1985); Jalkanen, et al., J. Cell Biol. 105:3087-3096 (1987)). Other antibody-based methods useful for detecting protein gene expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody

assay labels are known in the art and include enzyme labels, such as, glucose oxidase; radioisotopes, such as iodine (^{125}I , ^{121}I), carbon (^{14}C), sulfur (^{35}S), tritium (^3H), indium (^{112}In), and technetium (^{99}Tc); luminescent labels, such as luminol; and fluorescent labels, such as fluorescein and rhodamine, and biotin.

5 One aspect of the invention is the detection and diagnosis of a disease or disorder associated with aberrant expression of a polypeptide of interest in an animal, preferably a mammal and most preferably a human. In one embodiment, diagnosis comprises: a) administering (for example, parenterally, subcutaneously, or intraperitoneally) to a subject an effective amount of a labeled molecule which
10 specifically binds to the polypeptide of interest; b) waiting for a time interval following the administering for permitting the labeled molecule to preferentially concentrate at sites in the subject where the polypeptide is expressed (and for unbound labeled molecule to be cleared to background level); c) determining background level; and d) detecting the labeled molecule in the subject, such that
15 detection of labeled molecule above the background level indicates that the subject has a particular disease or disorder associated with aberrant expression of the polypeptide of interest. Background level can be determined by various methods including, comparing the amount of labeled molecule detected to a standard value previously determined for a particular system.

20 It will be understood in the art that the size of the subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the case of a radioisotope moiety, for a human subject, the quantity of radioactivity injected will normally range from about 5 to 20 millicuries of ^{99}mTc . The labeled antibody or antibody fragment will then preferentially
25 accumulate at the location of cells which contain the specific protein. In vivo tumor imaging is described in S.W. Burchiel et al., "Immunopharmacokinetics of

Radiolabeled Antibodies and Their Fragments.” (Chapter 13 in Tumor Imaging: The Radiochemical Detection of Cancer, S.W. Burchiel and B. A. Rhodes, eds., Masson Publishing Inc. (1982).

5 Depending on several variables, including the type of label used and the mode of administration, the time interval following the administration for permitting the labeled molecule to preferentially concentrate at sites in the subject and for unbound labeled molecule to be cleared to background level is 6 to 48 hours or 6 to 24 hours or 6 to 12 hours. In another embodiment the time interval following administration is 5 to 20 days or 5 to 10 days.

10 In an embodiment, monitoring of the disease or disorder is carried out by repeating the method for diagnosing the disease or disease, for example, one month after initial diagnosis, six months after initial diagnosis, one year after initial diagnosis, etc.

Presence of the labeled molecule can be detected in the patient using methods
15 known in the art for in vivo scanning. These methods depend upon the type of label used. Skilled artisans will be able to determine the appropriate method for detecting a particular label. Methods and devices that may be used in the diagnostic methods of the invention include, but are not limited to, computed tomography (CT), whole body scan such as position emission tomography (PET), magnetic resonance imaging
20 (MRI), and sonography.

In a specific embodiment, the molecule is labeled with a radioisotope and is detected in the patient using a radiation responsive surgical instrument (Thurston et al., U.S. Patent No. 5,441,050). In another embodiment, the molecule is labeled with a fluorescent compound and is detected in the patient using a fluorescence responsive
25 scanning instrument. In another embodiment, the molecule is labeled with a positron emitting metal and is detected in the patent using positron emission-tomography. In

yet another embodiment, the molecule is labeled with a paramagnetic label and is detected in a patient using magnetic resonance imaging (MRI). Kits

The present invention provides kits that can be used in the above methods. In one embodiment, a kit comprises an antibody of the invention, preferably a purified
5 antibody, in one or more containers. In a specific embodiment, the kits of the present invention contain a substantially isolated polypeptide comprising an epitope which is specifically immunoreactive with an antibody included in the kit. Preferably, the kits of the present invention further comprise a control antibody which does not react with the polypeptide of interest. In another specific embodiment, the kits of the present
10 invention contain a means for detecting the binding of an antibody to a polypeptide of interest (e.g., the antibody may be conjugated to a detectable substrate such as a fluorescent compound, an enzymatic substrate, a radioactive compound or a luminescent compound, or a second antibody which recognizes the first antibody may be conjugated to a detectable substrate).

15 In another specific embodiment of the present invention, the kit is a diagnostic kit for use in screening serum containing antibodies specific against proliferative and/or cancerous polynucleotides and polypeptides. Such a kit may include a control antibody that does not react with the polypeptide of interest. Such a kit may include a substantially isolated polypeptide antigen comprising an epitope which is specifically
20 immunoreactive with at least one anti-polypeptide antigen antibody. Further, such a kit includes means for detecting the binding of said antibody to the antigen (e.g., the antibody may be conjugated to a fluorescent compound such as fluorescein or rhodamine which can be detected by flow cytometry). In specific embodiments, the kit may include a recombinantly produced or chemically synthesized polypeptide
25 antigen. The polypeptide antigen of the kit may also be attached to a solid support.

In a more specific embodiment the detecting means of the above-described kit includes a solid support to which said polypeptide antigen is attached. Such a kit may also include a non-attached reporter-labeled anti-human antibody. In this embodiment, binding of the antibody to the polypeptide antigen can be detected by
5 binding of the said reporter-labeled antibody.

In an additional embodiment, the invention includes a diagnostic kit for use in screening serum containing antigens of the polypeptide of the invention. The diagnostic kit includes a substantially isolated antibody specifically immunoreactive with polypeptide or polynucleotide antigens, and means for detecting the binding of
10 the polynucleotide or polypeptide antigen to the antibody. In one embodiment, the antibody is attached to a solid support. In a specific embodiment, the antibody may be a monoclonal antibody. The detecting means of the kit may include a second, labeled monoclonal antibody. Alternatively, or in addition, the detecting means may include a labeled, competing antigen.

15 In one diagnostic configuration, test serum is reacted with a solid phase reagent having a surface-bound antigen obtained by the methods of the present invention. After binding with specific antigen antibody to the reagent and removing unbound serum components by washing, the reagent is reacted with reporter-labeled anti-human antibody to bind reporter to the reagent in proportion to the amount of
20 bound anti-antigen antibody on the solid support. The reagent is again washed to remove unbound labeled antibody, and the amount of reporter associated with the reagent is determined. Typically, the reporter is an enzyme which is detected by incubating the solid phase in the presence of a suitable fluorometric, luminescent or colorimetric substrate (Sigma, St. Louis, MO).

25 The solid surface reagent in the above assay is prepared by known techniques for attaching protein material to solid support material, such as polymeric beads, dip

sticks, 96-well plate or filter material. These attachment methods generally include non-specific adsorption of the protein to the support or covalent attachment of the protein, typically through a free amine group, to a chemically reactive group on the solid support, such as an activated carboxyl, hydroxyl, or aldehyde group.

5 Alternatively, streptavidin coated plates can be used in conjunction with biotinylated antigen(s).

Thus, the invention provides an assay system or kit for carrying out this diagnostic method. The kit generally includes a support with surface-bound recombinant antigens, and a reporter-labeled anti-human antibody for detecting
10 surface-bound anti-antigen antibody.

Fusion Proteins

Any polypeptide of the present invention can be used to generate fusion
15 proteins. For example, the polypeptide of the present invention, when fused to a second protein, can be used as an antigenic tag. Antibodies raised against the polypeptide of the present invention can be used to indirectly detect the second protein by binding to the polypeptide. Moreover, because secreted proteins target cellular locations based on trafficking signals, the polypeptides of the present
20 invention can be used as targeting molecules once fused to other proteins.

Examples of domains that can be fused to polypeptides of the present invention include not only heterologous signal sequences, but also other heterologous functional regions. The fusion does not necessarily need to be direct, but may occur through linker sequences.

25 Moreover, fusion proteins may also be engineered to improve characteristics of the polypeptide of the present invention. For instance, a region of additional amino

acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence during purification from the host cell or subsequent handling and storage. Also, peptide moieties may be added to the polypeptide to facilitate purification. Such regions may be removed prior to final
5 preparation of the polypeptide. The addition of peptide moieties to facilitate handling of polypeptides are familiar and routine techniques in the art.

Moreover, polypeptides of the present invention, including fragments, and specifically epitopes, can be combined with parts of the constant domain of immunoglobulins (IgA, IgE, IgG, IgM) or portions thereof (CH1, CH2, CH3, and any
10 combination thereof, including both entire domains and portions thereof), resulting in chimeric polypeptides. These fusion proteins facilitate purification and show an increased half-life in vivo. One reported example describes chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian
15 immunoglobulins. (EP A 394,827; Traunecker et al., Nature 331:84-86 (1988).) Fusion proteins having disulfide-linked dimeric structures (due to the IgG) can also be more efficient in binding and neutralizing other molecules, than the monomeric secreted protein or protein fragment alone. (Fountoulakis et al., J. Biochem. 270:3958-3964 (1995).)

20 Similarly, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties. (EP-A 0232 262.) Alternatively,
25 deleting the Fc part after the fusion protein has been expressed, detected, and purified, would be desired. For example, the Fc portion may hinder therapy and diagnosis if

the fusion protein is used as an antigen for immunizations. In drug discovery, for example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. (See, D. Bennett et al., J. Molecular Recognition 8:52-58 (1995); K. Johanson et al., J. Biol. Chem. 270:9459-9471 (1995).)

Moreover, the polypeptides of the present invention can be fused to marker sequences, such as a peptide which facilitates purification of the fused polypeptide. In preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., Proc. Natl. Acad. Sci. USA 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein. Another peptide tag useful for purification, the "HA" tag, corresponds to an epitope derived from the influenza hemagglutinin protein. (Wilson et al., Cell 37:767 (1984).)

Thus, any of these above fusions can be engineered using the polynucleotides or the polypeptides of the present invention.

Vectors, Host Cells, and Protein Production

The present invention also relates to vectors containing the polynucleotide of the present invention, host cells, and the production of polypeptides by recombinant techniques. The vector may be, for example, a phage, plasmid, viral, or retroviral vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it may be packaged in vitro using an appropriate packaging cell line and then transduced into host cells.

The polynucleotide insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the *E. coli* lac, trp, phoA and tac promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination, and, in the transcribed region, a ribosome binding site for translation. The coding portion of the transcripts expressed by the constructs will preferably include a translation initiating codon at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase, G418 or neomycin resistance for eukaryotic cell culture and tetracycline, kanamycin or ampicillin resistance genes for culturing in *E. coli* and other bacteria. Representative examples of appropriate hosts include, but are not limited to, bacterial cells, such as *E. coli*, *Streptomyces* and *Salmonella typhimurium* cells; fungal cells, such as yeast cells (e.g., *Saccharomyces cerevisiae* or *Pichia pastoris* (ATCC Accession No. 201178)); insect cells such as *Drosophila* S2 and *Spodoptera Sf9* cells; animal cells such as CHO, COS, 293, and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from QIAGEN, Inc.; pBluescript vectors, Phagescript vectors, pNH8A,

pNH16a, pNH18A, pNH46A, available from Stratagene Cloning Systems, Inc.; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia Biotech, Inc. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Preferred expression vectors for use in yeast systems include, but are not limited to pYES2, pYD1, pTEF1/Zeo, pYES2/GS, pPICZ, pGAPZ, pGAPZalph, pPIC9, pPIC3.5, pHIL-D2, pHIL-S1, pPIC3.5K, pPIC9K, and PAO815 (all available from Invitrogen, Carlsbad, CA). Other suitable vectors will be readily apparent to the skilled artisan.

10 Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, or other methods. Such methods are described in many standard laboratory manuals, such as Davis et al., Basic Methods In Molecular Biology (1986). It is specifically contemplated that the

15 polypeptides of the present invention may in fact be expressed by a host cell lacking a recombinant vector.

A polypeptide of this invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography,

20 phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification.

Polypeptides of the present invention, and preferably the secreted form, can

25 also be recovered from: products purified from natural sources, including bodily fluids, tissues and cells, whether directly isolated or cultured; products of chemical

synthetic procedures; and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect, and mammalian cells. Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated
5 or may be non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes. Thus, it is well known in the art that the N-terminal methionine encoded by the translation initiation codon generally is removed with high efficiency from any protein after translation in all eukaryotic cells. While the N-terminal
10 methionine on most proteins also is efficiently removed in most prokaryotes, for some proteins, this prokaryotic removal process is inefficient, depending on the nature of the amino acid to which the N-terminal methionine is covalently linked.

In one embodiment, the yeast *Pichia pastoris* is used to express the polypeptide of the present invention in a eukaryotic system. *Pichia pastoris* is a
15 methylotrophic yeast which can metabolize methanol as its sole carbon source. A main step in the methanol metabolism pathway is the oxidation of methanol to formaldehyde using O₂. This reaction is catalyzed by the enzyme alcohol oxidase. In order to metabolize methanol as its sole carbon source, *Pichia pastoris* must generate high levels of alcohol oxidase due, in part, to the relatively low affinity of alcohol
20 oxidase for O₂. Consequently, in a growth medium depending on methanol as a main carbon source, the promoter region of one of the two alcohol oxidase genes (*AOX1*) is highly active. In the presence of methanol, alcohol oxidase produced from the *AOX1* gene comprises up to approximately 30% of the total soluble protein in *Pichia pastoris*. See, Ellis, S.B., *et al.*, *Mol. Cell. Biol.* 5:1111-21 (1985); Koutz, P.J., *et al.*,
25 *Yeast* 5:167-77 (1989); Tschopp, J.F., *et al.*, *Nucl. Acids Res.* 15:3859-76 (1987).

Thus, a heterologous coding sequence, such as, for example, a polynucleotide of the present invention, under the transcriptional regulation of all or part of the *AOX1* regulatory sequence is expressed at exceptionally high levels in *Pichia* yeast grown in the presence of methanol.

5 In one example, the plasmid vector pPIC9K is used to express DNA encoding a polypeptide of the invention, as set forth herein, in a *Pichea* yeast system essentially as described in "*Pichia* Protocols: Methods in Molecular Biology," D.R. Higgins and J. Cregg, eds. The Humana Press, Totowa, NJ, 1998. This expression vector allows expression and secretion of a protein of the invention by virtue of the strong *AOX1*
10 promoter linked to the *Pichia pastoris* alkaline phosphatase (PHO) secretory signal peptide (i.e., leader) located upstream of a multiple cloning site.

Many other yeast vectors could be used in place of pPIC9K, such as, pYES2, pYD1, pTEF1/Zeo, pYES2/GS, pPICZ, pGAPZ, pGAPZalpha, pPIC9, pPIC3.5, pHIL-D2, pHIL-S1, pPIC3.5K, and PAO815, as one skilled in the art would readily
15 appreciate, as long as the proposed expression construct provides appropriately located signals for transcription, translation, secretion (if desired), and the like, including an in-frame AUG as required.

In another embodiment, high-level expression of a heterologous coding sequence, such as, for example, a polynucleotide of the present invention, may be
20 achieved by cloning the heterologous polynucleotide of the invention into an expression vector such as, for example, pGAPZ or pGAPZalpha, and growing the yeast culture in the absence of methanol.

In addition to encompassing host cells containing the vector constructs discussed herein, the invention also encompasses primary, secondary, and
25 immortalized host cells of vertebrate origin, particularly mammalian origin, that have

been engineered to delete or replace endogenous genetic material (e.g., coding sequence), and/or to include genetic material (e.g., heterologous polynucleotide sequences) that is operably associated with the polynucleotides of the invention, and which activates, alters, and/or amplifies endogenous polynucleotides. For example, techniques known in the art may be used to operably associate heterologous control regions (e.g., promoter and/or enhancer) and endogenous polynucleotide sequences via homologous recombination, resulting in the formation of a new transcription unit (see, e.g., U.S. Patent No. 5,641,670, issued June 24, 1997; U.S. Patent No. 5,733,761, issued March 31, 1998; International Publication No. WO 96/29411, published September 26, 1996; International Publication No. WO 94/12650, published August 4, 1994; Koller et al., *Proc. Natl. Acad. Sci. USA* 86:8932-8935 (1989); and Zijlstra et al., *Nature* 342:435-438 (1989), the disclosures of each of which are incorporated by reference in their entireties).

In addition, polypeptides of the invention can be chemically synthesized using techniques known in the art (e.g., see Creighton, 1983, *Proteins: Structures and Molecular Principles*, W.H. Freeman & Co., N.Y., and Hunkapiller et al., *Nature*, 310:105-111 (1984)). For example, a polypeptide corresponding to a fragment of a polypeptide sequence of the invention can be synthesized by use of a peptide synthesizer. Furthermore, if desired, nonclassical amino acids or chemical amino acid analogs can be introduced as a substitution or addition into the polypeptide sequence. Non-classical amino acids include, but are not limited to, to the D-isomers of the common amino acids, 2,4-diaminobutyric acid, α -amino isobutyric acid, 4-aminobutyric acid, Abu, 2-amino butyric acid, g-Abu, e-Ahx, 6-amino hexanoic acid, Aib, 2-amino isobutyric acid, 3-amino propionic acid, ornithine, norleucine, norvaline, hydroxyproline, sarcosine, citrulline, homocitrulline, cysteic acid, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine, b-alanine, fluoro-

amino acids, designer amino acids such as b-methyl amino acids, Ca-methyl amino acids, Na-methyl amino acids, and amino acid analogs in general. Furthermore, the amino acid can be D (dextrorotary) or L (levorotary).

The invention encompasses polypeptides which are differentially modified during or after translation, *e.g.*, by glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to an antibody molecule or other cellular ligand, etc. Any of numerous chemical modifications may be carried out by known techniques, including but not limited, to specific chemical cleavage by cyanogen bromide, trypsin, chymotrypsin, papain, V8 protease, NaBH_4 ; acetylation, formylation, oxidation, reduction; metabolic synthesis in the presence of tunicamycin; etc.

Additional post-translational modifications encompassed by the invention include, for example, *e.g.*, N-linked or O-linked carbohydrate chains, processing of N-terminal or C-terminal ends), attachment of chemical moieties to the amino acid backbone, chemical modifications of N-linked or O-linked carbohydrate chains, and addition or deletion of an N-terminal methionine residue as a result of procaryotic host cell expression. The polypeptides may also be modified with a detectable label, such as an enzymatic, fluorescent, isotopic or affinity label to allow for detection and isolation of the protein.

Also provided by the invention are chemically modified derivatives of the polypeptides of the invention which may provide additional advantages such as increased solubility, stability and circulating time of the polypeptide, or decreased immunogenicity (see U.S. Patent NO: 4,179,337). The chemical moieties for derivitization may be selected from water soluble polymers such as polyethylene glycol, ethylene glycol/propylene glycol copolymers, carboxymethylcellulose, dextran, polyvinyl alcohol and the like. The polypeptides may be modified at random

positions within the molecule, or at predetermined positions within the molecule and may include one, two, three or more attached chemical moieties.

The polymer may be of any molecular weight, and may be branched or unbranched. For polyethylene glycol, the preferred molecular weight is between
5 about 1 kDa and about 100 kDa (the term "about" indicating that in preparations of polyethylene glycol, some molecules will weigh more, some less, than the stated molecular weight) for ease in handling and manufacturing. Other sizes may be used, depending on the desired therapeutic profile (e.g., the duration of sustained release desired, the effects, if any on biological activity, the ease in handling, the degree or
10 lack of antigenicity and other known effects of the polyethylene glycol to a therapeutic protein or analog).

The polyethylene glycol molecules (or other chemical moieties) should be attached to the protein with consideration of effects on functional or antigenic domains of the protein. There are a number of attachment methods available to those
15 skilled in the art, e.g., EP 0 401 384, herein incorporated by reference (coupling PEG to G-CSF), see also Malik et al., Exp. Hematol. 20:1028-1035 (1992) (reporting pegylation of GM-CSF using tresyl chloride). For example, polyethylene glycol may be covalently bound through amino acid residues via a reactive group, such as, a free amino or carboxyl group. Reactive groups are those to which an activated
20 polyethylene glycol molecule may be bound. The amino acid residues having a free amino group may include lysine residues and the N-terminal amino acid residues; those having a free carboxyl group may include aspartic acid residues glutamic acid residues and the C-terminal amino acid residue. Sulfhydryl groups may also be used as a reactive group for attaching the polyethylene glycol molecules. Preferred for
25 therapeutic purposes is attachment at an amino group, such as attachment at the N-terminus or lysine group.

- One may specifically desire proteins chemically modified at the N-terminus. Using polyethylene glycol as an illustration of the present composition, one may select from a variety of polyethylene glycol molecules (by molecular weight, branching, etc.), the proportion of polyethylene glycol molecules to protein (polypeptide) molecules in the reaction mix, the type of pegylation reaction to be performed, and the method of obtaining the selected N-terminally pegylated protein. The method of obtaining the N-terminally pegylated preparation (i.e., separating this moiety from other monopegylated moieties if necessary) may be by purification of the N-terminally pegylated material from a population of pegylated protein molecules.
- 5 (polypeptide) molecules in the reaction mix, the type of pegylation reaction to be performed, and the method of obtaining the selected N-terminally pegylated protein. The method of obtaining the N-terminally pegylated preparation (i.e., separating this moiety from other monopegylated moieties if necessary) may be by purification of the N-terminally pegylated material from a population of pegylated protein molecules.
- 10 Selective proteins chemically modified at the N-terminus modification may be accomplished by reductive alkylation which exploits differential reactivity of different types of primary amino groups (lysine versus the N-terminal) available for derivatization in a particular protein. Under the appropriate reaction conditions, substantially selective derivatization of the protein at the N-terminus with a carbonyl
- 15 group containing polymer is achieved.

- The polypeptides of the invention may be in monomers or multimers (i.e., dimers, trimers, tetramers and higher multimers). Accordingly, the present invention relates to monomers and multimers of the polypeptides of the invention, their preparation, and compositions (preferably, *Therapeutics*) containing them. In specific
- 20 embodiments, the polypeptides of the invention are monomers, dimers, trimers or tetramers. In additional embodiments, the multimers of the invention are at least dimers, at least trimers, or at least tetramers.

- Multimers encompassed by the invention may be homomers or heteromers. As used herein, the term homomer, refers to a multimer containing only polypeptides
- 25 corresponding to the amino acid sequence of SEQ ID NO:Y or encoded by the cDNA contained in a deposited clone (including fragments, variants, splice variants, and

fusion proteins, corresponding to these polypeptides as described herein). These homomers may contain polypeptides having identical or different amino acid sequences. In a specific embodiment, a homomer of the invention is a multimer containing only polypeptides having an identical amino acid sequence. In another
5 specific embodiment, a homomer of the invention is a multimer containing polypeptides having different amino acid sequences. In specific embodiments, the multimer of the invention is a homodimer (*e.g.*, containing polypeptides having identical or different amino acid sequences) or a homotrimer (*e.g.*, containing polypeptides having identical and/or different amino acid sequences). In additional
10 embodiments, the homomeric multimer of the invention is at least a homodimer, at least a homotrimer, or at least a homotetramer.

As used herein, the term heteromer refers to a multimer containing one or more heterologous polypeptides (*i.e.*, polypeptides of different proteins) in addition to the polypeptides of the invention. In a specific embodiment, the multimer of the
15 invention is a heterodimer, a heterotrimer, or a heterotetramer. In additional embodiments, the heteromeric multimer of the invention is at least a heterodimer, at least a heterotrimer, or at least a heterotetramer.

Multimers of the invention may be the result of hydrophobic, hydrophilic, ionic and/or covalent associations and/or may be indirectly linked, by for example,
20 liposome formation. Thus, in one embodiment, multimers of the invention, such as, for example, homodimers or homotrimers, are formed when polypeptides of the invention contact one another in solution. In another embodiment, heteromultimers of the invention, such as, for example, heterotrimers or heterotetramers, are formed when polypeptides of the invention contact antibodies to the polypeptides of the
25 invention (including antibodies to the heterologous polypeptide sequence in a fusion protein of the invention) in solution. In other embodiments, multimers of the

invention are formed by covalent associations with and/or between the polypeptides of the invention. Such covalent associations may involve one or more amino acid residues contained in the polypeptide sequence (e.g., that recited in the sequence listing, or contained in the polypeptide encoded by a deposited clone). In one
5 instance, the covalent associations are cross-linking between cysteine residues located within the polypeptide sequences which interact in the native (i.e., naturally occurring) polypeptide. In another instance, the covalent associations are the consequence of chemical or recombinant manipulation. Alternatively, such covalent associations may involve one or more amino acid residues contained in the
10 heterologous polypeptide sequence in a fusion protein of the invention.

In one example, covalent associations are between the heterologous sequence contained in a fusion protein of the invention (see, e.g., US Patent Number 5,478,925). In a specific example, the covalent associations are between the heterologous sequence contained in an Fc fusion protein of the invention (as
15 described herein). In another specific example, covalent associations of fusion proteins of the invention are between heterologous polypeptide sequence from another protein that is capable of forming covalently associated multimers, such as for example, osteopontin (see, e.g., International Publication NO: WO 98/49305, the contents of which are herein incorporated by reference in its entirety). In another
20 embodiment, two or more polypeptides of the invention are joined through peptide linkers. Examples include those peptide linkers described in U.S. Pat. No. 5,073,627 (hereby incorporated by reference). Proteins comprising multiple polypeptides of the invention separated by peptide linkers may be produced using conventional recombinant DNA technology.

25 Another method for preparing multimer polypeptides of the invention involves use of polypeptides of the invention fused to a leucine zipper or isoleucine zipper

polypeptide sequence. Leucine zipper and isoleucine zipper domains are polypeptides that promote multimerization of the proteins in which they are found. Leucine zippers were originally identified in several DNA-binding proteins (Landschulz et al., Science 240:1759, (1988)), and have since been found in a variety of different

5 proteins. Among the known leucine zippers are naturally occurring peptides and derivatives thereof that dimerize or trimerize. Examples of leucine zipper domains suitable for producing soluble multimeric proteins of the invention are those described in PCT application WO 94/10308, hereby incorporated by reference. Recombinant fusion proteins comprising a polypeptide of the invention fused to a polypeptide

10 sequence that dimerizes or trimerizes in solution are expressed in suitable host cells, and the resulting soluble multimeric fusion protein is recovered from the culture supernatant using techniques known in the art.

Trimeric polypeptides of the invention may offer the advantage of enhanced biological activity. Preferred leucine zipper moieties and isoleucine moieties are

15 those that preferentially form trimers. One example is a leucine zipper derived from lung surfactant protein D (SPD), as described in Hoppe et al. (FEBS Letters 344:191, (1994)) and in U.S. patent application Ser. No. 08/446,922, hereby incorporated by reference. Other peptides derived from naturally occurring trimeric proteins may be employed in preparing trimeric polypeptides of the invention.

20 In another example, proteins of the invention are associated by interactions between Flag® polypeptide sequence contained in fusion proteins of the invention containing Flag® polypeptide sequence. In a further embodiment, associations proteins of the invention are associated by interactions between heterologous polypeptide sequence contained in Flag® fusion proteins of the invention and anti-

25 Flag® antibody.

The multimers of the invention may be generated using chemical techniques known in the art. For example, polypeptides desired to be contained in the multimers of the invention may be chemically cross-linked using linker molecules and linker molecule length optimization techniques known in the art (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety).

Additionally, multimers of the invention may be generated using techniques known in the art to form one or more inter-molecule cross-links between the cysteine residues located within the sequence of the polypeptides desired to be contained in the multimer (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). Further, polypeptides of the invention may be routinely modified by the addition of cysteine or biotin to the C terminus or N-terminus of the polypeptide and techniques known in the art may be applied to generate multimers containing one or more of these modified polypeptides (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). Additionally, techniques known in the art may be applied to generate liposomes containing the polypeptide components desired to be contained in the multimer of the invention (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety).

Alternatively, multimers of the invention may be generated using genetic engineering techniques known in the art. In one embodiment, polypeptides contained in multimers of the invention are produced recombinantly using fusion protein technology described herein or otherwise known in the art (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). In a specific embodiment, polynucleotides coding for a homodimer of the invention are generated by ligating a polynucleotide sequence encoding a polypeptide of the invention to a sequence encoding a linker polypeptide and then further to a synthetic

polynucleotide encoding the translated product of the polypeptide in the reverse orientation from the original C-terminus to the N-terminus (lacking the leader sequence) (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). In another embodiment, recombinant techniques described
5 herein or otherwise known in the art are applied to generate recombinant polypeptides of the invention which contain a transmembrane domain (or hydrophobic or signal peptide) and which can be incorporated by membrane reconstitution techniques into liposomes (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety).

10

Uses of the Polynucleotides

Each of the polynucleotides identified herein can be used in numerous ways as reagents. The following description should be considered exemplary and utilizes known techniques.

15 The polynucleotides of the present invention are useful for chromosome identification. There exists an ongoing need to identify new chromosome markers, since few chromosome marking reagents, based on actual sequence data (repeat polymorphisms), are presently available. Each polynucleotide of the present invention can be used as a chromosome marker.

20 Briefly, sequences can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp) from the sequences shown in SEQ ID NO:X. Primers can be selected using computer analysis so that primers do not span more than one predicted exon in the genomic DNA. These primers are then used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids
25 containing the human gene corresponding to the SEQ ID NO:X will yield an amplified fragment.

Similarly, somatic hybrids provide a rapid method of PCR mapping the polynucleotides to particular chromosomes. Three or more clones can be assigned per day using a single thermal cycler. Moreover, sublocalization of the polynucleotides can be achieved with panels of specific chromosome fragments. Other gene mapping strategies that can be used include in situ hybridization, prescreening with labeled flow-sorted chromosomes, and preselection by hybridization to construct chromosome specific-cDNA libraries.

Precise chromosomal location of the polynucleotides can also be achieved using fluorescence in situ hybridization (FISH) of a metaphase chromosomal spread. This technique uses polynucleotides as short as 500 or 600 bases; however, polynucleotides 2,000-4,000 bp are preferred. For a review of this technique, see Verma et al., "Human Chromosomes: a Manual of Basic Techniques," Pergamon Press, New York (1988).

For chromosome mapping, the polynucleotides can be used individually (to mark a single chromosome or a single site on that chromosome) or in panels (for marking multiple sites and/or multiple chromosomes). Preferred polynucleotides correspond to the noncoding regions of the cDNAs because the coding sequences are more likely conserved within gene families, thus increasing the chance of cross hybridization during chromosomal mapping.

Once a polynucleotide has been mapped to a precise chromosomal location, the physical position of the polynucleotide can be used in linkage analysis. Linkage analysis establishes coinheritance between a chromosomal location and presentation of a particular disease. (Disease mapping data are found, for example, in V. McKusick, Mendelian Inheritance in Man (available on line through Johns Hopkins University Welch Medical Library) .) Assuming 1 megabase mapping resolution and

one gene per 20 kb, a cDNA precisely localized to a chromosomal region associated with the disease could be one of 50-500 potential causative genes.

Thus, once coinheritance is established, differences in the polynucleotide and the corresponding gene between affected and unaffected individuals can be examined.

- 5 First, visible structural alterations in the chromosomes, such as deletions or translocations, are examined in chromosome spreads or by PCR. If no structural alterations exist, the presence of point mutations are ascertained. Mutations observed in some or all affected individuals, but not in normal individuals, indicates that the mutation may cause the disease. However, complete sequencing of the polypeptide
10 and the corresponding gene from several normal individuals is required to distinguish the mutation from a polymorphism. If a new polymorphism is identified, this polymorphic polypeptide can be used for further linkage analysis.

- Furthermore, increased or decreased expression of the gene in affected individuals as compared to unaffected individuals can be assessed using
15 polynucleotides of the present invention. Any of these alterations (altered expression, chromosomal rearrangement, or mutation) can be used as a diagnostic or prognostic marker.

- Thus, the invention also provides a diagnostic method useful during diagnosis of a disorder, involving measuring the expression level of polynucleotides of the
20 present invention in cells or body fluid from an individual and comparing the measured gene expression level with a standard level of polynucleotide expression level, whereby an increase or decrease in the gene expression level compared to the standard is indicative of a disorder.

- In still another embodiment, the invention includes a kit for analyzing samples
25 for the presence of proliferative and/or cancerous polynucleotides derived from a test subject. In a general embodiment, the kit includes at least one polynucleotide probe

containing a nucleotide sequence that will specifically hybridize with a polynucleotide of the present invention and a suitable container. In a specific embodiment, the kit includes two polynucleotide probes defining an internal region of the polynucleotide of the present invention, where each probe has one strand containing a 31'-mer-end internal to the region. In a further embodiment, the probes may be useful as primers for polymerase chain reaction amplification.

Where a diagnosis of a disorder, has already been made according to conventional methods, the present invention is useful as a prognostic indicator, whereby patients exhibiting enhanced or depressed polynucleotide of the present invention expression will experience a worse clinical outcome relative to patients expressing the gene at a level nearer the standard level.

By "measuring the expression level of polynucleotide of the present invention" is intended qualitatively or quantitatively measuring or estimating the level of the polypeptide of the present invention or the level of the mRNA encoding the polypeptide in a first biological sample either directly (e.g., by determining or estimating absolute protein level or mRNA level) or relatively (e.g., by comparing to the polypeptide level or mRNA level in a second biological sample). Preferably, the polypeptide level or mRNA level in the first biological sample is measured or estimated and compared to a standard polypeptide level or mRNA level, the standard being taken from a second biological sample obtained from an individual not having the disorder or being determined by averaging levels from a population of individuals not having a disorder. As will be appreciated in the art, once a standard polypeptide level or mRNA level is known, it can be used repeatedly as a standard for comparison.

By "biological sample" is intended any biological sample obtained from an individual, body fluid, cell line, tissue culture, or other source which contains the

polypeptide of the present invention or mRNA. As indicated, biological samples include body fluids (such as semen, lymph, sera, plasma, urine, synovial fluid and spinal fluid) which contain the polypeptide of the present invention, and other tissue sources found to express the polypeptide of the present invention. Methods for
5 obtaining tissue biopsies and body fluids from mammals are well known in the art. Where the biological sample is to include mRNA, a tissue biopsy is the preferred source.

The method(s) provided above may preferably be applied in a diagnostic method and/or kits in which polynucleotides and/or polypeptides are attached to a
10 solid support. In one exemplary method, the support may be a "gene chip" or a "biological chip" as described in US Patents 5,837,832, 5,874,219, and 5,856,174. Further, such a gene chip with polynucleotides of the present invention attached may be used to identify polymorphisms between the polynucleotide sequences, with polynucleotides isolated from a test subject. The knowledge of such polymorphisms
15 (i.e. their location, as well as, their existence) would be beneficial in identifying disease loci for many disorders, including cancerous diseases and conditions. Such a method is described in US Patents 5,858,659 and 5,856,104. The US Patents referenced supra are hereby incorporated by reference in their entirety herein.

The present invention encompasses polynucleotides of the present invention
20 that are chemically synthesized, or reproduced as peptide nucleic acids (PNA), or according to other methods known in the art. The use of PNAs would serve as the preferred form if the polynucleotides are incorporated onto a solid support, or gene chip. For the purposes of the present invention, a peptide nucleic acid (PNA) is a polyamide type of DNA analog and the monomeric units for adenine, guanine,
25 thymine and cytosine are available commercially (Perceptive Biosystems). Certain components of DNA, such as phosphorus, phosphorus oxides, or deoxyribose

derivatives, are not present in PNAs. As disclosed by P. E. Nielsen, M. Egholm, R. H. Berg and O. Buchardt, *Science* 254, 1497 (1991); and M. Egholm, O. Buchardt, L. Christensen, C. Behrens, S. M. Freier, D. A. Driver, R. H. Berg, S. K. Kim, B. Norden, and P. E. Nielsen, *Nature* 365, 666 (1993), PNAs bind specifically and tightly to complementary DNA strands and are not degraded by nucleases. In fact, PNA binds more strongly to DNA than DNA itself does. This is probably because there is no electrostatic repulsion between the two strands, and also the polyamide backbone is more flexible. Because of this, PNA/DNA duplexes bind under a wider range of stringency conditions than DNA/DNA duplexes, making it easier to perform multiplex hybridization. Smaller probes can be used than with DNA due to the strong binding. In addition, it is more likely that single base mismatches can be determined with PNA/DNA hybridization because a single mismatch in a PNA/DNA 15-mer lowers the melting point ($T_{sub.m}$) by 8°-20° C, vs. 4°-16° C for the DNA/DNA 15-mer duplex. Also, the absence of charge groups in PNA means that hybridization can be done at low ionic strengths and reduce possible interference by salt during the analysis.

The present invention is useful for detecting cancer in mammals. In particular the invention is useful during diagnosis of pathological cell proliferative neoplasias which include, but are not limited to: acute myelogenous leukemias including acute monocytic leukemia, acute myeloblastic leukemia, acute promyelocytic leukemia, acute myelomonocytic leukemia, acute erythroleukemia, acute megakaryocytic leukemia, and acute undifferentiated leukemia, etc.; and chronic myelogenous leukemias including chronic myelomonocytic leukemia, chronic granulocytic leukemia, etc. Preferred mammals include monkeys, apes, cats, dogs, cows, pigs, horses, rabbits and humans. Particularly preferred are humans.

Pathological cell proliferative diseases, disorders, and/or conditions are often associated with inappropriate activation of proto-oncogenes. (Germann, E. P. et al., "The Etiology of Acute Leukemia: Molecular Genetics and Viral Oncology," in Neoplastic Diseases of the Blood, Vol 1., Wiernik, P. H. et al. eds., 161-182 (1985)).

5 Neoplasias are now believed to result from the qualitative alteration of a normal cellular gene product, or from the quantitative modification of gene expression by insertion into the chromosome of a viral sequence, by chromosomal translocation of a gene to a more actively transcribed region, or by some other mechanism. (Germann et al., supra) It is likely that mutated or altered expression of specific genes is

10 involved in the pathogenesis of some leukemias, among other tissues and cell types. (Germann et al., supra) Indeed, the human counterparts of the oncogenes involved in some animal neoplasias have been amplified or translocated in some cases of human leukemia and carcinoma. (Germann et al., supra)

For example, c-myc expression is highly amplified in the non-lymphocytic leukemia

15 cell line HL-60. When HL-60 cells are chemically induced to stop proliferation, the level of c-myc is found to be downregulated. (International Publication Number WO 91/15580) However, it has been shown that exposure of HL-60 cells to a DNA construct that is complementary to the 5' end of c-myc or c-myb blocks translation of the corresponding mRNAs which downregulates expression of the c-myc or c-myb

20 proteins and causes arrest of cell proliferation and differentiation of the treated cells. (International Publication Number WO 91/15580; Wickstrom et al., Proc. Natl. Acad. Sci. 85:1028 (1988); Anfossi et al., Proc. Natl. Acad. Sci. 86:3379 (1989)). However, the skilled artisan would appreciate the present invention's usefulness would not be limited to treatment of proliferative diseases, disorders, and/or conditions of

25 hematopoietic cells and tissues, in light of the numerous cells and cell types of varying origins which are known to exhibit proliferative phenotypes.

In addition to the foregoing, a polynucleotide can be used to control gene expression through triple helix formation or antisense DNA or RNA. Antisense techniques are discussed, for example, in Okano, J. *Neurochem.* 56: 560 (1991); "Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca

5 Raton, FL (1988). Triple helix formation is discussed in, for instance Lee et al., *Nucleic Acids Research* 6: 3073 (1979); Cooney et al., *Science* 241: 456 (1988); and Dervan et al., *Science* 251: 1360 (1991). Both methods rely on binding of the polynucleotide to a complementary DNA or RNA. For these techniques, preferred polynucleotides are usually oligonucleotides 20 to 40 bases in length and
10 complementary to either the region of the gene involved in transcription (triple helix - see Lee et al., *Nucl. Acids Res.* 6:3073 (1979); Cooney et al., *Science* 241:456 (1988); and Dervan et al., *Science* 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. *Neurochem.* 56:560 (1991); Oligodeoxy-nucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988).) Triple helix
15 formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques are effective in model systems, and the information disclosed herein can be used to design antisense or triple helix polynucleotides in an effort to treat or prevent disease.

20 Polynucleotides of the present invention are also useful in gene therapy. One goal of gene therapy is to insert a normal gene into an organism having a defective gene, in an effort to correct the genetic defect. The polynucleotides disclosed in the present invention offer a means of targeting such genetic defects in a highly accurate manner. Another goal is to insert a new gene that was not present in the host genome,
25 thereby producing a new trait in the host cell.

The polynucleotides are also useful for identifying individuals from minute biological samples. The United States military, for example, is considering the use of restriction fragment length polymorphism (RFLP) for identification of its personnel. In this technique, an individual's genomic DNA is digested with one or more
5 restriction enzymes, and probed on a Southern blot to yield unique bands for identifying personnel. This method does not suffer from the current limitations of "Dog Tags" which can be lost, switched, or stolen, making positive identification difficult. The polynucleotides of the present invention can be used as additional DNA markers for RFLP.

10 The polynucleotides of the present invention can also be used as an alternative to RFLP, by determining the actual base-by-base DNA sequence of selected portions of an individual's genome. These sequences can be used to prepare PCR primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique, individuals can be identified because each individual will have a
15 unique set of DNA sequences. Once an unique ID database is established for an individual, positive identification of that individual, living or dead, can be made from extremely small tissue samples.

Forensic biology also benefits from using DNA-based identification techniques as disclosed herein. DNA sequences taken from very small biological
20 samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, semen, synovial fluid, amniotic fluid, breast milk, lymph, pulmonary sputum or surfactant, urine, fecal matter, etc., can be amplified using PCR. In one prior art technique, gene sequences amplified from polymorphic loci, such as DQa class II HLA gene, are used in forensic biology to identify individuals. (Erlich, H., PCR
25 Technology, Freeman and Co. (1992).) Once these specific polymorphic loci are amplified, they are digested with one or more restriction enzymes, yielding an

identifying set of bands on a Southern blot probed with DNA corresponding to the DQa class II HLA gene. Similarly, polynucleotides of the present invention can be used as polymorphic markers for forensic purposes.

There is also a need for reagents capable of identifying the source of a particular tissue. Such need arises, for example, in forensics when presented with tissue of unknown origin. Appropriate reagents can comprise, for example, DNA probes or primers specific to particular tissue prepared from the sequences of the present invention. Panels of such reagents can identify tissue by species and/or by organ type. In a similar fashion, these reagents can be used to screen tissue cultures for contamination.

In the very least, the polynucleotides of the present invention can be used as molecular weight markers on Southern gels, as diagnostic probes for the presence of a specific mRNA in a particular cell type, as a probe to "subtract-out" known sequences in the process of discovering novel polynucleotides, for selecting and making oligomers for attachment to a "gene chip" or other support, to raise anti-DNA antibodies using DNA immunization techniques, and as an antigen to elicit an immune response.

Uses of the Polypeptides

Each of the polypeptides identified herein can be used in numerous ways. The following description should be considered exemplary and utilizes known techniques.

A polypeptide of the present invention can be used to assay protein levels in a biological sample using antibody-based techniques. For example, protein expression in tissues can be studied with classical immunohistological methods. (Jalkanen, M., et al., J. Cell. Biol. 101:976-985 (1985); Jalkanen, M., et al., J. Cell . Biol. 105:3087-3096 (1987).) Other antibody-based methods useful for detecting protein gene

expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase, and radioisotopes, such as iodine (^{125}I , ^{121}I), carbon (^{14}C), sulfur (^{35}S), tritium (^3H), indium (^{112}In), and
5 technetium ($^{99\text{m}}\text{Tc}$), and fluorescent labels, such as fluorescein and rhodamine, and biotin.

In addition to assaying secreted protein levels in a biological sample, proteins can also be detected in vivo by imaging. Antibody labels or markers for in vivo imaging of protein include those detectable by X-radiography, NMR or ESR. For X-
10 radiography, suitable labels include radioisotopes such as barium or cesium, which emit detectable radiation but are not overtly harmful to the subject. Suitable markers for NMR and ESR include those with a detectable characteristic spin, such as deuterium, which may be incorporated into the antibody by labeling of nutrients for the relevant hybridoma.

15 A protein-specific antibody or antibody fragment which has been labeled with an appropriate detectable imaging moiety, such as a radioisotope (for example, ^{131}I , ^{112}In , $^{99\text{m}}\text{Tc}$), a radio-opaque substance, or a material detectable by nuclear magnetic resonance, is introduced (for example, parenterally, subcutaneously, or intraperitoneally) into the mammal. It will be understood in the art that the size of the
20 subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the case of a radioisotope moiety, for a human subject, the quantity of radioactivity injected will normally range from about 5 to 20 millicuries of $^{99\text{m}}\text{Tc}$. The labeled antibody or antibody fragment will then preferentially accumulate at the location of cells which contain the specific protein.
25 In vivo tumor imaging is described in S.W. Burchiel et al., "Immunopharmacokinetics of Radiolabeled Antibodies and Their Fragments." (Chapter 13 in Tumor Imaging:

The Radiochemical Detection of Cancer, S.W. Burchiel and B. A. Rhodes, eds.,
Masson Publishing Inc. (1982).)

Thus, the invention provides a diagnostic method of a disorder, which
involves (a) assaying the expression of a polypeptide of the present invention in cells
5 or body fluid of an individual; (b) comparing the level of gene expression with a
standard gene expression level, whereby an increase or decrease in the assayed
polypeptide gene expression level compared to the standard expression level is
indicative of a disorder. With respect to cancer, the presence of a relatively high
amount of transcript in biopsied tissue from an individual may indicate a
10 predisposition for the development of the disease, or may provide a means for
detecting the disease prior to the appearance of actual clinical symptoms. A more
definitive diagnosis of this type may allow health professionals to employ
preventative measures or aggressive treatment earlier thereby preventing the
development or further progression of the cancer.

15 Moreover, polypeptides of the present invention can be used to treat, prevent,
and/or diagnose disease. For example, patients can be administered a polypeptide of
the present invention in an effort to replace absent or decreased levels of the
polypeptide (e.g., insulin), to supplement absent or decreased levels of a different
polypeptide (e.g., hemoglobin S for hemoglobin B, SOD, catalase, DNA repair
20 proteins), to inhibit the activity of a polypeptide (e.g., an oncogene or tumor
suppressor), to activate the activity of a polypeptide (e.g., by binding to a receptor), to
reduce the activity of a membrane bound receptor by competing with it for free ligand
(e.g., soluble TNF receptors used in reducing inflammation), or to bring about a
desired response (e.g., blood vessel growth inhibition, enhancement of the immune
25 response to proliferative cells or tissues).

Similarly, antibodies directed to a polypeptide of the present invention can also be used to treat, prevent, and/or diagnose disease. For example, administration of an antibody directed to a polypeptide of the present invention can bind and reduce overproduction of the polypeptide. Similarly, administration of an antibody can
5 activate the polypeptide, such as by binding to a polypeptide bound to a membrane (receptor).

At the very least, the polypeptides of the present invention can be used as molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods well known to those of skill in the art. Polypeptides can also
10 be used to raise antibodies, which in turn are used to measure protein expression from a recombinant cell, as a way of assessing transformation of the host cell. Moreover, the polypeptides of the present invention can be used to test the following biological activities.

15 **Gene Therapy Methods**

Another aspect of the present invention is to gene therapy methods for treating or preventing disorders, diseases and conditions. The gene therapy methods relate to the introduction of nucleic acid (DNA, RNA and antisense DNA or RNA) sequences into an animal to achieve expression of a polypeptide of the present invention. This
20 method requires a polynucleotide which codes for a polypeptide of the invention that operatively linked to a promoter and any other genetic elements necessary for the expression of the polypeptide by the target tissue. Such gene therapy and delivery techniques are known in the art, see, for example, WO90/11092, which is herein incorporated by reference.

25 Thus, for example, cells from a patient may be engineered with a polynucleotide (DNA or RNA) comprising a promoter operably linked to a

polynucleotide of the invention *ex vivo*, with the engineered cells then being provided to a patient to be treated with the polypeptide. Such methods are well-known in the art. For example, see Beldegrun et al., J. Natl. Cancer Inst., 85:207-216 (1993); Ferrantini et al., Cancer Research, 53:107-1112 (1993); Ferrantini et al., J. Immunology 153: 4604-4615 (1994); Kaido, T., et al., Int. J. Cancer 60: 221-229 (1995); Ogura et al., Cancer Research 50: 5102-5106 (1990); Santodonato, et al., Human Gene Therapy 7:1-10 (1996); Santodonato, et al., Gene Therapy 4:1246-1255 (1997); and Zhang, et al., Cancer Gene Therapy 3: 31-38 (1996)), which are herein incorporated by reference. In one embodiment, the cells which are engineered are arterial cells. The arterial cells may be reintroduced into the patient through direct injection to the artery, the tissues surrounding the artery, or through catheter injection.

As discussed in more detail below, the polynucleotide constructs can be delivered by any method that delivers injectable materials to the cells of an animal, such as, injection into the interstitial space of tissues (heart, muscle, skin, lung, liver, and the like). The polynucleotide constructs may be delivered in a pharmaceutically acceptable liquid or aqueous carrier.

In one embodiment, the polynucleotide of the invention is delivered as a naked polynucleotide. The term "naked" polynucleotide, DNA or RNA refers to sequences that are free from any delivery vehicle that acts to assist, promote or facilitate entry into the cell, including viral sequences, viral particles, liposome formulations, lipofectin or precipitating agents and the like. However, the polynucleotides of the invention can also be delivered in liposome formulations and lipofectin formulations and the like can be prepared by methods well known to those skilled in the art. Such methods are described, for example, in U.S. Patent Nos. 5,593,972, 5,589,466, and 5,580,859, which are herein incorporated by reference.

The polynucleotide vector constructs of the invention used in the gene therapy method are preferably constructs that will not integrate into the host genome nor will they contain sequences that allow for replication. Appropriate vectors include pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; 5 pSVK3, pBPV, pMSG and pSVL available from Pharmacia; and pEF1/V5, pcDNA3.1, and pRc/CMV2 available from Invitrogen. Other suitable vectors will be readily apparent to the skilled artisan.

Any strong promoter known to those skilled in the art can be used for driving the expression of polynucleotide sequence of the invention. Suitable promoters 10 include adenoviral promoters, such as the adenoviral major late promoter; or heterologous promoters, such as the cytomegalovirus (CMV) promoter; the respiratory syncytial virus (RSV) promoter; inducible promoters, such as the MMT promoter, the metallothionein promoter; heat shock promoters; the albumin promoter; the ApoA1 promoter; human globin promoters; viral thymidine kinase promoters, 15 such as the Herpes Simplex thymidine kinase promoter; retroviral LTRs; the b-actin promoter; and human growth hormone promoters. The promoter also may be the native promoter for the polynucleotides of the invention.

Unlike other gene therapy techniques, one major advantage of introducing naked nucleic acid sequences into target cells is the transitory nature of the 20 polynucleotide synthesis in the cells. Studies have shown that non-replicating DNA sequences can be introduced into cells to provide production of the desired polypeptide for periods of up to six months.

The polynucleotide construct of the invention can be delivered to the interstitial space of tissues within the an animal, including of muscle, skin, brain, lung, liver, 25 spleen, bone marrow, thymus, heart, lymph, blood, bone, cartilage, pancreas, kidney, gall bladder, stomach, intestine, testis, ovary, uterus, rectum, nervous system, eye,

gland, and connective tissue. Interstitial space of the tissues comprises the intercellular, fluid, mucopolysaccharide matrix among the reticular fibers of organ tissues, elastic fibers in the walls of vessels or chambers, collagen fibers of fibrous tissues, or that same matrix within connective tissue ensheathing muscle cells or in the lacunae of bone. It is similarly the space occupied by the plasma of the circulation and the lymph fluid of the lymphatic channels. Delivery to the interstitial space of muscle tissue is preferred for the reasons discussed below. They may be conveniently delivered by injection into the tissues comprising these cells. They are preferably delivered to and expressed in persistent, non-dividing cells which are differentiated, although delivery and expression may be achieved in non-differentiated or less completely differentiated cells, such as, for example, stem cells of blood or skin fibroblasts. *In vivo* muscle cells are particularly competent in their ability to take up and express polynucleotides.

For the naked *nucleic acid* sequence injection, an effective dosage amount of DNA or RNA will be in the range of from about 0.05 mg/kg body weight to about 50 mg/kg body weight. Preferably the dosage will be from about 0.005 mg/kg to about 20 mg/kg and more preferably from about 0.05 mg/kg to about 5 mg/kg. Of course, as the artisan of ordinary skill will appreciate, this dosage will vary according to the tissue site of injection. The appropriate and effective dosage of nucleic acid sequence can readily be determined by those of ordinary skill in the art and may depend on the condition being treated and the route of administration.

The preferred route of administration is by the parenteral route of injection into the interstitial space of tissues. However, other parenteral routes may also be used, such as, inhalation of an aerosol formulation particularly for delivery to lungs or bronchial tissues, throat or mucous membranes of the nose. In addition, naked DNA constructs can be delivered to arteries during angioplasty by the catheter used in the procedure.

The naked polynucleotides are delivered by any method known in the art, including, but not limited to, direct needle injection at the delivery site, intravenous injection, topical administration, catheter infusion, and so-called "gene guns". These delivery methods are known in the art.

5 The constructs may also be delivered with delivery vehicles such as viral sequences, viral particles, liposome formulations, lipofectin, precipitating agents, etc. Such methods of delivery are known in the art.

In certain embodiments, the polynucleotide constructs of the invention are complexed in a liposome preparation. Liposomal preparations for use in the instant
10 invention include cationic (positively charged), anionic (negatively charged) and neutral preparations. However, cationic liposomes are particularly preferred because a tight charge complex can be formed between the cationic liposome and the polyanionic nucleic acid. Cationic liposomes have been shown to mediate intracellular delivery of plasmid DNA (Felgner et al., Proc. Natl. Acad. Sci. USA ,
15 84:7413-7416 (1987), which is herein incorporated by reference); mRNA (Malone et al., Proc. Natl. Acad. Sci. USA , 86:6077-6081 (1989), which is herein incorporated by reference); and purified transcription factors (Debs et al., J. Biol. Chem., 265:10189-10192 (1990), which is herein incorporated by reference), in functional form.

20 Cationic liposomes are readily available. For example, N[1-2,3-dioleoyloxy)propyl]-N,N,N-triethylammonium (DOTMA) liposomes are particularly useful and are available under the trademark Lipofectin, from GIBCO BRL, Grand Island, N.Y. (See, also, Felgner et al., Proc. Natl Acad. Sci. USA , 84:7413-7416 (1987), which is herein incorporated by reference). Other commercially
25 available liposomes include transfectace (DDAB/DOPE) and DOTAP/DOPE (Boehringer).

Other cationic liposomes can be prepared from readily available materials using techniques well known in the art. See, e.g. PCT Publication NO: WO 90/11092 (which is herein incorporated by reference) for a description of the synthesis of DOTAP (1,2-bis(oleoyloxy)-3-(trimethylammonio)propane) liposomes. Preparation of DOTMA liposomes is explained in the literature, see, e.g., Felgner et al., Proc. Natl. Acad. Sci. USA, 84:7413-7417, which is herein incorporated by reference. Similar methods can be used to prepare liposomes from other cationic lipid materials.

Similarly, anionic and neutral liposomes are readily available, such as from Avanti Polar Lipids (Birmingham, Ala.), or can be easily prepared using readily available materials. Such materials include phosphatidyl, choline, cholesterol, phosphatidyl ethanolamine, dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), dioleoylphosphatidyl ethanolamine (DOPE), among others. These materials can also be mixed with the DOTMA and DOTAP starting materials in appropriate ratios. Methods for making liposomes using these materials are well known in the art.

For example, commercially dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), and dioleoylphosphatidyl ethanolamine (DOPE) can be used in various combinations to make conventional liposomes, with or without the addition of cholesterol. Thus, for example, DOPG/DOPC vesicles can be prepared by drying 50 mg each of DOPG and DOPC under a stream of nitrogen gas into a sonication vial. The sample is placed under a vacuum pump overnight and is hydrated the following day with deionized water. The sample is then sonicated for 2 hours in a capped vial, using a Heat Systems model 350 sonicator equipped with an inverted cup (bath type) probe at the maximum setting while the bath is circulated at 15EC. Alternatively, negatively charged vesicles can be prepared without sonication to produce multilamellar vesicles or by extrusion through nucleopore membranes to

produce unilamellar vesicles of discrete size. Other methods are known and available to those of skill in the art.

The liposomes can comprise multilamellar vesicles (MLVs), small unilamellar vesicles (SUVs), or large unilamellar vesicles (LUVs), with SUVs being preferred.

- 5 The various liposome-nucleic acid complexes are prepared using methods well known in the art. See, e.g., Straubinger et al., *Methods of Immunology*, 101:512-527 (1983), which is herein incorporated by reference. For example, MLVs containing nucleic acid can be prepared by depositing a thin film of phospholipid on the walls of a glass tube and subsequently hydrating with a solution of the material to be encapsulated.
- 10 SUVs are prepared by extended sonication of MLVs to produce a homogeneous population of unilamellar liposomes. The material to be entrapped is added to a suspension of preformed MLVs and then sonicated. When using liposomes containing cationic lipids, the dried lipid film is resuspended in an appropriate solution such as sterile water or an isotonic buffer solution such as 10 mM Tris/NaCl, sonicated, and
- 15 then the preformed liposomes are mixed directly with the DNA. The liposome and DNA form a very stable complex due to binding of the positively charged liposomes to the cationic DNA. SUVs find use with small nucleic acid fragments. LUVs are prepared by a number of methods, well known in the art. Commonly used methods include Ca^{2+} -EDTA chelation (Papahadjopoulos et al., *Biochim. Biophys. Acta*, 394:483 (1975); Wilson et al., *Cell*, 17:77 (1979)); ether injection (Deamer et al., *Biochim. Biophys. Acta*, 443:629 (1976); Ostro et al., *Biochem. Biophys. Res. Commun.*, 76:836 (1977); Fraley et al., *Proc. Natl. Acad. Sci. USA*, 76:3348 (1979)); detergent dialysis (Enoch et al., *Proc. Natl. Acad. Sci. USA*, 76:145 (1979)); and reverse-phase evaporation (REV) (Fraley et al., *J. Biol. Chem.*, 255:10431 (1980);
- 20 Szoka et al., *Proc. Natl. Acad. Sci. USA*, 75:145 (1978); Schaefer-Ridder et al., *Science*, 215:166 (1982)), which are herein incorporated by reference.

Generally, the ratio of DNA to liposomes will be from about 10:1 to about 1:10. Preferably, the ratio will be from about 5:1 to about 1:5. More preferably, the ratio will be about 3:1 to about 1:3. Still more preferably, the ratio will be about 1:1.

U.S. Patent NO: 5,676,954 (which is herein incorporated by reference) reports
5 on the injection of genetic material, complexed with cationic liposomes carriers, into mice. U.S. Patent Nos. 4,897,355, 4,946,787, 5,049,386, 5,459,127, 5,589,466, 5,693,622, 5,580,859, 5,703,055, and international publication NO: WO 94/9469 (which are herein incorporated by reference) provide cationic lipids for use in transfecting DNA into cells and mammals. U.S. Patent Nos. 5,589,466, 5,693,622,
10 5,580,859, 5,703,055, and international publication NO: WO 94/9469 (which are herein incorporated by reference) provide methods for delivering DNA-cationic lipid complexes to mammals.

In certain embodiments, cells are engineered, *ex vivo* or *in vivo*, using a retroviral particle containing RNA which comprises a sequence encoding
15 polypeptides of the invention. Retroviruses from which the retroviral plasmid vectors may be derived include, but are not limited to, Moloney Murine Leukemia Virus, spleen necrosis virus, Rous sarcoma Virus, Harvey Sarcoma Virus, avian leukosis virus, gibbon ape leukemia virus, human immunodeficiency virus, Myeloproliferative Sarcoma Virus, and mammary tumor virus.

20 The retroviral plasmid vector is employed to transduce packaging cell lines to form producer cell lines. Examples of packaging cells which may be transfected include, but are not limited to, the PE501, PA317, R-2, R-AM, PA12, T19-14X, VT-19-17-H2, RCRE, RCRIP, GP+E-86, GP+envAm12, and DAN cell lines as described in Miller, Human Gene Therapy, 1:5-14 (1990), which is incorporated herein by
25 reference in its entirety. The vector may transduce the packaging cells through any means known in the art. Such means include, but are not limited to, electroporation,

the use of liposomes, and CaPO_4 precipitation. In one alternative, the retroviral plasmid vector may be encapsulated into a liposome, or coupled to a lipid, and then administered to a host.

The producer cell line generates infectious retroviral vector particles which
5 include polynucleotide encoding polypeptides of the invention. Such retroviral vector particles then may be employed, to transduce eukaryotic cells, either *in vitro* or *in vivo*. The transduced eukaryotic cells will express polypeptides of the invention.

In certain other embodiments, cells are engineered, *ex vivo* or *in vivo*, with polynucleotides of the invention contained in an adenovirus vector. Adenovirus can
10 be manipulated such that it encodes and expresses polypeptides of the invention, and at the same time is inactivated in terms of its ability to replicate in a normal lytic viral life cycle. Adenovirus expression is achieved without integration of the viral DNA into the host cell chromosome, thereby alleviating concerns about insertional mutagenesis. Furthermore, adenoviruses have been used as live enteric vaccines for
15 many years with an excellent safety profile (Schwartz et al., Am. Rev. Respir. Dis., 109:233-238 (1974)). Finally, adenovirus mediated gene transfer has been demonstrated in a number of instances including transfer of alpha-1-antitrypsin and CFTR to the lungs of cotton rats (Rosenfeld et al., Science, 252:431-434 (1991); Rosenfeld et al., Cell, 68:143-155 (1992)). Furthermore, extensive studies to attempt
20 to establish adenovirus as a causative agent in human cancer were uniformly negative (Green et al. Proc. Natl. Acad. Sci. USA, 76:6606 (1979)).

Suitable adenoviral vectors useful in the present invention are described, for example, in Kozarsky and Wilson, Curr. Opin. Genet. Devel., 3:499-503 (1993); Rosenfeld et al., Cell, 68:143-155 (1992); Engelhardt et al., Human Genet. Ther.,
25 4:759-769 (1993); Yang et al., Nature Genet., 7:362-369 (1994); Wilson et al., Nature, 365:691-692 (1993); and U.S. Patent NO: 5,652,224, which are herein

incorporated by reference. For example, the adenovirus vector Ad2 is useful and can be grown in human 293 cells. These cells contain the E1 region of adenovirus and constitutively express E1a and E1b, which complement the defective adenoviruses by providing the products of the genes deleted from the vector. In addition to Ad2, other
5 varieties of adenovirus (e.g., Ad3, Ad5, and Ad7) are also useful in the present invention.

Preferably, the adenoviruses used in the present invention are replication deficient. Replication deficient adenoviruses require the aid of a helper virus and/or packaging cell line to form infectious particles. The resulting virus is capable of
10 infecting cells and can express a polynucleotide of interest which is operably linked to a promoter, but cannot replicate in most cells. Replication deficient adenoviruses may be deleted in one or more of all or a portion of the following genes: E1a, E1b, E3, E4, E2a, or L1 through L5.

In certain other embodiments, the cells are engineered, *ex vivo* or *in vivo*,
15 using an adeno-associated virus (AAV). AAVs are naturally occurring defective viruses that require helper viruses to produce infectious particles (Muzyczka, Curr. Topics in Microbiol. Immunol., 158:97 (1992)). It is also one of the few viruses that may integrate its DNA into non-dividing cells. Vectors containing as little as 300 base pairs of AAV can be packaged and can integrate, but space for exogenous DNA is
20 limited to about 4.5 kb. Methods for producing and using such AAVs are known in the art. See, for example, U.S. Patent Nos. 5,139,941, 5,173,414, 5,354,678, 5,436,146, 5,474,935, 5,478,745, and 5,589,377.

For example, an appropriate AAV vector for use in the present invention will include all the sequences necessary for DNA replication, encapsidation, and host-cell
25 integration. The polynucleotide construct containing polynucleotides of the invention is inserted into the AAV vector using standard cloning methods, such as those found

in Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press (1989). The recombinant AAV vector is then transfected into packaging cells which are infected with a helper virus, using any standard technique, including lipofection, electroporation, calcium phosphate precipitation, etc. Appropriate helper
5 viruses include adenoviruses, cytomegaloviruses, vaccinia viruses, or herpes viruses. Once the packaging cells are transfected and infected, they will produce infectious AAV viral particles which contain the polynucleotide construct of the invention. These viral particles are then used to transduce eukaryotic cells, either *ex vivo* or *in vivo*. The transduced cells will contain the polynucleotide construct integrated into its
10 genome, and will express the desired gene product.

Another method of gene therapy involves operably associating heterologous control regions and endogenous polynucleotide sequences (e.g. encoding the polypeptide sequence of interest) via homologous recombination (see, e.g., U.S. Patent NO: 5,641,670, issued June 24, 1997; International Publication NO: WO
15 96/29411, published September 26, 1996; International Publication NO: WO 94/12650, published August 4, 1994; Koller et al., Proc. Natl. Acad. Sci. USA, 86:8932-8935 (1989); and Zijlstra et al., Nature, 342:435-438 (1989). This method involves the activation of a gene which is present in the target cells, but which is not normally expressed in the cells, or is expressed at a lower level than desired.

20 Polynucleotide constructs are made, using standard techniques known in the art, which contain the promoter with targeting sequences flanking the promoter. Suitable promoters are described herein. The targeting sequence is sufficiently complementary to an endogenous sequence to permit homologous recombination of the promoter-targeting sequence with the endogenous sequence. The targeting
25 sequence will be sufficiently near the 5' end of the desired endogenous

polynucleotide sequence so the promoter will be operably linked to the endogenous sequence upon homologous recombination.

The promoter and the targeting sequences can be amplified using PCR.

Preferably, the amplified promoter contains distinct restriction enzyme sites on the 5'

5 and 3' ends. Preferably, the 3' end of the first targeting sequence contains the same restriction enzyme site as the 5' end of the amplified promoter and the 5' end of the second targeting sequence contains the same restriction site as the 3' end of the amplified promoter. The amplified promoter and targeting sequences are digested and ligated together.

10 The promoter-targeting sequence construct is delivered to the cells, either as naked polynucleotide, or in conjunction with transfection-facilitating agents, such as liposomes, viral sequences, viral particles, whole viruses, lipofection, precipitating agents, etc., described in more detail above. The P promoter-targeting sequence can be delivered by any method, included direct needle injection, intravenous injection,
15 topical administration, catheter infusion, particle accelerators, etc. The methods are described in more detail below.

The promoter-targeting sequence construct is taken up by cells. Homologous recombination between the construct and the endogenous sequence takes place, such that an endogenous sequence is placed under the control of the promoter. The
20 promoter then drives the expression of the endogenous sequence.

The polynucleotides encoding polypeptides of the present invention may be administered along with other polynucleotides encoding other angiogenic proteins. Angiogenic proteins include, but are not limited to, acidic and basic fibroblast growth factors, VEGF-1, VEGF-2 (VEGF-C), VEGF-3 (VEGF-B), epidermal growth factor
25 alpha and beta, platelet-derived endothelial cell growth factor, platelet-derived growth factor, tumor necrosis factor alpha, hepatocyte growth factor, insulin like growth

factor, colony stimulating factor, macrophage colony stimulating factor, granulocyte/macrophage colony stimulating factor, and nitric oxide synthase.

Preferably, the polynucleotide encoding a polypeptide of the invention contains a secretory signal sequence that facilitates secretion of the protein.

5 Typically, the signal sequence is positioned in the coding region of the polynucleotide to be expressed towards or at the 5' end of the coding region. The signal sequence may be homologous or heterologous to the polynucleotide of interest and may be homologous or heterologous to the cells to be transfected. Additionally, the signal sequence may be chemically synthesized using methods known in the art.

10 Any mode of administration of any of the above-described polynucleotides constructs can be used so long as the mode results in the expression of one or more molecules in an amount sufficient to provide a therapeutic effect. This includes direct needle injection, systemic injection, catheter infusion, biolistic injectors, particle accelerators (i.e., "gene guns"), gelfoam sponge depots, other commercially available
15 depot materials, osmotic pumps (e.g., Alza minipumps), oral or suppositorial solid (tablet or pill) pharmaceutical formulations, and decanting or topical applications during surgery. For example, direct injection of naked calcium phosphate-precipitated plasmid into rat liver and rat spleen or a protein-coated plasmid into the portal vein has resulted in gene expression of the foreign gene in the
20 rat livers. (Kaneda et al., Science, 243:375 (1989)).

A preferred method of local administration is by direct injection. Preferably, a recombinant molecule of the present invention complexed with a delivery vehicle is administered by direct injection into or locally within the area of arteries.

Administration of a composition locally within the area of arteries refers to injecting
25 the composition centimeters and preferably, millimeters within arteries.

Another method of local administration is to contact a polynucleotide construct of the present invention in or around a surgical wound. For example, a patient can undergo surgery and the polynucleotide construct can be coated on the surface of tissue inside the wound or the construct can be injected into areas of tissue
5 inside the wound.

Therapeutic compositions useful in systemic administration, include recombinant molecules of the present invention complexed to a targeted delivery vehicle of the present invention. Suitable delivery vehicles for use with systemic administration comprise liposomes comprising ligands for targeting the vehicle to a
10 particular site.

Preferred methods of systemic administration, include intravenous injection, aerosol, oral and percutaneous (topical) delivery. Intravenous injections can be performed using methods standard in the art. Aerosol delivery can also be performed using methods standard in the art (see, for example, Stribling et al., Proc. Natl. Acad.
15 Sci. USA , 189:11277-11281 (1992), which is incorporated herein by reference). Oral delivery can be performed by complexing a polynucleotide construct of the present invention to a carrier capable of withstanding degradation by digestive enzymes in the gut of an animal. Examples of such carriers, include plastic capsules or tablets, such as those known in the art. Topical delivery can be performed by mixing a
20 polynucleotide construct of the present invention with a lipophilic reagent (e.g., DMSO) that is capable of passing into the skin.

Determining an effective amount of substance to be delivered can depend upon a number of factors including, for example, the chemical structure and biological activity of the substance, the age and weight of the animal, the precise
25 condition requiring treatment and its severity, and the route of administration. The frequency of treatments depends upon a number of factors, such as the amount of

polynucleotide constructs administered per dose, as well as the health and history of the subject. The precise amount, number of doses, and timing of doses will be determined by the attending physician or veterinarian. Therapeutic compositions of the present invention can be administered to any animal, preferably to mammals and
5 birds. Preferred mammals include humans, dogs, cats, mice, rats, rabbits sheep, cattle, horses and pigs, with humans being particularly

Biological Activities

The polynucleotides or polypeptides, or agonists or antagonists of the present
10 invention can be used in assays to test for one or more biological activities. If these polynucleotides and polypeptides do exhibit activity in a particular assay, it is likely that these molecules may be involved in the diseases associated with the biological activity. Thus, the polynucleotides or polypeptides, or agonists or antagonists could be used to treat the associated disease.

15

Immune Activity

The polynucleotides or polypeptides, or agonists or antagonists of the present invention may be useful in treating, preventing, and/or diagnosing diseases, disorders, and/or conditions of the immune system, by activating or inhibiting the proliferation,
20 differentiation, or mobilization (chemotaxis) of immune cells. Immune cells develop through a process called hematopoiesis, producing myeloid (platelets, red blood cells, neutrophils, and macrophages) and lymphoid (B and T lymphocytes) cells from pluripotent stem cells. The etiology of these immune diseases, disorders, and/or conditions may be genetic, somatic, such as cancer or some autoimmune diseases,
25 disorders, and/or conditions, acquired (e.g., by chemotherapy or toxins), or infectious. Moreover, a polynucleotides or polypeptides, or agonists or antagonists of the present

invention can be used as a marker or detector of a particular immune system disease or disorder.

A polynucleotides or polypeptides, or agonists or antagonists of the present invention may be useful in treating, preventing, and/or diagnosing diseases, disorders, and/or conditions of hematopoietic cells. A polynucleotides or polypeptides, or agonists or antagonists of the present invention could be used to increase differentiation and proliferation of hematopoietic cells, including the pluripotent stem cells, in an effort to treat or prevent those diseases, disorders, and/or conditions associated with a decrease in certain (or many) types hematopoietic cells. Examples of immunologic deficiency syndromes include, but are not limited to: blood protein diseases, disorders, and/or conditions (e.g. agammaglobulinemia, dysgammaglobulinemia), ataxia telangiectasia, common variable immunodeficiency, Digeorge Syndrome, HIV infection, HTLV-BLV infection, leukocyte adhesion deficiency syndrome, lymphopenia, phagocyte bactericidal dysfunction, severe combined immunodeficiency (SCIDs), Wiskott-Aldrich Disorder, anemia, thrombocytopenia, or hemoglobinuria.

Moreover, a polynucleotides or polypeptides, or agonists or antagonists of the present invention could also be used to modulate hemostatic (the stopping of bleeding) or thrombolytic activity (clot formation). For example, by increasing hemostatic or thrombolytic activity, a polynucleotides or polypeptides, or agonists or antagonists of the present invention could be used to treat or prevent blood coagulation diseases, disorders, and/or conditions (e.g., afibrinogenemia, factor deficiencies), blood platelet diseases, disorders, and/or conditions (e.g. thrombocytopenia), or wounds resulting from trauma, surgery, or other causes. Alternatively, a polynucleotides or polypeptides, or agonists or antagonists of the present invention that can decrease hemostatic or thrombolytic activity could be used

to inhibit or dissolve clotting. These molecules could be important in the treatment or prevention of heart attacks (infarction), strokes, or scarring.

A polynucleotides or polypeptides, or agonists or antagonists of the present invention may also be useful in treating, preventing, and/or diagnosing autoimmune diseases, disorders, and/or conditions. Many autoimmune diseases, disorders, and/or conditions result from inappropriate recognition of self as foreign material by immune cells. This inappropriate recognition results in an immune response leading to the destruction of the host tissue. Therefore, the administration of a polynucleotides or polypeptides, or agonists or antagonists of the present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing autoimmune diseases, disorders, and/or conditions.

Examples of autoimmune diseases, disorders, and/or conditions that can be treated, prevented, and/or diagnosed or detected by the present invention include, but are not limited to: Addison's Disease, hemolytic anemia, antiphospholipid syndrome, rheumatoid arthritis, dermatitis, allergic encephalomyelitis, glomerulonephritis, Goodpasture's Syndrome, Graves' Disease, Multiple Sclerosis, Myasthenia Gravis, Neuritis, Ophthalmia, Bullous Pemphigoid, Pemphigus, Polyendocrinopathies, Purpura, Reiter's Disease, Stiff-Man Syndrome, Autoimmune Thyroiditis, Systemic Lupus Erythematosus, Autoimmune Pulmonary Inflammation, Guillain-Barre Syndrome, insulin dependent diabetes mellitus, and autoimmune inflammatory eye disease.

Similarly, allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems, may also be treated, prevented, and/or diagnosed by polynucleotides or polypeptides, or agonists or antagonists of the

present invention. Moreover, these molecules can be used to treat anaphylaxis, hypersensitivity to an antigenic molecule, or blood group incompatibility.

A polynucleotides or polypeptides, or agonists or antagonists of the present invention may also be used to treat, prevent, and/or diagnose organ rejection or graft-versus-host disease (GVHD). Organ-rejection occurs by host immune cell destruction of the transplanted tissue through an immune response. Similarly, an immune response is also involved in GVHD, but, in this case, the foreign transplanted immune cells destroy the host tissues. The administration of a polynucleotides or polypeptides, or agonists or antagonists of the present invention that inhibits an
10 immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing organ rejection or GVHD.

Similarly, a polynucleotides or polypeptides, or agonists or antagonists of the present invention may also be used to modulate inflammation. For example, the polypeptide or polynucleotide or agonists
15 or antagonist may inhibit the proliferation and differentiation of cells involved in an inflammatory response. These molecules can be used to treat, prevent, and/or diagnose inflammatory conditions, both chronic and acute conditions, including chronic prostatitis, granulomatous prostatitis and malacoplakia, inflammation associated with infection (e.g., septic shock, sepsis, or systemic inflammatory
20 response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, or resulting from over production of cytokines (e.g., TNF or IL-1.)

25 **Hyperproliferative Disorders**

A polynucleotides or polypeptides, or agonists or antagonists of the invention can be used to treat, prevent, and/or diagnose hyperproliferative diseases, disorders, including neoplasms. A polynucleotides or polypeptides, or agonists or antagonists of the present invention may inhibit the proliferation of the disorder through direct or
5 indirect interactions. Alternatively, a polynucleotides or polypeptides, or agonists or antagonists of the present invention may proliferate other cells which can inhibit the hyperproliferative disorder.

For example, by increasing an immune response, particularly increasing antigenic qualities of the hyperproliferative disorder or by proliferating,
10 differentiating, or mobilizing T-cells, hyperproliferative diseases, disorders, and/or conditions can be treated, prevented, and/or diagnosed. This immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, decreasing an immune response may also be a method of treating, preventing, and/or diagnosing hyperproliferative diseases,
15 disorders, and/or conditions, such as a chemotherapeutic agent.

Examples of hyperproliferative diseases, disorders, and/or conditions that can be treated, prevented, and/or diagnosed by polynucleotides or polypeptides, or agonists or antagonists of the present invention include, but are not limited to neoplasms located in the: colon, abdomen, bone, breast, digestive system, liver,
20 pancreas, peritoneum, endocrine glands (adrenal, parathyroid, pituitary, testicles, ovary, thymus, thyroid), eye, head and neck, nervous (central and peripheral), lymphatic system, pelvic, skin, soft tissue, spleen, thoracic, and urogenital.

Similarly, other hyperproliferative diseases, disorders, and/or conditions can also be treated, prevented, and/or diagnosed by a polynucleotides or polypeptides, or
25 agonists or antagonists of the present invention. Examples of such hyperproliferative diseases, disorders, and/or conditions include, but are not limited to:

hypergammaglobulinemia, lymphoproliferative diseases, disorders, and/or conditions, paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenstrom's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease, besides neoplasia, located in an organ system listed above.

5 One preferred embodiment utilizes polynucleotides of the present invention to inhibit aberrant cellular division, by gene therapy using the present invention, and/or protein fusions or fragments thereof.

 Thus, the present invention provides a method for treating or preventing cell proliferative diseases, disorders, and/or conditions by inserting into an abnormally
10 proliferating cell a polynucleotide of the present invention, wherein said polynucleotide represses said expression.

 Another embodiment of the present invention provides a method of treating or preventing cell-proliferative diseases, disorders, and/or conditions in individuals comprising administration of one or more active gene copies of the present invention
15 to an abnormally proliferating cell or cells. In a preferred embodiment, polynucleotides of the present invention is a DNA construct comprising a recombinant expression vector effective in expressing a DNA sequence encoding said polynucleotides. In another preferred embodiment of the present invention, the DNA construct encoding the polynucleotides of the present invention is inserted into cells to
20 be treated utilizing a retrovirus, or more preferably an adenoviral vector (See G J. Nabel, et. al., PNAS 1999 96: 324-326, which is hereby incorporated by reference). In a most preferred embodiment, the viral vector is defective and will not transform non-proliferating cells, only proliferating cells. Moreover, in a preferred embodiment, the polynucleotides of the present invention inserted into proliferating
25 cells either alone, or in combination with or fused to other polynucleotides, can then be modulated via an external stimulus (i.e. magnetic, specific small molecule,

chemical, or drug administration, etc.), which acts upon the promoter upstream of said polynucleotides to induce expression of the encoded protein product. As such the beneficial therapeutic affect of the present invention may be expressly modulated (i.e. to increase, decrease, or inhibit expression of the present invention) based upon said
5 external stimulus.

Polynucleotides of the present invention may be useful in repressing expression of oncogenic genes or antigens. By "repressing expression of the oncogenic genes " is intended the suppression of the transcription of the gene, the degradation of the gene transcript (pre-message RNA), the inhibition of splicing, the
10 destruction of the messenger RNA, the prevention of the post-translational modifications of the protein, the destruction of the protein, or the inhibition of the normal function of the protein.

For local administration to abnormally proliferating cells, polynucleotides of the present invention may be administered by any method known to those of skill in
15 the art including, but not limited to transfection, electroporation, microinjection of cells, or in vehicles such as liposomes, lipofectin, or as naked polynucleotides, or any other method described throughout the specification. The polynucleotide of the present invention may be delivered by known gene delivery systems such as, but not limited to, retroviral vectors (Gilboa, J. Virology 44:845 (1982); Hocke, Nature
20 320:275 (1986); Wilson, et al., Proc. Natl. Acad. Sci. U.S.A. 85:3014), vaccinia virus system (Chakrabarty et al., Mol. Cell Biol. 5:3403 (1985) or other efficient DNA delivery systems (Yates et al., Nature 313:812 (1985)) known to those skilled in the art. These references are exemplary only and are hereby incorporated by reference. In order to specifically deliver or transfect cells which are abnormally proliferating
25 and spare non-dividing cells, it is preferable to utilize a retrovirus, or adenoviral (as described in the art and elsewhere herein) delivery system known to those of skill in

the art. Since host DNA replication is required for retroviral DNA to integrate and the retrovirus will be unable to self replicate due to the lack of the retrovirus genes needed for its life cycle. Utilizing such a retroviral delivery system for polynucleotides of the present invention will target said gene and constructs to

5 abnormally proliferating cells and will spare the non-dividing normal cells.

The polynucleotides of the present invention may be delivered directly to cell proliferative disorder/disease sites in internal organs, body cavities and the like by use of imaging devices used to guide an injecting needle directly to the disease site. The polynucleotides of the present invention may also be administered to disease sites at

10 the time of surgical intervention.

By "cell proliferative disease" is meant any human or animal disease or disorder, affecting any one or any combination of organs, cavities, or body parts, which is characterized by single or multiple local abnormal proliferations of cells, groups of cells, or tissues, whether benign or malignant.

15 Any amount of the polynucleotides of the present invention may be administered as long as it has a biologically inhibiting effect on the proliferation of the treated cells. Moreover, it is possible to administer more than one of the polynucleotide of the present invention simultaneously to the same site. By "biologically inhibiting" is meant partial or total growth inhibition as well as

20 decreases in the rate of proliferation or growth of the cells. The biologically inhibitory dose may be determined by assessing the effects of the polynucleotides of the present invention on target malignant or abnormally proliferating cell growth in tissue culture, tumor growth in animals and cell cultures, or any other method known to one of ordinary skill in the art.

25 The present invention is further directed to antibody-based therapies which involve administering of anti-polypeptides and anti-polynucleotide antibodies to a

mammalian, preferably human, patient for treating, preventing, and/or diagnosing one or more of the described diseases, disorders, and/or conditions. Methods for producing anti-polypeptides and anti-polynucleotide antibodies polyclonal and monoclonal antibodies are described in detail elsewhere herein. Such antibodies may
5 be provided in pharmaceutically acceptable compositions as known in the art or as described herein.

A summary of the ways in which the antibodies of the present invention may be used therapeutically includes binding polynucleotides or polypeptides of the present invention locally or systemically in the body or by direct cytotoxicity of the
10 antibody, e.g. as mediated by complement (CDC) or by effector cells (ADCC). Some of these approaches are described in more detail below. Armed with the teachings provided herein, one of ordinary skill in the art will know how to use the antibodies of the present invention for diagnostic, monitoring or therapeutic purposes without undue experimentation.

15 In particular, the antibodies, fragments and derivatives of the present invention are useful for treating, preventing, and/or diagnosing a subject having or developing cell proliferative and/or differentiation diseases, disorders, and/or conditions as described herein. Such treatment comprises administering a single or multiple doses of the antibody, or a fragment, derivative, or a conjugate thereof.

20 The antibodies of this invention may be advantageously utilized in combination with other monoclonal or chimeric antibodies, or with lymphokines or hematopoietic growth factors, for example, which serve to increase the number or activity of effector cells which interact with the antibodies.

It is preferred to use high affinity and/or potent in vivo inhibiting and/or
25 neutralizing antibodies against polypeptides or polynucleotides of the present invention, fragments or regions thereof, for both immunoassays directed to and

therapy of diseases, disorders, and/or conditions related to polynucleotides or polypeptides, including fragments thereof, of the present invention. Such antibodies, fragments, or regions, will preferably have an affinity for polynucleotides or polypeptides, including fragments thereof. Preferred binding affinities include those
5 with a dissociation constant or K_d less than $5 \times 10^{-6}M$, $10^{-6}M$, $5 \times 10^{-7}M$, $10^{-7}M$, $5 \times 10^{-8}M$, $10^{-8}M$, $5 \times 10^{-9}M$, $10^{-9}M$, $5 \times 10^{-10}M$, $10^{-10}M$, $5 \times 10^{-11}M$, $10^{-11}M$, $5 \times 10^{-12}M$, $10^{-12}M$, $5 \times 10^{-13}M$, $10^{-13}M$, $5 \times 10^{-14}M$, $10^{-14}M$, $5 \times 10^{-15}M$, and $10^{-15}M$.

Moreover, polypeptides of the present invention are useful in inhibiting the angiogenesis of proliferative cells or tissues, either alone, as a protein fusion, or in
10 combination with other polypeptides directly or indirectly, as described elsewhere herein. In a most preferred embodiment, said anti-angiogenesis effect may be achieved indirectly, for example, through the inhibition of hematopoietic, tumor-specific cells, such as tumor-associated macrophages (See Joseph IB, et al. J Natl Cancer Inst, 90(21):1648-53 (1998), which is hereby incorporated by reference).
15 Antibodies directed to polypeptides or polynucleotides of the present invention may also result in inhibition of angiogenesis directly, or indirectly (See Witte L, et al., Cancer Metastasis Rev. 17(2):155-61 (1998), which is hereby incorporated by reference)).

Polypeptides, including protein fusions, of the present invention, or fragments
20 thereof may be useful in inhibiting proliferative cells or tissues through the induction of apoptosis. Said polypeptides may act either directly, or indirectly to induce apoptosis of proliferative cells and tissues, for example in the activation of a death-domain receptor, such as tumor necrosis factor (TNF) receptor-1, CD95 (Fas/APO-1), TNF-receptor-related apoptosis-mediated protein (TRAMP) and TNF-related
25 apoptosis-inducing ligand (TRAIL) receptor-1 and -2 (See Schulze-Osthoff K, et al., Eur J Biochem 254(3):439-59 (1998), which is hereby incorporated by reference).

Moreover, in another preferred embodiment of the present invention, said polypeptides may induce apoptosis through other mechanisms, such as in the activation of other proteins which will activate apoptosis, or through stimulating the expression of said proteins, either alone or in combination with small molecule drugs or adjuvants, such as apoptonin, galectins, thioredoxins, antiinflammatory proteins (See for example, Mutat Res 400(1-2):447-55 (1998), Med Hypotheses.50(5):423-33 (1998), Chem Biol Interact. Apr 24;111-112:23-34 (1998), J Mol Med.76(6):402-12 (1998), Int J Tissue React;20(1):3-15 (1998), which are all hereby incorporated by reference).

10 Polypeptides, including protein fusions to, or fragments thereof, of the present invention are useful in inhibiting the metastasis of proliferative cells or tissues. Inhibition may occur as a direct result of administering polypeptides, or antibodies directed to said polypeptides as described elsewhere herein, or indirectly, such as activating the expression of proteins known to inhibit metastasis, for example alpha 4
15 integrins, (See, e.g., Curr Top Microbiol Immunol 1998;231:125-41, which is hereby incorporated by reference). Such therapeutic affects of the present invention may be achieved either alone, or in combination with small molecule drugs or adjuvants.

In another embodiment, the invention provides a method of delivering compositions containing the polypeptides of the invention (e.g., compositions
20 containing polypeptides or polypeptide antibodies associated with heterologous polypeptides, heterologous nucleic acids, toxins, or prodrugs) to targeted cells expressing the polypeptide of the present invention. Polypeptides or polypeptide antibodies of the invention may be associated with with heterologous polypeptides, heterologous nucleic acids, toxins, or prodrugs via hydrophobic, hydrophilic, ionic
25 and/or covalent interactions.

Polypeptides, protein fusions to, or fragments thereof, of the present invention are useful in enhancing the immunogenicity and/or antigenicity of proliferating cells or tissues, either directly, such as would occur if the polypeptides of the present invention 'vaccinated' the immune response to respond to proliferative antigens and immunogens, or indirectly, such as in activating the expression of proteins known to enhance the immune response (e.g. chemokines), to said antigens and immunogens.

Cardiovascular Disorders

Polynucleotides or polypeptides, or agonists or antagonists of the invention may be used to treat, prevent, and/or diagnose cardiovascular diseases, disorders, and/or conditions, including peripheral artery disease, such as limb ischemia.

Cardiovascular diseases, disorders, and/or conditions include cardiovascular abnormalities, such as arterio-arterial fistula, arteriovenous fistula, cerebral arteriovenous malformations, congenital heart defects, pulmonary atresia, and Scimitar Syndrome. Congenital heart defects include aortic coarctation, cor triatriatum, coronary vessel anomalies, crisscross heart, dextrocardia, patent ductus arteriosus, Ebstein's anomaly, Eisenmenger complex, hypoplastic left heart syndrome, levocardia, tetralogy of fallot, transposition of great vessels, double outlet right ventricle, tricuspid atresia, persistent truncus arteriosus, and heart septal defects, such as aortopulmonary septal defect, endocardial cushion defects, Lutembacher's Syndrome, trilogly of Fallot, ventricular heart septal defects.

Cardiovascular diseases, disorders, and/or conditions also include heart disease, such as arrhythmias, carcinoid heart disease, high cardiac output, low cardiac output, cardiac tamponade, endocarditis (including bacterial), heart aneurysm, cardiac arrest, congestive heart failure, congestive cardiomyopathy, paroxysmal dyspnea, cardiac edema, heart hypertrophy, congestive cardiomyopathy, left ventricular

hypertrophy, right ventricular hypertrophy, post-infarction heart rupture, ventricular septal rupture, heart valve diseases, myocardial diseases, myocardial ischemia, pericardial effusion, pericarditis (including constrictive and tuberculous), pneumopericardium, postpericardiotomy syndrome, pulmonary heart disease,
5 rheumatic heart disease, ventricular dysfunction, hyperemia, cardiovascular pregnancy complications, Scimitar Syndrome, cardiovascular syphilis, and cardiovascular tuberculosis.

Arrhythmias include sinus arrhythmia, atrial fibrillation, atrial flutter, bradycardia, extrasystole, Adams-Stokes Syndrome, bundle-branch block, sinoatrial
10 block, long QT syndrome, parasystole, Lown-Ganong-Levine Syndrome, Mahaim-type pre-excitation syndrome, Wolff-Parkinson-White syndrome, sick sinus syndrome, tachycardias, and ventricular fibrillation. Tachycardias include paroxysmal tachycardia, supraventricular tachycardia, accelerated idioventricular rhythm, atrioventricular nodal reentry tachycardia, ectopic atrial tachycardia, ectopic
15 junctional tachycardia, sinoatrial nodal reentry tachycardia, sinus tachycardia, Torsades de Pointes, and ventricular tachycardia.

Heart valve disease include aortic valve insufficiency, aortic valve stenosis, hear murmurs, aortic valve prolapse, mitral valve prolapse, tricuspid valve prolapse, mitral valve insufficiency, mitral valve stenosis, pulmonary atresia, pulmonary valve
20 insufficiency, pulmonary valve stenosis, tricuspid atresia, tricuspid valve insufficiency, and tricuspid valve stenosis.

Myocardial diseases include alcoholic cardiomyopathy, congestive cardiomyopathy, hypertrophic cardiomyopathy, aortic subvalvular stenosis, pulmonary subvalvular stenosis, restrictive cardiomyopathy, Chagas cardiomyopathy,
25 endocardial fibroelastosis, endomyocardial fibrosis, Kearns Syndrome, myocardial reperfusion injury, and myocarditis.

Myocardial ischemias include coronary disease, such as angina pectoris, coronary aneurysm, coronary arteriosclerosis, coronary thrombosis, coronary vasospasm, myocardial infarction and myocardial stunning.

Cardiovascular diseases also include vascular diseases such as aneurysms, 5 angiodyplasia, angiomatosis, bacillary angiomatosis, Hippel-Lindau Disease, Klippel-Trenaunay-Weber Syndrome, Sturge-Weber Syndrome, angioneurotic edema, aortic diseases, Takayasu's Arteritis, aortitis, Leriche's Syndrome, arterial occlusive diseases, arteritis, enarteritis, polyarteritis nodosa, cerebrovascular diseases, disorders, and/or conditions, diabetic angiopathies, diabetic retinopathy, embolisms, thrombosis, 10 erythromelalgia, hemorrhoids, hepatic veno-occlusive disease, hypertension, hypotension, ischemia, peripheral vascular diseases, phlebitis, pulmonary veno-occlusive disease, Raynaud's disease, CREST syndrome, retinal vein occlusion, Scimitar syndrome, superior vena cava syndrome, telangiectasia, atacia telangiectasia, hereditary hemorrhagic telangiectasia, varicocele, varicose veins, varicose ulcer, 15 vasculitis, and venous insufficiency.

Aneurysms include dissecting aneurysms, false aneurysms, infected aneurysms, ruptured aneurysms, aortic aneurysms, cerebral aneurysms, coronary aneurysms, heart aneurysms, and iliac aneurysms.

Arterial occlusive diseases include arteriosclerosis, intermittent claudication, 20 carotid stenosis, fibromuscular dysplasias, mesenteric vascular occlusion, Moyamoya disease, renal artery obstruction, retinal artery occlusion, and thromboangiitis obliterans.

Cerebrovascular diseases, disorders, and/or conditions include carotid artery diseases, cerebral amyloid angiopathy, cerebral aneurysm, cerebral anoxia, cerebral 25 arteriosclerosis, cerebral arteriovenous malformation, cerebral artery diseases, cerebral embolism and thrombosis, carotid artery thrombosis, sinus thrombosis,

Wallenberg's syndrome, cerebral hemorrhage, epidural hematoma, subdural hematoma, subarachnoid hemorrhage, cerebral infarction, cerebral ischemia (including transient), subclavian steal syndrome, periventricular leukomalacia, vascular headache, cluster headache, migraine, and vertebrobasilar insufficiency.

5 Embolisms include air embolisms, amniotic fluid embolisms, cholesterol embolisms, blue toe syndrome, fat embolisms, pulmonary embolisms, and thromboembolisms. Thrombosis include coronary thrombosis, hepatic vein thrombosis, retinal vein occlusion, carotid artery thrombosis, sinus thrombosis, Wallenberg's syndrome, and thrombophlebitis.

10 Ischemia includes cerebral ischemia, ischemic colitis, compartment syndromes, anterior compartment syndrome, myocardial ischemia, reperfusion injuries, and peripheral limb ischemia. Vasculitis includes aortitis, arteritis, Behcet's Syndrome, Churg-Strauss Syndrome, mucocutaneous lymph node syndrome, thromboangiitis obliterans, hypersensitivity vasculitis, Schoenlein-Henoch purpura,
15 allergic cutaneous vasculitis, and Wegener's granulomatosis.

Polynucleotides or polypeptides, or agonists or antagonists of the invention, are especially effective for the treatment of critical limb ischemia and coronary disease.

Polypeptides may be administered using any method known in the art,
20 including, but not limited to, direct needle injection at the delivery site, intravenous injection, topical administration, catheter infusion, biolistic injectors, particle accelerators, gelfoam sponge depots, other commercially available depot materials, osmotic pumps, oral or suppository solid pharmaceutical formulations, decanting or topical applications during surgery, aerosol delivery. Such methods are known in the
25 art. Polypeptides of the invention may be administered as part of a *Therapeutic*,

described in more detail below. Methods of delivering polynucleotides of the invention are described in more detail herein.

Anti-Angiogenesis Activity

- 5 The naturally occurring balance between endogenous stimulators and inhibitors of angiogenesis is one in which inhibitory influences predominate. Rastinejad *et al.*, *Cell* 56:345-355 (1989). In those rare instances in which neovascularization occurs under normal physiological conditions, such as wound healing, organ regeneration, embryonic development, and female reproductive
- 10 processes, angiogenesis is stringently regulated and spatially and temporally delimited. Under conditions of pathological angiogenesis such as that characterizing solid tumor growth, these regulatory controls fail. Unregulated angiogenesis becomes pathologic and sustains progression of many neoplastic and non-neoplastic diseases. A number of serious diseases are dominated by abnormal neovascularization
- 15 including solid tumor growth and metastases, arthritis, some types of eye diseases, disorders, and/or conditions, and psoriasis. See, e.g., reviews by Moses *et al.*, *Biotech.* 9:630-634 (1991); Folkman *et al.*, *N. Engl. J. Med.*, 333:1757-1763 (1995); Auerbach *et al.*, *J. Microvasc. Res.* 29:401-411 (1985); Folkman, *Advances in Cancer Research*, eds. Klein and Weinhouse, Academic Press, New York, pp. 175-
- 20 203 (1985); Patz, *Am. J. Ophthalmol.* 94:715-743 (1982); and Folkman *et al.*, *Science* 221:719-725 (1983). In a number of pathological conditions, the process of angiogenesis contributes to the disease state. For example, significant data have accumulated which suggest that the growth of solid tumors is dependent on angiogenesis. Folkman and Klagsbrun, *Science* 235:442-447 (1987).
- 25 The present invention provides for treatment of diseases, disorders, and/or conditions associated with neovascularization by administration of the

polynucleotides and/or polypeptides of the invention, as well as agonists or antagonists of the present invention. Malignant and metastatic conditions which can be treated with the polynucleotides and polypeptides, or agonists or antagonists of the invention include, but are not limited to, malignancies, solid tumors, and cancers

5 described herein and otherwise known in the art (for a review of such disorders, see Fishman *et al.*, Medicine, 2d Ed., J. B. Lippincott Co., Philadelphia (1985)). Thus, the present invention provides a method of treating, preventing, and/or diagnosing an angiogenesis-related disease and/or disorder, comprising administering to an individual in need thereof a therapeutically effective amount of a polynucleotide,

10 polypeptide, antagonist and/or agonist of the invention. For example, polynucleotides, polypeptides, antagonists and/or agonists may be utilized in a variety of additional methods in order to therapeutically treat or prevent a cancer or tumor. Cancers which may be treated, prevented, and/or diagnosed with polynucleotides, polypeptides, antagonists and/or agonists include, but are not limited to solid tumors,

15 including prostate, lung, breast, ovarian, stomach, pancreas, larynx, esophagus, testes, liver, parotid, biliary tract, colon, rectum, cervix, uterus, endometrium, kidney, bladder, thyroid cancer; primary tumors and metastases; melanomas; glioblastoma; Kaposi's sarcoma; leiomyosarcoma; non-small cell lung cancer; colorectal cancer; advanced malignancies; and blood born tumors such as leukemias. For example,

20 polynucleotides, polypeptides, antagonists and/or agonists may be delivered topically, in order to treat or prevent cancers such as skin cancer, head and neck tumors, breast tumors, and Kaposi's sarcoma.

Within yet other aspects, polynucleotides, polypeptides, antagonists and/or agonists may be utilized to treat superficial forms of bladder cancer by, for example,

25 intravesical administration. Polynucleotides, polypeptides, antagonists and/or agonists may be delivered directly into the tumor, or near the tumor site, via injection or a

catheter. Of course, as the artisan of ordinary skill will appreciate, the appropriate mode of administration will vary according to the cancer to be treated. Other modes of delivery are discussed herein.

Polynucleotides, polypeptides, antagonists and/or agonists may be useful in
5 treating, preventing, and/or diagnosing other diseases, disorders, and/or conditions,
besides cancers, which involve angiogenesis. These diseases, disorders, and/or
conditions include, but are not limited to: benign tumors, for example hemangiomas,
acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas;
arteriosclerotic plaques; ocular angiogenic diseases, for example, diabetic retinopathy,
10 retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular
glaucoma, retrolental fibroplasia, rubeosis, retinoblastoma, uveitis and Pterygia
(abnormal blood vessel growth) of the eye; rheumatoid arthritis; psoriasis; delayed
wound healing; endometriosis; vasculogenesis; granulations; hypertrophic scars
(keloids); nonunion fractures; scleroderma; trachoma; vascular adhesions; myocardial
15 angiogenesis; coronary collaterals; cerebral collaterals; arteriovenous malformations;
ischemic limb angiogenesis; Osler-Webber Syndrome; plaque neovascularization;
telangiectasia; hemophilic joints; angiofibroma; fibromuscular dysplasia; wound
granulation; Crohn's disease; and atherosclerosis.

For example, within one aspect of the present invention methods are provided
20 for treating, preventing, and/or diagnosing hypertrophic scars and keloids, comprising
the step of administering a polynucleotide, polypeptide, antagonist and/or agonist of
the invention to a hypertrophic scar or keloid.

Within one embodiment of the present invention polynucleotides,
polypeptides, antagonists and/or agonists are directly injected into a hypertrophic scar
25 or keloid, in order to prevent the progression of these lesions. This therapy is of
particular value in the prophylactic treatment of conditions which are known to result

in the development of hypertrophic scars and keloids (e.g., burns), and is preferably initiated after the proliferative phase has had time to progress (approximately 14 days after the initial injury), but before hypertrophic scar or keloid development. As noted above, the present invention also provides methods for treating, preventing, and/or

5 diagnosing neovascular diseases of the eye, including for example, corneal neovascularization, neovascular glaucoma, proliferative diabetic retinopathy, retrolental fibroplasia and macular degeneration.

Moreover, Ocular diseases, disorders, and/or conditions associated with neovascularization which can be treated, prevented, and/or diagnosed with the

10 polynucleotides and polypeptides of the present invention (including agonists and/or antagonists) include, but are not limited to: neovascular glaucoma, diabetic retinopathy, retinoblastoma, retrolental fibroplasia, uveitis, retinopathy of prematurity macular degeneration, corneal graft neovascularization, as well as other eye inflammatory diseases, ocular tumors and diseases associated with choroidal or iris

15 neovascularization. See, e.g., reviews by Waltman *et al.*, *Am. J. Ophthalm.* 85:704-710 (1978) and Gartner *et al.*, *Surv. Ophthalm.* 22:291-312 (1978).

Thus, within one aspect of the present invention methods are provided for treating or preventing neovascular diseases of the eye such as corneal neovascularization (including corneal graft neovascularization), comprising the step

20 of administering to a patient a therapeutically effective amount of a compound (as described above) to the cornea, such that the formation of blood vessels is inhibited. Briefly, the cornea is a tissue which normally lacks blood vessels. In certain pathological conditions however, capillaries may extend into the cornea from the pericorneal vascular plexus of the limbus. When the cornea becomes vascularized, it

25 also becomes clouded, resulting in a decline in the patient's visual acuity. Visual loss may become complete if the cornea completely opacitates. A wide variety of

diseases, disorders, and/or conditions can result in corneal neovascularization, including for example, corneal infections (e.g., trachoma, herpes simplex keratitis, leishmaniasis and onchocerciasis), immunological processes (e.g., graft rejection and Stevens-Johnson's syndrome), alkali burns, trauma, inflammation (of any cause),
5 toxic and nutritional deficiency states, and as a complication of wearing contact lenses.

Within particularly preferred embodiments of the invention, may be prepared for topical administration in saline (combined with any of the preservatives and antimicrobial agents commonly used in ocular preparations), and administered in
10 eyedrop form. The solution or suspension may be prepared in its pure form and administered several times daily. Alternatively, anti-angiogenic compositions, prepared as described above, may also be administered directly to the cornea. Within preferred embodiments, the anti-angiogenic composition is prepared with a muco-adhesive polymer which binds to cornea. Within further embodiments, the anti-
15 angiogenic factors or anti-angiogenic compositions may be utilized as an adjunct to conventional steroid therapy. Topical therapy may also be useful prophylactically in corneal lesions which are known to have a high probability of inducing an angiogenic response (such as chemical burns). In these instances the treatment, likely in combination with steroids, may be instituted immediately to help prevent subsequent
20 complications.

Within other embodiments, the compounds described above may be injected directly into the corneal stroma by an ophthalmologist under microscopic guidance. The preferred site of injection may vary with the morphology of the individual lesion, but the goal of the administration would be to place the composition at the advancing
25 front of the vasculature (i.e., interspersed between the blood vessels and the normal cornea). In most cases this would involve perilimbic corneal injection to "protect" the

cornea from the advancing blood vessels. This method may also be utilized shortly after a corneal insult in order to prophylactically prevent corneal neovascularization. In this situation the material could be injected in the perilimbic cornea interspersed between the corneal lesion and its undesired potential limbic blood supply. Such
5 methods may also be utilized in a similar fashion to prevent capillary invasion of transplanted corneas. In a sustained-release form injections might only be required 2-3 times per year. A steroid could also be added to the injection solution to reduce inflammation resulting from the injection itself.

Within another aspect of the present invention, methods are provided for
10 treating or preventing neovascular glaucoma, comprising the step of administering to a patient a therapeutically effective amount of a polynucleotide, polypeptide, antagonist and/or agonist to the eye, such that the formation of blood vessels is inhibited. In one embodiment, the compound may be administered topically to the eye in order to treat or prevent early forms of neovascular glaucoma. Within other
15 embodiments, the compound may be implanted by injection into the region of the anterior chamber angle. Within other embodiments, the compound may also be placed in any location such that the compound is continuously released into the aqueous humor. Within another aspect of the present invention, methods are provided for treating or preventing proliferative diabetic retinopathy, comprising the step of
20 administering to a patient a therapeutically effective amount of a polynucleotide, polypeptide, antagonist and/or agonist to the eyes, such that the formation of blood vessels is inhibited.

Within particularly preferred embodiments of the invention, proliferative diabetic retinopathy may be treated by injection into the aqueous humor or the
25 vitreous, in order to increase the local concentration of the polynucleotide, polypeptide, antagonist and/or agonist in the retina. Preferably, this treatment should

be initiated prior to the acquisition of severe disease requiring photocoagulation.

Within another aspect of the present invention, methods are provided for treating or preventing retrolental fibroplasia, comprising the step of administering to a patient a therapeutically effective amount of a polynucleotide, polypeptide, antagonist and/or agonist to the eye, such that the formation of blood vessels is inhibited. The compound may be administered topically, via intravitreal injection and/or via intraocular implants.

Additionally, diseases, disorders, and/or conditions which can be treated, prevented, and/or diagnosed with the polynucleotides, polypeptides, agonists and/or agonists include, but are not limited to, hemangioma, arthritis, psoriasis, angiofibroma, atherosclerotic plaques, delayed wound healing, granulations, hemophilic joints, hypertrophic scars, nonunion fractures, Osler-Weber syndrome, pyogenic granuloma, scleroderma, trachoma, and vascular adhesions.

Moreover, diseases, disorders, and/or conditions and/or states, which can be treated, prevented, and/or diagnosed with the the polynucleotides, polypeptides, agonists and/or agonists include, but are not limited to, solid tumors, blood born tumors such as leukemias, tumor metastasis, Kaposi's sarcoma, benign tumors, for example hemangiomas, acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas, rheumatoid arthritis, psoriasis, ocular angiogenic diseases, for example, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, retinoblastoma, and uveitis, delayed wound healing, endometriosis, vasculogenesis, granulations, hypertrophic scars (keloids), nonunion fractures, scleroderma, trachoma, vascular adhesions, myocardial angiogenesis, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischemic limb angiogenesis, Osler-Webber Syndrome, plaque neovascularization, telangiectasia, hemophilic joints, angiofibroma

- fibromuscular dysplasia, wound granulation, Crohn's disease, atherosclerosis, birth control agent by preventing vascularization required for embryo implantation controlling menstruation, diseases that have angiogenesis as a pathologic consequence such as cat scratch disease (*Rochela minalia quintosa*), ulcers (*Helicobacter pylori*),
- 5 Bartonellosis and bacillary angiomatosis.

- In one aspect of the birth control method, an amount of the compound sufficient to block embryo implantation is administered before or after intercourse and fertilization have occurred, thus providing an effective method of birth control, possibly a "morning after" method. Polynucleotides, polypeptides, agonists and/or
- 10 agonists may also be used in controlling menstruation or administered as either a peritoneal lavage fluid or for peritoneal implantation in the treatment of endometriosis.

- Polynucleotides, polypeptides, agonists and/or agonists of the present invention may be incorporated into surgical sutures in order to prevent stitch
- 15 granulomas.

- Polynucleotides, polypeptides, agonists and/or agonists may be utilized in a wide variety of surgical procedures. For example, within one aspect of the present invention a compositions (in the form of, for example, a spray or film) may be utilized to coat or spray an area prior to removal of a tumor, in order to isolate normal
- 20 surrounding tissues from malignant tissue, and/or to prevent the spread of disease to surrounding tissues. Within other aspects of the present invention, compositions (e.g., in the form of a spray) may be delivered via endoscopic procedures in order to coat tumors, or inhibit angiogenesis in a desired locale. Within yet other aspects of the present invention, surgical meshes which have been coated with anti- angiogenic
- 25 compositions of the present invention may be utilized in any procedure wherein a surgical mesh might be utilized. For example, within one embodiment of the

invention a surgical mesh laden with an anti-angiogenic composition may be utilized during abdominal cancer resection surgery (e.g., subsequent to colon resection) in order to provide support to the structure, and to release an amount of the anti-angiogenic factor.

5 Within further aspects of the present invention, methods are provided for treating tumor excision sites, comprising administering a polynucleotide, polypeptide, agonist and/or agonist to the resection margins of a tumor subsequent to excision, such that the local recurrence of cancer and the formation of new blood vessels at the site is inhibited. Within one embodiment of the invention, the anti-angiogenic
10 compound is administered directly to the tumor excision site (e.g., applied by swabbing, brushing or otherwise coating the resection margins of the tumor with the anti-angiogenic compound). Alternatively, the anti-angiogenic compounds may be incorporated into known surgical pastes prior to administration. Within particularly preferred embodiments of the invention, the anti-angiogenic compounds are applied
15 after hepatic resections for malignancy, and after neurosurgical operations.

 Within one aspect of the present invention, polynucleotides, polypeptides, agonists and/or agonists may be administered to the resection margin of a wide variety of tumors, including for example, breast, colon, brain and hepatic tumors. For example, within one embodiment of the invention, anti-angiogenic compounds may
20 be administered to the site of a neurological tumor subsequent to excision, such that the formation of new blood vessels at the site are inhibited.

 The polynucleotides, polypeptides, agonists and/or agonists of the present invention may also be administered along with other anti-angiogenic factors. Representative examples of other anti-angiogenic factors include: Anti-Invasive
25 Factor, retinoic acid and derivatives thereof, paclitaxel, Suramin, Tissue Inhibitor of Metalloproteinase-1, Tissue Inhibitor of Metalloproteinase-2, Plasminogen Activator

Inhibitor-1, Plasminogen Activator Inhibitor-2, and various forms of the lighter "d group" transition metals.

Lighter "d group" transition metals include, for example, vanadium, molybdenum, tungsten, titanium, niobium, and tantalum species. Such transition
5 metal species may form transition metal complexes. Suitable complexes of the above-mentioned transition metal species include oxo transition metal complexes.

Representative examples of vanadium complexes include oxo vanadium complexes such as vanadate and vanadyl complexes. Suitable vanadate complexes include metavanadate and orthovanadate complexes such as, for example, ammonium
10 metavanadate, sodium metavanadate, and sodium orthovanadate. Suitable vanadyl complexes include, for example, vanadyl acetylacetonate and vanadyl sulfate including vanadyl sulfate hydrates such as vanadyl sulfate mono- and trihydrates.

Representative examples of tungsten and molybdenum complexes also include oxo complexes. Suitable oxo tungsten complexes include tungstate and tungsten
15 oxide complexes. Suitable tungstate complexes include ammonium tungstate, calcium tungstate, sodium tungstate dihydrate, and tungstic acid. Suitable tungsten oxides include tungsten (IV) oxide and tungsten (VI) oxide. Suitable oxo molybdenum complexes include molybdate, molybdenum oxide, and molybdenyl complexes. Suitable molybdate complexes include ammonium molybdate and its
20 hydrates, sodium molybdate and its hydrates, and potassium molybdate and its hydrates. Suitable molybdenum oxides include molybdenum (VI) oxide, molybdenum (VI) oxide, and molybdic acid. Suitable molybdenyl complexes include, for example, molybdenyl acetylacetonate. Other suitable tungsten and molybdenum complexes include hydroxo derivatives derived from, for example, glycerol, tartaric acid, and
25 sugars.

- A wide variety of other anti-angiogenic factors may also be utilized within the context of the present invention. Representative examples include platelet factor 4; protamine sulphate; sulphated chitin derivatives (prepared from queen crab shells), (Murata et al., Cancer Res. 51:22-26, 1991); Sulphated Polysaccharide Peptidoglycan
- 5 -- Complex (SP- PG) (the function of this compound may be enhanced by the presence of steroids such as estrogen, and tamoxifen citrate); Staurosporine; modulators of matrix metabolism, including for example, proline analogs, cishydroxyproline, d,L-3,4-dehydroproline, Thiaproline, alpha,alpha-dipyridyl, aminopropionitrile fumarate; 4-propyl-5-(4-pyridinyl)-2(3H)-oxazolone; Methotrexate; Mitoxantrone; Heparin;
- 10 Interferons; 2 Macroglobulin-serum; ChIMP-3 (Pavloff et al., J. Bio. Chem. 267:17321-17326, 1992); Chymostatin (Tomkinson et al., Biochem J. 286:475-480, 1992); Cyclodextrin Tetradasulfate; Eponemycin; Camptothecin; Fumagillin (Ingber et al., Nature 348:555-557, 1990); Gold Sodium Thiomalate ("GST"; Matsubara and Ziff, J. Clin. Invest. 79:1440-1446, 1987); anticollagenase-serum;
- 15 alpha2-antiplasmin (Holmes et al., J. Biol. Chem. 262(4):1659-1664, 1987); Bisantrene (National Cancer Institute); Lobenzarit disodium (N-(2)-carboxyphenyl-4-chloroanthronilic acid disodium or "CCA"; Takeuchi et al., Agents Actions 36:312-316, 1992); Thalidomide; Angostatic steroid; AGM-1470; carboxynaminolmidazole; and metalloproteinase inhibitors such as BB94.

20

Diseases at the Cellular Level

- Diseases associated with increased cell survival or the inhibition of apoptosis that could be treated, prevented, and/or diagnosed by the polynucleotides or polypeptides and/or antagonists or agonists of the invention, include cancers (such as
- 25 follicular lymphomas, carcinomas with p53 mutations, and hormone-dependent tumors, including, but not limited to colon cancer, cardiac tumors, pancreatic cancer,

melanoma, retinoblastoma, glioblastoma, lung cancer, intestinal cancer, testicular cancer, stomach cancer, neuroblastoma, myxoma, myoma, lymphoma, endothelioma, osteoblastoma, osteoclastoma, osteosarcoma, chondrosarcoma, adenoma, breast cancer, prostate cancer, Kaposi's sarcoma and ovarian cancer); autoimmune diseases, disorders, and/or conditions (such as, multiple sclerosis, Sjogren's syndrome, Hashimoto's thyroiditis, biliary cirrhosis, Behcet's disease, Crohn's disease, polymyositis, systemic lupus erythematosus and immune-related glomerulonephritis and rheumatoid arthritis) and viral infections (such as herpes viruses, pox viruses and adenoviruses), inflammation, graft v. host disease, acute graft rejection, and chronic graft rejection. In preferred embodiments, the polynucleotides or polypeptides, and/or agonists or antagonists of the invention are used to inhibit growth, progression, and/or metasis of cancers, in particular those listed above.

Additional diseases or conditions associated with increased cell survival that could be treated, prevented or diagnosed by the polynucleotides or polypeptides, or agonists or antagonists of the invention, include, but are not limited to, progression, and/or metastases of malignancies and related disorders such as leukemia (including acute leukemias (e.g., acute lymphocytic leukemia, acute myelocytic leukemia (including myeloblastic, promyelocytic, myelomonocytic, monocytic, and erythroleukemia)) and chronic leukemias (e.g., chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia)), polycythemia vera, lymphomas (e.g., Hodgkin's disease and non-Hodgkin's disease), multiple myeloma, Waldenstrom's macroglobulinemia, heavy chain disease, and solid tumors including, but not limited to, sarcomas and carcinomas such as fibrosarcoma, myxosarcoma, liposarcoma, chondrosarcoma, osteogenic sarcoma, chordoma, angiosarcoma, endotheliosarcoma, lymphangiosarcoma, lymphangioendotheliosarcoma, synovioma, mesothelioma, Ewing's tumor, leiomyosarcoma, rhabdomyosarcoma, colon carcinoma, pancreatic

- cancer, breast cancer, ovarian cancer, prostate cancer, squamous cell carcinoma, basal cell carcinoma, adenocarcinoma, sweat gland carcinoma, sebaceous gland carcinoma, papillary carcinoma, papillary adenocarcinomas, cystadenocarcinoma, medullary carcinoma, bronchogenic carcinoma, renal cell carcinoma, hepatoma, bile duct carcinoma, choriocarcinoma, seminoma, embryonal carcinoma, Wilm's tumor, cervical cancer, testicular tumor, lung carcinoma, small cell lung carcinoma, bladder carcinoma, epithelial carcinoma, glioma, astrocytoma, medulloblastoma, craniopharyngioma, ependymoma, pinealoma, hemangioblastoma, acoustic neuroma, oligodendroglioma, menangioma, melanoma, neuroblastoma, and retinoblastoma.
- 10 Diseases associated with increased apoptosis that could be treated, prevented, and/or diagnosed by the polynucleotides or polypeptides, and/or agonists or antagonists of the invention, include AIDS; neurodegenerative diseases, disorders, and/or conditions (such as Alzheimer's disease, Parkinson's disease, Amyotrophic lateral sclerosis, Retinitis pigmentosa, Cerebellar degeneration and brain tumor or
- 15 prior associated disease); autoimmune diseases, disorders, and/or conditions (such as, multiple sclerosis, Sjogren's syndrome, Hashimoto's thyroiditis, biliary cirrhosis, Behcet's disease, Crohn's disease, polymyositis, systemic lupus erythematosus and immune-related glomerulonephritis and rheumatoid arthritis) myelodysplastic syndromes (such as aplastic anemia), graft v. host disease, ischemic injury (such as
- 20 that caused by myocardial infarction, stroke and reperfusion injury), liver injury (e.g., hepatitis related liver injury, ischemia/reperfusion injury, cholestasis (bile duct injury) and liver cancer); toxin-induced liver disease (such as that caused by alcohol), septic shock, cachexia and anorexia.

Wound Healing and Epithelial Cell Proliferation

In accordance with yet a further aspect of the present invention, there is provided a process for utilizing the polynucleotides or polypeptides, and/or agonists or antagonists of the invention, for therapeutic purposes, for example, to stimulate
5 epithelial cell proliferation and basal keratinocytes for the purpose of wound healing, and to stimulate hair follicle production and healing of dermal wounds.

Polynucleotides or polypeptides, as well as agonists or antagonists of the invention, may be clinically useful in stimulating wound healing including surgical wounds, excisional wounds, deep wounds involving damage of the dermis and epidermis, eye
10 tissue wounds, dental tissue wounds, oral cavity wounds, diabetic ulcers, dermal ulcers, cubitus ulcers, arterial ulcers, venous stasis ulcers, burns resulting from heat exposure or chemicals, and other abnormal wound healing conditions such as uremia, malnutrition, vitamin deficiencies and complications associated with systemic treatment with steroids, radiation therapy and antineoplastic drugs and
15 antimetabolites. Polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could be used to promote dermal reestablishment subsequent to dermal loss

The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could be used to increase the adherence of skin grafts to a wound bed and
20 to stimulate re-epithelialization from the wound bed. The following are a non-exhaustive list of grafts that polynucleotides or polypeptides, agonists or antagonists of the invention, could be used to increase adherence to a wound bed: autografts, artificial skin, allografts, autodermic graft, autoepdermic grafts, avacular grafts, Blair-Brown grafts, bone graft, brephoplastic grafts, cutis graft, delayed graft, dermic graft,
25 epidermic graft, fascia graft, full thickness graft, heterologous graft, xenograft, homologous graft, hyperplastic graft, lamellar graft, mesh graft, mucosal graft, Ollier-

Thiersch graft, omentoplastic graft, patch graft, pedicle graft, penetrating graft, split skin graft, thick split graft. The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, can be used to promote skin strength and to improve the appearance of aged skin.

5 It is believed that the polynucleotides or polypeptides, and/or agonists or antagonists of the invention, will also produce changes in hepatocyte proliferation, and epithelial cell proliferation in the lung, breast, pancreas, stomach, small intestine, and large intestine. The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could promote proliferation of epithelial cells such as
10 sebocytes, hair follicles, hepatocytes, type II pneumocytes, mucin-producing goblet cells, and other epithelial cells and their progenitors contained within the skin, lung, liver, and gastrointestinal tract. The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, may promote proliferation of endothelial cells, keratinocytes, and basal keratinocytes.

15 The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could also be used to reduce the side effects of gut toxicity that result from radiation, chemotherapy treatments or viral infections. The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, may have a cytoprotective effect on the small intestine mucosa. The polynucleotides or
20 polypeptides, and/or agonists or antagonists of the invention, may also stimulate healing of mucositis (mouth ulcers) that result from chemotherapy and viral infections.

 The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could further be used in full regeneration of skin in full and partial
25 thickness skin defects, including burns, (i.e., repopulation of hair follicles, sweat glands, and sebaceous glands), treatment of other skin defects such as psoriasis. The

polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could be used to treat epidermolysis bullosa, a defect in adherence of the epidermis to the underlying dermis which results in frequent, open and painful blisters by accelerating reepithelialization of these lesions. The polynucleotides or polypeptides, and/or

5 agonists or antagonists of the invention, could also be used to treat gastric and duodenal ulcers and help heal by scar formation of the mucosal lining and regeneration of glandular mucosa and duodenal mucosal lining more rapidly.

Inflammatory bowel diseases, such as Crohn's disease and ulcerative colitis, are diseases which result in destruction of the mucosal surface of the small or large

10 intestine, respectively. Thus, the polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could be used to promote the resurfacing of the mucosal surface to aid more rapid healing and to prevent progression of inflammatory bowel disease. Treatment with the polynucleotides or polypeptides, and/or agonists or antagonists of the invention, is expected to have a significant effect on the production

15 of mucus throughout the gastrointestinal tract and could be used to protect the intestinal mucosa from injurious substances that are ingested or following surgery.

The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could be used to treat diseases associate with the under expression of the polynucleotides of the invention.

20 Moreover, the polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could be used to prevent and heal damage to the lungs due to various pathological states. A growth factor such as the polynucleotides or polypeptides, and/or agonists or antagonists of the invention, which could stimulate proliferation and differentiation and promote the repair of alveoli and brochiolar epithelium to

25 prevent or treat acute or chronic lung damage. For example, emphysema, which results in the progressive loss of aveoli, and inhalation injuries, i.e., resulting from

smoke inhalation and burns, that cause necrosis of the bronchiolar epithelium and alveoli could be effectively treated, prevented, and/or diagnosed using the polynucleotides or polypeptides, and/or agonists or antagonists of the invention.

Also, the polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could be used to stimulate the proliferation of and differentiation of type II pneumocytes, which may help treat or prevent disease such as hyaline membrane diseases, such as infant respiratory distress syndrome and bronchopulmonary dysplasia, in premature infants.

The polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could stimulate the proliferation and differentiation of hepatocytes and, thus, could be used to alleviate or treat liver diseases and pathologies such as fulminant liver failure caused by cirrhosis, liver damage caused by viral hepatitis and toxic substances (i.e., acetaminophen, carbon tetrachloride and other hepatotoxins known in the art).

In addition, the polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could be used to treat or prevent the onset of diabetes mellitus. In patients with newly diagnosed Types I and II diabetes, where some islet cell function remains, the polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could be used to maintain the islet function so as to alleviate, delay or prevent permanent manifestation of the disease. Also, the polynucleotides or polypeptides, and/or agonists or antagonists of the invention, could be used as an auxiliary in islet cell transplantation to improve or promote islet cell function.

Neurological Diseases

Nervous system diseases, disorders, and/or conditions, which can be treated, prevented, and/or diagnosed with the compositions of the invention (e.g., polypeptides, polynucleotides, and/or agonists or antagonists), include, but are not limited to, nervous system injuries, and diseases, disorders, and/or conditions which

5 result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated, prevented, and/or diagnosed in a patient (including human and non-human mammalian patients) according to the invention, include but are not limited to, the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems: (1)

10 ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia; (2) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries; (3) malignant lesions, in which a portion of

15 the nervous system is destroyed or injured by malignant tissue which is either a nervous system associated malignancy or a malignancy derived from non-nervous system tissue; (4) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex

20 virus or with Lyme disease, tuberculosis, syphilis; (5) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis (ALS); (6) lesions associated with nutritional diseases, disorders, and/or conditions, in which a

25 portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic

acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration; (7) neurological lesions associated with systemic diseases including, but not limited to, diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis; (8) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and (9) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including, but not limited to, multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

In a preferred embodiment, the polypeptides, polynucleotides, or agonists or antagonists of the invention are used to protect neural cells from the damaging effects of cerebral hypoxia. According to this embodiment, the compositions of the invention are used to treat, prevent, and/or diagnose neural cell injury associated with cerebral hypoxia. In one aspect of this embodiment, the polypeptides, polynucleotides, or agonists or antagonists of the invention are used to treat, prevent, and/or diagnose neural cell injury associated with cerebral ischemia. In another aspect of this embodiment, the polypeptides, polynucleotides, or agonists or antagonists of the invention are used to treat, prevent, and/or diagnose neural cell injury associated with cerebral infarction. In another aspect of this embodiment, the polypeptides, polynucleotides, or agonists or antagonists of the invention are used to treat, prevent, and/or diagnose or prevent neural cell injury associated with a stroke. In a further aspect of this embodiment, the polypeptides, polynucleotides, or agonists or antagonists of the invention are used to treat, prevent, and/or diagnose neural cell injury associated with a heart attack.

The compositions of the invention which are useful for treating or preventing a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, compositions of the invention which elicit any of the following effects may be useful according to the invention: (1) increased survival time of neurons in culture; (2) increased sprouting of neurons in culture or *in vivo*; (3) increased production of a neuron-associated molecule in culture or *in vivo*, e.g., choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or (4) decreased symptoms of neuron dysfunction *in vivo*. Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may routinely be measured using a method set forth herein or otherwise known in the art, such as, for example, the method set forth in Arakawa et al. (J. Neurosci. 10:3507-3515 (1990)); increased sprouting of neurons may be detected by methods known in the art, such as, for example, the methods set forth in Pestronk et al. (Exp. Neurol. 70:65-82 (1980)) or Brown et al. (Ann. Rev. Neurosci. 4:17-42 (1981)); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, etc., using techniques known in the art and depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, e.g., weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron diseases, disorders, and/or conditions that may be treated, prevented, and/or diagnosed according to the invention include, but are not limited to, diseases, disorders, and/or conditions such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous

system, as well as diseases, disorders, and/or conditions that selectively affect neurons such as amyotrophic lateral sclerosis, and including, but not limited to, progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-

5 Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary
Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

Infectious Disease

A polypeptide or polynucleotide and/or agonist or antagonist of the present
10 invention can be used to treat, prevent, and/or diagnose infectious agents. For
example, by increasing the immune response, particularly increasing the proliferation
and differentiation of B and/or T cells, infectious diseases may be treated, prevented,
and/or diagnosed. The immune response may be increased by either enhancing an
existing immune response, or by initiating a new immune response. Alternatively,
15 polypeptide or polynucleotide and/or agonist or antagonist of the present invention
may also directly inhibit the infectious agent, without necessarily eliciting an immune
response.

Viruses are one example of an infectious agent that can cause disease or
symptoms that can be treated, prevented, and/or diagnosed by a polynucleotide or
20 polypeptide and/or agonist or antagonist of the present invention. Examples of
viruses, include, but are not limited to Examples of viruses, include, but are not
limited to the following DNA and RNA viruses and viral families: Arbovirus,
Adenoviridae, Arenaviridae, Arterivirus, Birnaviridae, Bunyaviridae, Caliciviridae,
Circoviridae, Coronaviridae, Dengue, EBV, HIV, Flaviviridae, Hepadnaviridae
25 (Hepatitis), Herpesviridae (such as, Cytomegalovirus, Herpes Simplex, Herpes
Zoster), Mononegavirus (e.g., Paramyxoviridae, Morbillivirus, Rhabdoviridae),

Orthomyxoviridae (e.g., Influenza A, Influenza B, and parainfluenza), Papiloma virus, Papovaviridae, Parvoviridae, Picornaviridae, Poxviridae (such as Smallpox or Vaccinia), Reoviridae (e.g., Rotavirus), Retroviridae (HTLV-I, HTLV-II, Lentivirus), and Togaviridae (e.g., Rubivirus). Viruses falling within these families can cause a

5 variety of diseases or symptoms, including, but not limited to: arthritis, bronchiollitis, respiratory syncytial virus, encephalitis, eye infections (e.g., conjunctivitis, keratitis), chronic fatigue syndrome, hepatitis (A, B, C, E, Chronic Active, Delta), Japanese B encephalitis, Junin, Chikungunya, Rift Valley fever, yellow fever, meningitis, opportunistic infections (e.g., AIDS), pneumonia, Burkitt's Lymphoma, chickenpox,

10 hemorrhagic fever, Measles, Mumps, Parainfluenza, Rabies, the common cold, Polio, leukemia, Rubella, sexually transmitted diseases, skin diseases (e.g., Kaposi's, warts), and viremia. polynucleotides or polypeptides, or agonists or antagonists of the invention, can be used to treat, prevent, and/or diagnose any of these symptoms or diseases. In specific embodiments, polynucleotides, polypeptides, or agonists or

15 antagonists of the invention are used to treat, prevent, and/or diagnose: meningitis, Dengue, EBV, and/or hepatitis (e.g., hepatitis B). In an additional specific embodiment polynucleotides, polypeptides, or agonists or antagonists of the invention are used to treat patients nonresponsive to one or more other commercially available hepatitis vaccines. In a further specific embodiment polynucleotides, polypeptides, or

20 agonists or antagonists of the invention are used to treat, prevent, and/or diagnose AIDS.

Similarly, bacterial or fungal agents that can cause disease or symptoms and that can be treated, prevented, and/or diagnosed by a polynucleotide or polypeptide and/or agonist or antagonist of the present invention include, but not limited to,

25 include, but not limited to, the following Gram-Negative and Gram-positive bacteria and bacterial families and fungi: Actinomycetales (e.g., Corynebacterium,

- Mycobacterium, Norcardia), Cryptococcus neoformans, Aspergillosis, Bacillaceae (e.g., Anthrax, Clostridium), Bacteroidaceae, Blastomycosis, Bordetella, Borrelia (e.g., Borrelia burgdorferi), Brucellosis, Candidiasis, Campylobacter, Coccidioidomycosis, Cryptococcosis, Dermatocycoses, E. coli (e.g., Enterotoxigenic E. coli and Enterohemorrhagic-E. coli), Enterobacteriaceae (Klebsiella, Salmonella (e.g., Salmonella typhi, and Salmonella paratyphi), Serratia, Yersinia), Erysipelothrix, Helicobacter, Legionellosis, Leptospirosis, Listeria, Mycoplasmatales, Mycobacterium leprae, Vibrio cholerae, Neisseriaceae (e.g., Acinetobacter, Gonorrhea, Meningococcal), Meisseria meningitidis, Pasteurellacea Infections (e.g., Actinobacillus, Heamophilus (e.g., Heamophilus influenza type B), Pasteurella), Pseudomonas, Rickettsiaceae, Chlamydiaceae, Syphilis, Shigella spp., Staphylococcal, Meningiococcal, Pneumococcal and Streptococcal (e.g., Streptococcus pneumoniae and Group B Streptococcus). These bacterial or fungal families can cause the following diseases or symptoms, including, but not limited to:
- bacteremia, endocarditis, eye infections (conjunctivitis, tuberculosis, uveitis), gingivitis, opportunistic infections (e.g., AIDS related infections), paronychia, prosthesis-related infections, Reiter's Disease, respiratory tract infections, such as Whooping Cough or Empyema, sepsis, Lyme Disease, Cat-Scratch Disease, Dysentery, Paratyphoid Fever, food poisoning, Typhoid, pneumonia, Gonorrhea, meningitis (e.g., meningitis types A and B), Chlamydia, Syphilis, Diphtheria, Leprosy, Paratuberculosis, Tuberculosis, Lupus, Botulism, gangrene, tetanus, impetigo, Rheumatic Fever, Scarlet Fever, sexually transmitted diseases, skin diseases (e.g., cellulitis, dermatocycoses), toxemia, urinary tract infections, wound infections.
- Polynucleotides or polypeptides, agonists or antagonists of the invention, can be used to treat, prevent, and/or diagnose any of these symptoms or diseases. In specific embodiments, polynucleotides, polypeptides, agonists or antagonists of the invention

are used to treat, prevent, and/or diagnose: tetanus, Diphtheria, botulism, and/or meningitis type B.

Moreover, parasitic agents causing disease or symptoms that can be treated, prevented, and/or diagnosed by a polynucleotide or polypeptide and/or agonist or antagonist of the present invention include, but not limited to, the following families or class: Amebiasis, Babesiosis, Coccidiosis, Cryptosporidiosis, Dientamoebiasis, 5 Dourine, Ectoparasitic, Giardiasis, Helminthiasis, Leishmaniasis, Theileriasis, Toxoplasmosis, Trypanosomiasis, and Trichomonas and Sporozoans (e.g., Plasmodium virax, Plasmodium falciparum, Plasmodium malariae and Plasmodium 10 ovale). These parasites can cause a variety of diseases or symptoms, including, but not limited to: Scabies, Trombiculiasis, eye infections, intestinal disease (e.g., dysentery, giardiasis), liver disease, lung disease, opportunistic infections (e.g., AIDS related), malaria, pregnancy complications, and toxoplasmosis. polynucleotides or polypeptides, or agonists or antagonists of the invention, can be used to treat, prevent, 15 and/or diagnose any of these symptoms or diseases. In specific embodiments, polynucleotides, polypeptides, or agonists or antagonists of the invention are used to treat, prevent, and/or diagnose malaria.

Preferably, treatment or prevention using a polypeptide or polynucleotide and/or agonist or antagonist of the present invention could either be by administering 20 an effective amount of a polypeptide to the patient, or by removing cells from the patient, supplying the cells with a polynucleotide of the present invention, and returning the engineered cells to the patient (ex vivo therapy). Moreover, the polypeptide or polynucleotide of the present invention can be used as an antigen in a vaccine to raise an immune response against infectious disease.

25

Regeneration

A polynucleotide or polypeptide and/or agonist or antagonist of the present invention can be used to differentiate, proliferate, and attract cells, leading to the regeneration of tissues. (See, Science 276:59-87 (1997).) The regeneration of tissues could be used to repair, replace, or protect tissue damaged by congenital defects, 5 trauma (wounds, burns, incisions, or ulcers), age, disease (e.g. osteoporosis, osteoarthritis, periodontal disease, liver failure), surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, or systemic cytokine damage.

Tissues that could be regenerated using the present invention include organs (e.g., pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal 10 or cardiac), vasculature (including vascular and lymphatics), nervous, hematopoietic, and skeletal (bone, cartilage, tendon, and ligament) tissue. Preferably, regeneration occurs without or decreased scarring. Regeneration also may include angiogenesis.

Moreover, a polynucleotide or polypeptide and/or agonist or antagonist of the present invention may increase regeneration of tissues difficult to heal. For example, 15 increased tendon/ligament regeneration would quicken recovery time after damage.

A polynucleotide or polypeptide and/or agonist or antagonist of the present invention could also be used prophylactically in an effort to avoid damage. Specific diseases that could be treated, prevented, and/or diagnosed include of tendinitis, carpal tunnel syndrome, and other tendon or ligament defects. A further example of tissue 20 regeneration of non-healing wounds includes pressure ulcers, ulcers associated with vascular insufficiency, surgical, and traumatic wounds.

Similarly, nerve and brain tissue could also be regenerated by using a polynucleotide or polypeptide and/or agonist or antagonist of the present invention to proliferate and differentiate nerve cells. Diseases that could be treated, prevented, 25 and/or diagnosed using this method include central and peripheral nervous system diseases, neuropathies, or mechanical and traumatic diseases, disorders, and/or

conditions (e.g., spinal cord disorders, head trauma, cerebrovascular disease, and stroke). Specifically, diseases associated with peripheral nerve injuries, peripheral neuropathy (e.g., resulting from chemotherapy or other medical therapies), localized neuropathies, and central nervous system diseases (e.g., Alzheimer's disease,

- 5 Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome), could all be treated, prevented, and/or diagnosed using the polynucleotide or polypeptide and/or agonist or antagonist of the present invention.

Chemotaxis

- 10 A polynucleotide or polypeptide and/or agonist or antagonist of the present invention may have chemotaxis activity. A chemotactic molecule attracts or mobilizes cells (e.g., monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells) to a particular site in the body, such as inflammation, infection, or site of hyperproliferation. The mobilized cells can then
- 15 fight off and/or heal the particular trauma or abnormality.

- A polynucleotide or polypeptide and/or agonist or antagonist of the present invention may increase chemotactic activity of particular cells. These chemotactic molecules can then be used to treat, prevent, and/or diagnose inflammation, infection, hyperproliferative diseases, disorders, and/or conditions, or any immune system
- 20 disorder by increasing the number of cells targeted to a particular location in the body. For example, chemotactic molecules can be used to treat, prevent, and/or diagnose wounds and other trauma to tissues by attracting immune cells to the injured location. Chemotactic molecules of the present invention can also attract fibroblasts, which can be used to treat, prevent, and/or diagnose wounds.

- 25 It is also contemplated that a polynucleotide or polypeptide and/or agonist or antagonist of the present invention may inhibit chemotactic activity. These molecules

could also be used to treat, prevent, and/or diagnose diseases, disorders, and/or conditions. Thus, a polynucleotide or polypeptide and/or agonist or antagonist of the present invention could be used as an inhibitor of chemotaxis.

5

Binding Activity

A polypeptide of the present invention may be used to screen for molecules that bind to the polypeptide or for molecules to which the polypeptide binds. The binding of the polypeptide and the molecule may activate (agonist), increase, inhibit
10 (antagonist), or decrease activity of the polypeptide or the molecule bound. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

Preferably, the molecule is closely related to the natural ligand of the polypeptide, e.g., a fragment of the ligand, or a natural substrate, a ligand, a structural
15 or functional mimetic. (See, Coligan et al., Current Protocols in Immunology 1(2):Chapter 5 (1991).) Similarly, the molecule can be closely related to the natural receptor to which the polypeptide binds, or at least, a fragment of the receptor capable of being bound by the polypeptide (e.g., active site). In either case, the molecule can be rationally designed using known techniques.

20 Preferably, the screening for these molecules involves producing appropriate cells which express the polypeptide, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, *Drosophila*, or *E. coli*. Cells expressing the polypeptide (or cell membrane containing the expressed polypeptide) are then preferably contacted with a test compound potentially
25 containing the molecule to observe binding, stimulation, or inhibition of activity of either the polypeptide or the molecule.

The assay may simply test binding of a candidate compound to the polypeptide, wherein binding is detected by a label, or in an assay involving competition with a labeled competitor. Further, the assay may test whether the candidate compound results in a signal generated by binding to the polypeptide.

5 Alternatively, the assay can be carried out using cell-free preparations, polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide, measuring polypeptide/molecule activity or binding, and comparing the polypeptide/molecule activity or binding to a
10 standard.

Preferably, an ELISA assay can measure polypeptide level or activity in a sample (e.g., biological sample) using a monoclonal or polyclonal antibody. The antibody can measure polypeptide level or activity by either binding, directly or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

15 Additionally, the receptor to which a polypeptide of the invention binds can be identified by numerous methods known to those of skill in the art, for example, ligand panning and FACS sorting (Coligan, et al., *Current Protocols in Immun.*, 1(2), Chapter 5, (1991)). For example, expression cloning is employed wherein polyadenylated RNA is prepared from a cell responsive to the polypeptides, for
20 example, NIH3T3 cells which are known to contain multiple receptors for the FGF family proteins, and SC-3 cells, and a cDNA library created from this RNA is divided into pools and used to transfect COS cells or other cells that are not responsive to the polypeptides. Transfected cells which are grown on glass slides are exposed to the polypeptide of the present invention, after they have been labelled. The polypeptides
25 can be labeled by a variety of means including iodination or inclusion of a recognition site for a site-specific protein kinase.

Following fixation and incubation, the slides are subjected to auto-radiographic analysis. Positive pools are identified and sub-pools are prepared and re-transfected using an iterative sub-pooling and re-screening process, eventually yielding a single clones that encodes the putative receptor.

5 As an alternative approach for receptor identification, the labeled polypeptides can be photoaffinity linked with cell membrane or extract preparations that express the receptor molecule. Cross-linked material is resolved by PAGE analysis and exposed to X-ray film. The labeled complex containing the receptors of the polypeptides can be excised, resolved into peptide fragments, and subjected to protein
10 microsequencing. The amino acid sequence obtained from microsequencing would be used to design a set of degenerate oligonucleotide probes to screen a cDNA library to identify the genes encoding the putative receptors.

Moreover, the techniques of gene-shuffling, motif-shuffling, exon-shuffling, and/or codon-shuffling (collectively referred to as "DNA shuffling") may be
15 employed to modulate the activities of polypeptides of the invention thereby effectively generating agonists and antagonists of polypeptides of the invention. See generally, U.S. Patent Nos. 5,605,793, 5,811,238, 5,830,721, 5,834,252, and 5,837,458, and Patten, P. A., et al., Curr. Opinion Biotechnol. 8:724-33 (1997); Harayama, S. Trends Biotechnol. 16(2):76-82 (1998); Hansson, L. O., et al., J. Mol.
20 Biol. 287:265-76 (1999); and Lorenzo, M. M. and Blasco, R. Biotechniques 24(2):308-13 (1998) (each of these patents and publications are hereby incorporated by reference). In one embodiment, alteration of polynucleotides and corresponding polypeptides of the invention may be achieved by DNA shuffling. DNA shuffling involves the assembly of two or more DNA segments into a desired polynucleotide
25 sequence of the invention molecule by homologous, or site-specific, recombination. In another embodiment, polynucleotides and corresponding polypeptides of the

invention may be altered by being subjected to random mutagenesis by error-prone PCR, random nucleotide insertion or other methods prior to recombination. In another embodiment, one or more components, motifs, sections, parts, domains, fragments, etc., of the polypeptides of the invention may be recombined with one or more components, motifs, sections, parts, domains, fragments, etc. of one or more heterologous molecules. In preferred embodiments, the heterologous molecules are family members. In further preferred embodiments, the heterologous molecule is a growth factor such as, for example, platelet-derived growth factor (PDGF), insulin-like growth factor (IGF-I), transforming growth factor (TGF)-alpha, epidermal growth factor (EGF), fibroblast growth factor (FGF), TGF-beta, bone morphogenetic protein (BMP)-2, BMP-4, BMP-5, BMP-6, BMP-7, activins A and B, decapentaplegic(dpp), 60A, OP-2, dorsalin, growth differentiation factors (GDFs), nodal, MIS, inhibin-alpha, TGF-beta1, TGF-beta2, TGF-beta3, TGF-beta5, and glial-derived neurotrophic factor (GDNF).

Other preferred fragments are biologically active fragments of the polypeptides of the invention. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

Additionally, this invention provides a method of screening compounds to identify those which modulate the action of the polypeptide of the present invention. An example of such an assay comprises combining a mammalian fibroblast cell, a the polypeptide of the present invention, the compound to be screened and ^3H thymidine under cell culture conditions where the fibroblast cell would normally proliferate. A control assay may be performed in the absence of the compound to be screened and compared to the amount of fibroblast proliferation in the presence of the

compound to determine if the compound stimulates proliferation by determining the uptake of 3[H] thymidine in each case. The amount of fibroblast cell proliferation is measured by liquid scintillation chromatography which measures the incorporation of 3[H] thymidine. Both agonist and antagonist compounds may be identified by this
5 procedure.

In another method, a mammalian cell or membrane preparation expressing a receptor for a polypeptide of the present invention is incubated with a labeled polypeptide of the present invention in the presence of the compound. The ability of the compound to enhance or block this interaction could then be measured.

- 10 Alternatively, the response of a known second messenger system following interaction of a compound to be screened and the receptor is measured and the ability of the compound to bind to the receptor and elicit a second messenger response is measured to determine if the compound is a potential agonist or antagonist. Such second messenger systems include but are not limited to, cAMP guanylate cyclase,
15 ion channels or phosphoinositide hydrolysis.

All of these above assays can be used as diagnostic or prognostic markers. The molecules discovered using these assays can be used to treat, prevent, and/or diagnose disease or to bring about a particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the polypeptide/molecule. Moreover, the assays
20 can discover agents which may inhibit or enhance the production of the polypeptides of the invention from suitably manipulated cells or tissues. Therefore, the invention includes a method of identifying compounds which bind to the polypeptides of the invention comprising the steps of: (a) incubating a candidate binding compound with the polypeptide; and (b) determining if binding has occurred. Moreover, the
25 invention includes a method of identifying agonists/antagonists comprising the steps of: (a) incubating a candidate compound with the polypeptide, (b) assaying a

biological activity , and (b) determining if a biological activity of the polypeptide has been altered.

Also, one could identify molecules bind a polypeptide of the invention experimentally by using the beta-pleated sheet regions contained in the polypeptide sequence of the protein. Accordingly, specific embodiments of the invention are directed to polynucleotides encoding polypeptides which comprise, or alternatively consist of, the amino acid sequence of each beta pleated sheet regions in a disclosed polypeptide sequence. Additional embodiments of the invention are directed to polynucleotides encoding polypeptides which comprise, or alternatively consist of, any combination or all of contained in the polypeptide sequences of the invention. Additional preferred embodiments of the invention are directed to polypeptides which comprise, or alternatively consist of, the amino acid sequence of each of the beta pleated sheet regions in one of the polypeptide sequences of the invention. Additional embodiments of the invention are directed to polypeptides which comprise, or alternatively consist of, any combination or all of the beta pleated sheet regions in one of the polypeptide sequences of the invention.

Targeted Delivery

In another embodiment, the invention provides a method of delivering compositions to targeted cells expressing a receptor for a polypeptide of the invention, or cells expressing a cell bound form of a polypeptide of the invention.

As discussed herein, polypeptides or antibodies of the invention may be associated with heterologous polypeptides, heterologous nucleic acids, toxins, or prodrugs via hydrophobic, hydrophilic, ionic and/or covalent interactions. In one embodiment, the invention provides a method for the specific delivery of compositions of the invention to cells by administering polypeptides of the invention

(including antibodies) that are associated with heterologous polypeptides or nucleic acids. In one example, the invention provides a method for delivering a therapeutic protein into the targeted cell. In another example, the invention provides a method for delivering a single stranded nucleic acid (e.g., antisense or ribozymes) or double stranded nucleic acid (e.g., DNA that can integrate into the cell's genome or replicate epismally and that can be transcribed) into the targeted cell.

In another embodiment, the invention provides a method for the specific destruction of cells (e.g., the destruction of tumor cells) by administering polypeptides of the invention (e.g., polypeptides of the invention or antibodies of the invention) in association with toxins or cytotoxic prodrugs.

By "toxin" is meant compounds that bind and activate endogenous cytotoxic effector systems, radioisotopes, holotoxins, modified toxins, catalytic subunits of toxins, or any molecules or enzymes not normally present in or on the surface of a cell that under defined conditions cause the cell's death. Toxins that may be used according to the methods of the invention include, but are not limited to, radioisotopes known in the art, compounds such as, for example, antibodies (or complement fixing containing portions thereof) that bind an inherent or induced endogenous cytotoxic effector system, thymidine kinase, endonuclease, RNase, alpha toxin, ricin, abrin, *Pseudomonas* exotoxin A, diphtheria toxin, saporin, momordin, gelonin, pokeweed antiviral protein, alpha-sarcin and cholera toxin. By "cytotoxic prodrug" is meant a non-toxic compound that is converted by an enzyme, normally present in the cell, into a cytotoxic compound. Cytotoxic prodrugs that may be used according to the methods of the invention include, but are not limited to, glutamyl derivatives of benzoic acid mustard alkylating agent, phosphate derivatives of etoposide or mitomycin C, cytosine arabinoside, daunorubisin, and phenoxyacetamide derivatives of doxorubicin.

Drug Screening

Further contemplated is the use of the polypeptides of the present invention, or the polynucleotides encoding these polypeptides, to screen for molecules which
5 modify the activities of the polypeptides of the present invention. Such a method would include contacting the polypeptide of the present invention with a selected compound(s) suspected of having antagonist or agonist activity, and assaying the activity of these polypeptides following binding.

This invention is particularly useful for screening therapeutic compounds by
10 using the polypeptides of the present invention, or binding fragments thereof, in any of a variety of drug screening techniques. The polypeptide or fragment employed in such a test may be affixed to a solid support, expressed on a cell surface, free in solution, or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids
15 expressing the polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. One may measure, for example, the formulation of complexes between the agent being tested and a polypeptide of the present invention.

Thus, the present invention provides methods of screening for drugs or any
20 other agents which affect activities mediated by the polypeptides of the present invention. These methods comprise contacting such an agent with a polypeptide of the present invention or a fragment thereof and assaying for the presence of a complex between the agent and the polypeptide or a fragment thereof, by methods well known in the art. In such a competitive binding assay, the agents to screen are typically
25 labeled. Following incubation, free agent is separated from that present in bound

form, and the amount of free or uncomplexed label is a measure of the ability of a particular agent to bind to the polypeptides of the present invention.

Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to the polypeptides of the present invention, and is described in great detail in European Patent Application 84/03564, published on September 13, 1984, which is incorporated herein by reference herein. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. The peptide test compounds are reacted with polypeptides of the present invention and washed. Bound polypeptides are then detected by methods well known in the art. Purified polypeptides are coated directly onto plates for use in the aforementioned drug screening techniques. In addition, non-neutralizing antibodies may be used to capture the peptide and immobilize it on the solid support.

This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding polypeptides of the present invention specifically compete with a test compound for binding to the polypeptides or fragments thereof. In this manner, the antibodies are used to detect the presence of any peptide which shares one or more antigenic epitopes with a polypeptide of the invention.

20

Antisense And Ribozyme (Antagonists)

In specific embodiments, antagonists according to the present invention are nucleic acids corresponding to the sequences contained in SEQ ID NO:X, or the complementary strand thereof, and/or to nucleotide sequences contained a deposited clone. In one embodiment, antisense sequence is generated internally by the organism, in another embodiment, the antisense sequence is separately administered

25

(see, for example, O'Connor, *Neurochem.*, 56:560 (1991). *Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression*, CRC Press, Boca Raton, FL (1988).

Antisense technology can be used to control gene expression through antisense DNA or RNA, or through triple-helix formation. Antisense techniques are discussed for

5 example, in Okano, *Neurochem.*, 56:560 (1991); *Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression*, CRC Press, Boca Raton, FL (1988). Triple helix formation is discussed in, for instance, Lee et al., *Nucleic Acids Research*, 6:3073 (1979); Cooney et al., *Science*, 241:456 (1988); and Dervan et al., *Science*, 251:1300 (1991). The methods are based on binding of a polynucleotide to a complementary
10 DNA or RNA.

For example, the use of c-myc and c-myb antisense RNA constructs to inhibit the growth of the non-lymphocytic leukemia cell line HL-60 and other cell lines was previously described. (Wickstrom et al. (1988); Anfossi et al. (1989)). These experiments were performed in vitro by incubating cells with the oligoribonucleotide.

15 A similar procedure for in vivo use is described in WO 91/15580. Briefly, a pair of oligonucleotides for a given antisense RNA is produced as follows: A sequence complimentary to the first 15 bases of the open reading frame is flanked by an EcoRI site on the 5' end and a HindIII site on the 3' end. Next, the pair of oligonucleotides is heated at 90°C for one minute and then annealed in 2X ligation buffer (20mM TRIS
20 HCl pH 7.5, 10mM MgCl₂, 10mM dithiothreitol (DTT) and 0.2 mM ATP) and then ligated to the EcoRI/Hind III site of the retroviral vector PMV7 (WO 91/15580).

For example, the 5' coding portion of a polynucleotide that encodes the mature polypeptide of the present invention may be used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide
25 is designed to be complementary to a region of the gene involved in transcription thereby preventing transcription and the production of the receptor. The antisense

RNA oligonucleotide hybridizes to the mRNA in vivo and blocks translation of the mRNA molecule into receptor polypeptide.

In one embodiment, the antisense nucleic acid of the invention is produced intracellularly by transcription from an exogenous sequence. For example, a vector or
5 a portion thereof, is transcribed, producing an antisense nucleic acid (RNA) of the invention. Such a vector would contain a sequence encoding the antisense nucleic acid of the invention. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard
10 in the art. Vectors can be plasmid, viral, or others known in the art, used for replication and expression in vertebrate cells. Expression of the sequence encoding a polypeptide of the invention, or fragments thereof, can be by any promoter known in the art to act in vertebrate, preferably human cells. Such promoters can be inducible or constitutive. Such promoters include, but are not limited to, the SV40 early
15 promoter region (Bernoist and Chambon, Nature, 29:304-310 (1981), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto et al., Cell, 22:787-797 (1980), the herpes thymidine promoter (Wagner et al., Proc. Natl. Acad. Sci. U.S.A., 78:1441-1445 (1981), the regulatory sequences of the metallothionein gene (Brinster et al., Nature, 296:39-42 (1982)), etc.

20 The antisense nucleic acids of the invention comprise a sequence complementary to at least a portion of an RNA transcript of a gene of interest. However, absolute complementarity, although preferred, is not required. A sequence "complementary to at least a portion of an RNA," referred to herein, means a sequence having sufficient complementarity to be able to hybridize with the RNA,
25 forming a stable duplex; in the case of double stranded antisense nucleic acids of the invention, a single strand of the duplex DNA may thus be tested, or triplex formation

may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the larger the hybridizing nucleic acid, the more base mismatches with a RNA sequence of the invention it may contain and still form a stable duplex (or triplex as the case may be).

- 5 One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

- Oligonucleotides that are complementary to the 5' end of the message, *e.g.*, the 5' untranslated sequence up to and including the AUG initiation codon, should work most efficiently at inhibiting translation. However, sequences complementary to the 3' untranslated sequences of mRNAs have been shown to be effective at inhibiting translation of mRNAs as well. See generally, Wagner, R., *Nature*, 372:333-335 (1994). Thus, oligonucleotides complementary to either the 5' - or 3' - non-translated, non-coding regions of a polynucleotide sequence of the invention could be used in an antisense approach to inhibit translation of endogenous mRNA.
- 10 Oligonucleotides complementary to the 5' untranslated region of the mRNA should include the complement of the AUG start codon. Antisense oligonucleotides complementary to mRNA coding regions are less efficient inhibitors of translation but could be used in accordance with the invention. Whether designed to hybridize to the 5' -, 3' - or coding region of mRNA, antisense nucleic acids should be at least six
- 15 nucleotides in length, and are preferably oligonucleotides ranging from 6 to about 50 nucleotides in length. In specific aspects the oligonucleotide is at least 10 nucleotides, at least 17 nucleotides, at least 25 nucleotides or at least 50 nucleotides.

- The polynucleotides of the invention can be DNA or RNA or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-
- 25 stranded. The oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization,

etc. The oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors in vivo), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556 (1989); Lemaitre et al., Proc. Natl. Acad. Sci., 84:648-652 (1987); PCT Publication NO: WO88/09810, published December 15, 1988) or the blood-brain barrier (see, e.g., PCT Publication NO: WO89/10134, published April 25, 1988), hybridization-triggered cleavage agents. (See, e.g., Krol et al., BioTechniques, 6:958-976 (1988)) or intercalating agents. (See, e.g., Zon, Pharm. Res., 5:539-549 (1988)). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

The antisense oligonucleotide may comprise at least one modified base moiety which is selected from the group including, but not limited to, 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xantine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine.

The antisense oligonucleotide may also comprise at least one modified sugar moiety selected from the group including, but not limited to, arabinose, 2-fluoroarabinose, xylulose, and hexose.

In yet another embodiment, the antisense oligonucleotide comprises at least
5 one modified phosphate backbone selected from the group including, but not limited to, a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, and a formacetal or analog thereof.

In yet another embodiment, the antisense oligonucleotide is an a-anomeric
10 oligonucleotide. An a-anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual b-units, the strands run parallel to each other (Gautier et al., Nucl. Acids Res., 15:6625-6641 (1987)). The oligonucleotide is a 2-O-methylribonucleotide (Inoue et al., Nucl. Acids Res., 15:6131-6148 (1987)), or a chimeric RNA-DNA analogue (Inoue et al., FEBS Lett.
15 215:327-330 (1987)).

Polynucleotides of the invention may be synthesized by standard methods known in the art, e.g. by use of an automated DNA synthesizer (such as are commercially available from Biosearch, Applied Biosystems, etc.). As examples, phosphorothioate oligonucleotides may be synthesized by the method of Stein et al.
20 (Nucl. Acids Res., 16:3209 (1988)), methylphosphonate oligonucleotides can be prepared by use of controlled pore glass polymer supports (Sarin et al., Proc. Natl. Acad. Sci. U.S.A., 85:7448-7451 (1988)), etc.

While antisense nucleotides complementary to the coding region sequence of the invention could be used, those complementary to the transcribed untranslated
25 region are most preferred.

Potential antagonists according to the invention also include catalytic RNA, or a ribozyme (See, e.g., PCT International Publication WO 90/11364, published October 4, 1990; Sarver et al, Science, 247:1222-1225 (1990). While ribozymes that cleave mRNA at site specific recognition sequences can be used to destroy mRNAs corresponding to the polynucleotides of the invention, the use of hammerhead ribozymes is preferred. Hammerhead ribozymes cleave mRNAs at locations dictated by flanking regions that form complementary base pairs with the target mRNA. The sole requirement is that the target mRNA have the following sequence of two bases: 5' -UG-3'. The construction and production of hammerhead ribozymes is well known in the art and is described more fully in Haseloff and Gerlach, Nature, 334:585-591 (1988). There are numerous potential hammerhead ribozyme cleavage sites within each nucleotide sequence disclosed in the sequence listing. Preferably, the ribozyme is engineered so that the cleavage recognition site is located near the 5' end of the mRNA corresponding to the polynucleotides of the invention; i.e., to increase efficiency and minimize the intracellular accumulation of non-functional mRNA transcripts.

As in the antisense approach, the ribozymes of the invention can be composed of modified oligonucleotides (e.g. for improved stability, targeting, etc.) and should be delivered to cells which express the polynucleotides of the invention in vivo. DNA constructs encoding the ribozyme may be introduced into the cell in the same manner as described above for the introduction of antisense encoding DNA. A preferred method of delivery involves using a DNA construct "encoding" the ribozyme under the control of a strong constitutive promoter, such as, for example, pol III or pol II promoter, so that transfected cells will produce sufficient quantities of the ribozyme to destroy endogenous messages and inhibit translation. Since

ribozymes unlike antisense molecules, are catalytic, a lower intracellular concentration is required for efficiency.

Antagonist/agonist compounds may be employed to inhibit the cell growth and proliferation effects of the polypeptides of the present invention on neoplastic
5 cells and tissues, i.e. stimulation of angiogenesis of tumors, and, therefore, retard or prevent abnormal cellular growth and proliferation, for example, in tumor formation or growth.

The antagonist/agonist may also be employed to prevent hyper-vascular diseases, and prevent the proliferation of epithelial lens cells after extracapsular
10 cataract surgery. Prevention of the mitogenic activity of the polypeptides of the present invention may also be desirable in cases such as restenosis after balloon angioplasty.

The antagonist/agonist may also be employed to prevent the growth of scar tissue during wound healing.

15 The antagonist/agonist may also be employed to treat, prevent, and/or diagnose the diseases described herein.

Thus, the invention provides a method of treating or preventing diseases, disorders, and/or conditions, including but not limited to the diseases, disorders, and/or conditions listed throughout this application, associated with
20 overexpression of a polynucleotide of the present invention by administering to a patient (a) an antisense molecule directed to the polynucleotide of the present invention, and/or (b) a ribozyme directed to the polynucleotide of the present invention.

invention, and/or (b) a ribozyme directed to the polynucleotide of the present
25 invention.

Other Activities

The polypeptide of the present invention, as a result of the ability to stimulate vascular endothelial cell growth, may be employed in treatment for stimulating re-vascularization of ischemic tissues due to various disease conditions such as

5 thrombosis, arteriosclerosis, and other cardiovascular conditions. These polypeptide may also be employed to stimulate angiogenesis and limb regeneration, as discussed above.

The polypeptide may also be employed for treating wounds due to injuries, burns, post-operative tissue repair, and ulcers since they are mitogenic to various cells

10 of different origins, such as fibroblast cells and skeletal muscle cells, and therefore, facilitate the repair or replacement of damaged or diseased tissue.

The polypeptide of the present invention may also be employed stimulate neuronal growth and to treat, prevent, and/or diagnose neuronal damage which occurs in certain neuronal disorders or neuro-degenerative conditions such as Alzheimer's

15 disease, Parkinson's disease, and AIDS-related complex. The polypeptide of the invention may have the ability to stimulate chondrocyte growth, therefore, they may be employed to enhance bone and periodontal regeneration and aid in tissue transplants or bone grafts.

The polypeptide of the present invention may be also be employed to prevent

20 skin aging due to sunburn by stimulating keratinocyte growth.

The polypeptide of the invention may also be employed for preventing hair loss, since FGF family members activate hair-forming cells and promotes melanocyte growth. Along the same lines, the polypeptides of the present invention may be employed to stimulate growth and differentiation of hematopoietic cells and bone

25 marrow cells when used in combination with other cytokines.

The polypeptide of the invention may also be employed to maintain organs before transplantation or for supporting cell culture of primary tissues.

The polypeptide of the present invention may also be employed for inducing tissue of mesodermal origin to differentiate in early embryos.

5

The polypeptide or polynucleotides and/or agonist or antagonists of the present invention may also increase or decrease the differentiation or proliferation of embryonic stem cells, besides, as discussed above, hematopoietic lineage.

10 The polypeptide or polynucleotides and/or agonist or antagonists of the present invention may also be used to modulate mammalian characteristics, such as body height, weight, hair color, eye color, skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic surgery). Similarly, polypeptides or polynucleotides and/or agonist or antagonists of the present invention may be used to modulate mammalian metabolism affecting catabolism, anabolism, processing,
15 utilization, and storage of energy.

Polypeptide or polynucleotides and/or agonist or antagonists of the present invention may be used to change a mammal's mental state or physical state by influencing biorhythms, cardiac rhythms, depression (including depressive diseases, disorders, and/or conditions), tendency for violence, tolerance for pain, reproductive
20 capabilities (preferably by Activin or Inhibin-like activity), hormonal or endocrine levels, appetite, libido, memory, stress, or other cognitive qualities.

Polypeptide or polynucleotides and/or agonist or antagonists of the present invention may also be used as a food additive or preservative, such as to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins,
25 minerals, cofactors or other nutritional components.

Other Preferred Embodiments

Other preferred embodiments of the claimed invention include an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 50 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Clone Sequence and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Start Codon and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Similarly preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the First Amino Acid of the Signal Peptide and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 150 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

Further preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 500 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

A further preferred embodiment is a nucleic acid molecule comprising a
5 nucleotide sequence which is at least 95% identical to the nucleotide sequence of SEQ ID NO:X beginning with the nucleotide at about the position of the 5' Nucleotide of the First Amino Acid of the Signal Peptide and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

10 A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence of SEQ ID NO:X.

Also preferred is an isolated nucleic acid molecule which hybridizes under stringent hybridization conditions to a nucleic acid molecule, wherein said nucleic
15 acid molecule which hybridizes does not hybridize under stringent hybridization conditions to a nucleic acid molecule having a nucleotide sequence consisting of only A residues or of only T residues.

Also preferred is a composition of matter comprising a DNA molecule which comprises a human cDNA clone identified by a cDNA Clone Identifier in Table 1,
20 which DNA molecule is contained in the material deposited with the American Type Culture Collection and given the ATCC Deposit Number shown in Table 1 for said cDNA Clone Identifier.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous
25 nucleotides in the nucleotide sequence of a human cDNA clone identified by a cDNA

Clone Identifier in Table 1, which DNA molecule is contained in the deposit given the ATCC Deposit Number shown in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said sequence of at least 50 contiguous nucleotides is included in the nucleotide sequence of the

5 complete open reading frame sequence encoded by said human cDNA clone.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 150 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is an isolated nucleic acid molecule
10 comprising a nucleotide sequence which is at least 95% identical to sequence of at least 500 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete
15 nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is a method for detecting in a biological sample a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X
20 wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method comprises a step of comparing a nucleotide sequence of at least one nucleic acid molecule in said sample with a sequence selected from said group and
25 determining whether the sequence of said nucleic acid molecule in said sample is at least 95% identical to said selected sequence.

Also preferred is the above method wherein said step of comparing sequences comprises determining the extent of nucleic acid hybridization between nucleic acid molecules in said sample and a nucleic acid molecule comprising said sequence selected from said group. Similarly, also preferred is the above method wherein said
5 step of comparing sequences is performed by comparing the nucleotide sequence determined from a nucleic acid molecule in said sample with said sequence selected from said group. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

A further preferred embodiment is a method for identifying the species, tissue
10 or cell type of a biological sample which method comprises a step of detecting nucleic acid molecules in said sample, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by
15 a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

The method for identifying the species, tissue or cell type of a biological sample can comprise a step of detecting nucleic acid molecules comprising a
20 nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted
25 protein identified in Table 1, which method comprises a step of detecting in a biological sample obtained from said subject nucleic acid molecules, if any,

comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA

- 5 Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

The method for diagnosing a pathological condition can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least
10 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a composition of matter comprising isolated nucleic acid molecules wherein the nucleotide sequences of said nucleic acid molecules comprise a panel of at least two nucleotide sequences, wherein at least one sequence in said
15 panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA
20 clone in Table 1. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1.

25 Also preferred is a polypeptide, wherein said sequence of contiguous amino acids is included in the amino acid sequence of SEQ ID NO:Y in the range of

positions beginning with the residue at about the position of the First Amino Acid of the Secreted Portion and ending with the residue at about the Last Amino Acid of the Open Reading Frame as set forth for SEQ ID NO:Y in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence
5 at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

10 Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the complete amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino
15 acids in the complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is a polypeptide wherein said sequence of contiguous amino acids is included in the amino acid sequence of a secreted portion of the secreted
20 protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the
25 amino acid sequence of the secreted portion of the protein encoded by a human cDNA

clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is an isolated antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is a method for detecting in a biological sample a polypeptide comprising an amino acid sequence which is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained

in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method comprises a step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group and determining whether the sequence of said polypeptide molecule in said sample is
5 at least 90% identical to said sequence of at least 10 contiguous amino acids.

Also preferred is the above method wherein said step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group comprises determining the extent of specific binding of polypeptides in said sample to an antibody which binds specifically to a polypeptide
10 comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit
15 with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is the above method wherein said step of comparing sequences is performed by comparing the amino acid sequence determined from a polypeptide molecule in said sample with said sequence selected from said group.

Also preferred is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting polypeptide molecules
20 in said sample, if any, comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted
25 protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in

Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is the above method for identifying the species, tissue or cell type of a biological sample, which method comprises a step of detecting polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the above group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table 1, which method comprises a step of detecting in a biological sample obtained from said subject polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

In any of these methods, the step of detecting said polypeptide molecules includes using an antibody.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a nucleotide sequence encoding a polypeptide wherein said polypeptide comprises an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y

wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

5 Also preferred is an isolated nucleic acid molecule, wherein said nucleotide sequence encoding a polypeptide has been optimized for expression of said polypeptide in a prokaryotic host.

 Also preferred is an isolated nucleic acid molecule, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of: an amino
10 acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

 Further preferred is a method of making a recombinant vector comprising
15 inserting any of the above isolated nucleic acid molecule into a vector. Also preferred is the recombinant vector produced by this method. Also preferred is a method of making a recombinant host cell comprising introducing the vector into a host cell, as well as the recombinant host cell produced by this method.

 Also preferred is a method of making an isolated polypeptide comprising
20 culturing this recombinant host cell under conditions such that said polypeptide is expressed and recovering said polypeptide. Also preferred is this method of making an isolated polypeptide, wherein said recombinant host cell is a eukaryotic cell and said polypeptide is a secreted portion of a human secreted protein comprising an amino acid sequence selected from the group consisting of: an amino acid sequence of
25 SEQ ID NO:Y beginning with the residue at the position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y wherein Y is an integer set forth in Table 1 and

said position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y is defined in Table 1; and an amino acid sequence of a secreted portion of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The isolated polypeptide produced by this method is also preferred.

Also preferred is a method of treatment of an individual in need of an increased level of a secreted protein activity, which method comprises administering to such an individual a pharmaceutical composition comprising an amount of an isolated polypeptide, polynucleotide, or antibody of the claimed invention effective to increase the level of said protein activity in said individual.

The above-recited applications have uses in a wide variety of hosts. Such hosts include, but are not limited to, human, murine, rabbit, goat, guinea pig, camel, horse, mouse, rat, hamster, pig, micro-pig, chicken, goat, cow, sheep, dog, cat, non-human primate, and human. In specific embodiments, the host is a mouse, rabbit, goat, guinea pig, chicken, rat, hamster, pig, sheep, dog or cat. In preferred embodiments, the host is a mammal. In most preferred embodiments, the host is a human.

In specific embodiments of the invention, for each "Contig ID" listed in the fourth column of Table 2, preferably excluded are one or more polynucleotides comprising, or alternatively consisting of, a nucleotide sequence referenced in the fifth column of Table 2 and described by the general formula of a-b, whereas a and b are uniquely determined for the corresponding SEQ ID NO:X referred to in column 3 of Table 2. Further specific embodiments are directed to polynucleotide sequences excluding one, two, three, four, or more of the specific polynucleotide sequences referred to in the fifth column of Table 2. In no way is this listing meant to encompass all of the sequences which may be excluded by the general formula, it is just a

representative example. All references available through these accessions are hereby incorporated by reference in their entirety.

TABLE 2

Gene No.	cDNA Clone ID	NT SEQ ID NO: X	Contig ID	Public Accession Numbers
1	HTXOL30	11	838462	None
2	HTXOW27	12	839280	T53073, T53074, T60082, R17799, R34863, R43004, R43004, R61536, R61592, AA045280, AA046561, AA227495, AA236925, AA631391, AA569384, AA713835, AA761720, AA769524, AA825309, AA825495, Z78338, Z78337, AA399251, AA412234, AA644225, AA843899, AA854424, AI003333, AI039680, AI040474, T24506, Z38952, Z42809
3	HTXPD86	13	834772	T81937, R36282, R89681, N53821, N64739, N91752, W90483, AA040245, AA040246, AA147087, AA147144, AA261983, AA488962, AA490411, AA505052, AA737797
4	HWLGP26	14	834770	N49757, N52685, AA046576, AA046663, AA507121, AA605050, AA766124, AA769270, AA814924, AA815032, AA832314, AA910584, AA928729, AI025113, AI057140
5	HWLHO31	15	837480	W73267, W86465, W86466
6	HOGAR36	16	834684	R69465, R70454
7	HOGCC26	17	834792	T98236, T98237, R14574, R21981, R21982, R41348, R41348, H00175, H00222, H29775, H29774, N21638, N28879, N36793, N45953, N67785, W03588, W39247, W78769, W81121, AA075627, AA075737, AA082254, AA128583, AA164651, AA164650, AA167794, AA181995, AA169453, AA232076, AA232075, AA418291, AA282145, AA291318, AA291317, AA563842, AA714868, AA742838, AA911349
11	HSVCF53	21	846129	AA252019, AA765909, AA933872
17	HNKAA76	27	802009	R42232, R42232, AA035137, AA427665
18	HNTSQ23	28	645176	R52664, R52712, N50428, N50483, N92658, N94800, N99604
19	HOABP31	29	835084	T52858, T52859, T57464, T57488, T59403, T59448, T59449, T59707, T61472, T40823, T62477, T69853, T90480, T91503, T91531, T91603, T92747, T94522, T94877, T94923, T79634, T98620, R06276, R82351, H13665, H23734, H23947, H25430, H26258, H28473, H29839, H30884, H38812, H46729, R87096, R87727, R92991, R98012, R98704, H48574, H49955, H56360, H56909, H57921, H59052, H59734, H60410, H61987, H67853, H69037,

				H75682, H80238, H82211, H88070, H88071, H90411, H90523, H67853, H98710, H99649, N20377, N21511, N22122, N22168, N22944, N26521, N58030, N58352, N59419, N63667, N66143, N70869, N71217, N73779, N74172, N74325, N74647, N74689, N75303, N75313, N75577, N75969, N76725, N79470, N79475, N93046, N95056, N95378, N99213, N99400, W05182, W15372, W15553, W31294, W37886, W39403, W42492, W42929, W42978, W45645, W47486, W47496, W48578, W48595, W48603, W52195, W51834, W67567, W67614, W94128, W94023, W94272, W94249, N90040, N90259, N90696, AA036778, AA064639, AA070506, AA070709, AA079801, AA084682, AA100889, AA129704, AA133305, AA133735, AA131222, AA131231, AA132113, AA143137, AA147231, AA152370, AA152374, AA156113, AA158142, AA164283, AA169591, AA172262, AA181887, AA181923, AA186633, AA186705, AA188301, AA223735, AA223823, AA397467, AA501621, AA541327, AA548588, F17428, AA582753, AA586988, AA617741, AA618134, AA622633, AA622640, AA622660, AA576419, AA576993, AA565882, AA665276, AA689360, AA814485, AA834350, AA836934, AA961385, AA970283, AA973176, AA976481, AA983344, AA991420, A1003788, A1015373, W15463, C14368, C14474, AA642949, AA181920, AA650243, AA650406
20	HODAW64	30	840069	T63890, T68174, T86591, T86592, R34557, R55728, R62185, R73464, H00490, H27268, H30352, H40100, H45540, H45548, H49309, H64695, N24348, N44922, N45701, N50614, N79961, W07221, W24522, W40361, W72659, W84736, W84762, AA026874, AA037721, AA082063, AA083629, AA099538, AA159322, AA187572, AA459720, AA460678, AA470902, AA565576, AA811563, AA832414, AA904245, AA912052, AA928641, N83839, W39447, N88427, C03907, R29746, C21239, AA096344, AA651757, AA248793, AA496857, AA634015, AA724013, A1077523, A1086884, Z43558, D45448, F07291
22	HLQBX64	32	772803	T40113, T40914, T41019, T51148, T67818, T68167, T69598, T69670, T71679, R26189, R26437, R46148, R46148, H04754, H04844, H42697, N53433, N69299, AA165482, AA169335, AA171694, AA171782, AA172005, AA172094, AA191647
23	HOSCZ41	33	665525	AA233152
27	HPFDB66	37	829318	T89615, T89889, R16089, R15723, R81451, R81653, W81021, W81057, AA043862, AA085581, AA111916, AA115256, AA115257, AA180208, AA180840, AA602660, AA806736, A1000600
28	HPJAN76	38	826185	R11723, R14544, R17696, R20352, R41205, R43737, R41205, R43737, H06707, H06756, H17189, H17965, AA075743, AA082074,

				AA084248, AA084249, AA102212, AA173383, AA173739, AA419229, AA419214
29	HPBJ51	39	829114	R14675, R42399, R42399, R80272, H17533, H43227, H84163, H84164, N28981, N46086, N46087, W58010, W58093, AA129954, AA147570, AA156442, AA188999, AA515022, C01168, AA090341
30	HPMBW95	40	639092	R19233, R39170, R44496, R44496, N66954
31	HGBBR29	41	823106	T83401, R17472, R42818, R42818, R68485, R68486, R79980, R80080, H89552, H99877, N20299, N27568, N28562, N34775, N44501, N67848, W69116, W69241, W72484, W75942, AA010377, AA010473, AA062665, AA112285, AA167756, AA194650, AA233543, AA256044, AA255978
32	HPMDD27	42	830748	H29506, AA182641, AA505767, AA516054, AA581961, AA603342, AA638984, AA962704
33	HPMEG72	43	795709	W72392, W76410, AA164841, AA258828
35	HBXAT27	45	815571	R00252, R00362, R40811, R40811, R80822, R81028, H15801, R87999, R88050, R88812, R88873, R88984, R89532, R92997, R93038, H71528, H90510, H90606, W69506, W69628, AA024542, AA024541, AA085564, AA085693, AA098955, AA111893, AA172279, AA173255, AA173246, AA461514, AA460587
36	HPRCM72	46	813512	T59146, T59184, T87592, R07789, T97283, T97395, R21170, R22788, R63213, R63261, H05748, H05855, R93582, R93581, H65072, H65071, H65630, H79991, H79992, H82449, N21046, N27877, N50967, N66225, N76786, N98297, W38747, W46356, W46192, W94368, W94477, AA044925, AA076057, AA076152, AA121295, AA121467, AA149241, AA150022, AA150087, AA460935, AA461239
37	HOHCH71	47	823101	R11788, T96282, T96281, R18963, R33113, R33261, R37707, R43974, R52405, R52406, R52462, R52463, R43974, R55831, R55917, R56079, R56190, R63506, R63551, R66072, R67672, H04652, H04674, H14855, H88794, H89018, H88794, N29740, N57160, W45643, W45596, W69792, W69880, AA043192, AA043594, AA127419, AA127418, AA213537, AA214551
38	HPTRM02	48	812879	T62995, T63138, R07062, R37100, R73151, R73214, R75945, R76783, R82480, R82530, H28650, AA057835, AA149920, AA193433, AA427422
39	HPTRW28	49	822865	H49149
41	HPWDK06	51	839825	T57230, T87655, T91972, T85020, T96978, R00476, R25223, R46358, R46453, R49872, R54859, R72616, R72686, R75603, R75675, R75929, R77973, R78348, H02284, H02388, H10988, H39868, H68844, H68682, H70519, N80819, W15619, AA045287, AA046510, AA115201, AA115200, AA126650, AA136043, AA180862, AA226349, AA226348, AA226432,

				AA228435, AA229915, AA483567, AA555151, AA595655, AA602785, AA612746, AA614242, AA740442, AA873708, AA974018, W22494, C01231, C04788, F21664, AA496366, AA834942, AA835081, AI003183, AI015006
42	HRAAZ12	52	834637	T96296, T96297, T99900, R19850, R23539, R44289, R44289, R61144, R61862, R67833, R67834, H01050, H01803, H29595, H29681, R98622, R98621, R99444, R99592, R99697, H51139, H52434, H72212, H89687, H89721, H89784, H97683, H99253, H99620, N20176, N20668, N20808, N24184, N24408, N25760, N25995, N26379, N29046, N29077, N30533, N31512, N31684, N31777, N33546, N34920, N36627, N41524, N46649, N47687, N47688, N48154, N50190, N53300, N54402, N79568, W16605, W16999, W72221, W77965, W92085, W92118, AA009871, AA034447, AA046600, AA046728, AA047104, AA055473, AA057388, AA057640, AA057680, AA081096, AA081254, AA099129, AA099166, AA127691, AA126383, AA156964, AA255756, AA418398, AA418495, H72110, AA828181, AA857005, AA976518, N26125, W19201, N90777, AA047241, AA093313, AA127790
43	HRABP28	53	823344	T83292
44	HRDEX93	54	816046	T95860, T95866, T95955, T95961, R38031, R38117, R69693, R77485, H13222, H13591, H26512, H54187, H72140, H91107, H91459, N30739, N35164, N59649, N78203, W67484, W80351, W80352, N90770, AA031456, AA031577, AA037422, AA040058, AA040044, AA054553, AA054613, AA173027, AA176708, AA226924, AA226888
45	HRDFE30	55	750872	T49242, T50079, T57819, R23586, R32658, R51340, R94122, N68670, N68745, N91638, W17226, W65457, W65456, W88489, W89165, W89166, W90016, N89729, AA031751, AA032251, AA133738, AA133739, AA130423, AA130422, AA191749, AA461493, AA460568
48	HHSBI06	58	639097	N59786, AA088744

Having generally described the invention, the same will be more readily understood by reference to the following examples, which are provided by way of illustration and are not intended as limiting.

5

Examples

Example 1: Isolation of a Selected cDNA Clone From the Deposited Sample

Each cDNA clone in a cited ATCC deposit is contained in a plasmid vector.

10 Table 1 identifies the vectors used to construct the cDNA library from which each clone was isolated. In many cases, the vector used to construct the library is a phage vector from which a plasmid has been excised. The table immediately below correlates the related plasmid for each phage vector used in constructing the cDNA library. For example, where a particular clone is identified in Table 1 as being

15 isolated in the vector "Lambda Zap," the corresponding deposited clone is in "pBluescript."

	<u>Vector Used to Construct Library</u>	<u>Corresponding Deposited</u>
	<u>Plasmid</u>	
	Lambda Zap	pBluescript (pBS)
20	Uni-Zap XR	pBluescript (pBS)
	Zap Express	pBK
	lafmid BA	plafmid BA
	pSport1	pSport1
	pCMVSPORT 2.0	pCMVSPORT 2.0
25	pCMVSPORT 3.0	pCMVSPORT 3.0
	pCR [®] 2.1	pCR [®] 2.1

Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128, 256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., Nucleic Acids Res. 16:7583-7600 (1988); Alting-Mees, M. A. and Short, J. M., Nucleic Acids Res. 17:9494 (1989)) and pBK (Alting-Mees, M. A. et al., Strategies 5:58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Both can be transformed into E. coli strain XL-1 Blue, also available from Stratagene. pBS comes in 4 forms SK+, SK-, KS+ and KS. The S and K refers to the orientation of the polylinker to the T7 and T3 primer sequences which flank the polylinker region ("S" is for SacI and "K" is for KpnI which are the first sites on each respective end of the linker). "+" or "-" refer to the orientation of the f1 origin of replication ("ori"), such that in one orientation, single stranded rescue initiated from the f1 ori generates sense strand DNA and in the other, antisense.

Vectors pSport1, pCMVSport 2.0 and pCMVSport 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an ampicillin resistance gene and may be transformed into E. coli strain DH10B, also available from Life Technologies. (See, for instance, Gruber, C. E., et al., Focus 15:59 (1993).) Vector lafmid BA (Bento Soares, Columbia University, NY) contains an ampicillin resistance gene and can be transformed into E. coli strain XL-1 Blue. Vector pCR[®]2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into E. coli strain DH10B, available from Life Technologies. (See, for instance, Clark, J. M., Nuc. Acids Res. 16:9677-9686 (1988) and Mead, D. et al., Bio/Technology 9: (1991).) Preferably, a polynucleotide of the present invention

does not comprise the phage vector sequences identified for the particular clone in Table 1, as well as the corresponding plasmid vector sequences designated above.

The deposited material in the sample assigned the ATCC Deposit Number cited in Table 1 for any given cDNA clone also may contain one or more additional
5 plasmids, each comprising a cDNA clone different from that given clone. Thus, deposits sharing the same ATCC Deposit Number contain at least a plasmid for each cDNA clone identified in Table 1. Typically, each ATCC deposit sample cited in Table 1 comprises a mixture of approximately equal amounts (by weight) of about 50 plasmid DNAs, each containing a different cDNA clone; but such a deposit sample
10 may include plasmids for more or less than 50 cDNA clones, up to about 500 cDNA clones.

Two approaches can be used to isolate a particular clone from the deposited sample of plasmid DNAs cited for that clone in Table 1. First, a plasmid is directly isolated by screening the clones using a polynucleotide probe corresponding to SEQ
15 ID NO:X.

Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported. The oligonucleotide is labeled, for instance, with ^{32}P - γ -ATP using T4 polynucleotide kinase and purified according to routine methods. (E.g., Maniatis et al., Molecular
20 Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring, NY (1982).) The plasmid mixture is transformed into a suitable host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art, such as those provided by the vector supplier or in related publications or patents cited above. The transformants are plated on 1.5% agar plates (containing the appropriate selection
25 agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for

bacterial colony screening (e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Edit., (1989), Cold Spring Harbor Laboratory Press, pages 1.93 to 1.104), or other techniques known to those of skill in the art.

Alternatively, two primers of 17-20 nucleotides derived from both ends of the
5 SEQ ID NO:X (i.e., within the region of SEQ ID NO:X bounded by the 5' NT and
the 3' NT of the clone defined in Table 1) are synthesized and used to amplify the
desired cDNA using the deposited cDNA plasmid as a template. The polymerase
chain reaction is carried out under routine conditions, for instance, in 25 ul of reaction
mixture with 0.5 ug of the above cDNA template. A convenient reaction mixture is
10 1.5-5 mM MgCl₂, 0.01% (w/v) gelatin, 20 uM each of dATP, dCTP, dGTP, dTTP, 25
pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR
(denaturation at 94 degree C for 1 min; annealing at 55 degree C for 1 min; elongation
at 72 degree C for 1 min) are performed with a Perkin-Elmer Cetus automated
thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and
15 the DNA band with expected molecular weight is excised and purified. The PCR
product is verified to be the selected sequence by subcloning and sequencing the
DNA product.

Several methods are available for the identification of the 5' or 3' non-coding
portions of a gene which may not be present in the deposited clone. These methods
20 include but are not limited to, filter probing, clone enrichment using specific probes,
and protocols similar or identical to 5' and 3' "RACE" protocols which are well
known in the art. For instance, a method similar to 5' RACE is available for
generating the missing 5' end of a desired full-length transcript. (Fromont-Racine et
al., *Nucleic Acids Res.* 21(7):1683-1684 (1993).)

25 Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a
population of RNA presumably containing full-length gene RNA transcripts. A

primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest is used to PCR amplify the 5' portion of the desired full-length gene. This amplified product may then be sequenced and used to generate the full length gene.

- 5 This above method starts with total RNA isolated from the desired source, although poly-A+ RNA can be used. The RNA preparation can then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase should then be inactivated and the RNA treated with tobacco acid pyrophosphatase in order
10 to remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase.

- This modified RNA preparation is used as a template for first strand cDNA synthesis using a gene specific oligonucleotide. The first strand synthesis reaction is
15 used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the gene of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the desired gene.

20 **Example 2: Isolation of Genomic Clones Corresponding to a Polynucleotide**

 A human genomic P1 library (Genomic Systems, Inc.) is screened by PCR using primers selected for the cDNA sequence corresponding to SEQ ID NO:X., according to the method described in Example 1. (See also, Sambrook.)

25 **Example 3: Tissue Distribution of Polypeptide**

Tissue distribution of mRNA expression of polynucleotides of the present invention is determined using protocols for Northern blot analysis, described by; among others, Sambrook et al. For example, a cDNA probe produced by the method described in Example 1 is labeled with P^{32} using the rediprime™ DNA labeling system (Amersham Life Science), according to manufacturer's instructions. After labeling, the probe is purified using CHROMA SPIN-100™ column (Clontech Laboratories, Inc.), according to manufacturer's protocol number PT1200-1. The purified labeled probe is then used to examine various human tissues for mRNA expression.

Multiple Tissue Northern (MTN) blots containing various human tissues (H) or human immune system tissues (IM) (Clontech) are examined with the labeled probe using ExpressHyb™ hybridization solution (Clontech) according to manufacturer's protocol number PT1190-1. Following hybridization and washing, the blots are mounted and exposed to film at -70 degree C overnight, and the films developed according to standard procedures.

Example 4: Chromosomal Mapping of the Polynucleotides

An oligonucleotide primer set is designed according to the sequence at the 5' end of SEQ ID NO:X. This primer preferably spans about 100 nucleotides. This primer set is then used in a polymerase chain reaction under the following set of conditions : 30 seconds, 95 degree C; 1 minute, 56 degree C; 1 minute, 70 degree C. This cycle is repeated 32 times followed by one 5 minute cycle at 70 degree C. Human, mouse, and hamster DNA is used as template in addition to a somatic cell hybrid panel containing individual chromosomes or chromosome fragments (Bios, Inc). The reactions is analyzed on either 8% polyacrylamide gels or 3.5 % agarose

gels. Chromosome mapping is determined by the presence of an approximately 100 bp PCR fragment in the particular somatic cell hybrid.

Example 5: Bacterial Expression of a Polypeptide

5 A polynucleotide encoding a polypeptide of the present invention is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' ends of the DNA sequence, as outlined in Example 1, to synthesize insertion fragments. The primers used to amplify the cDNA insert should preferably contain restriction sites, such as BamHI and XbaI, at the 5' end of the primers in order to clone the amplified product
10 into the expression vector. For example, BamHI and XbaI correspond to the restriction enzyme sites on the bacterial expression vector pQE-9. (Qiagen, Inc., Chatsworth, CA). This plasmid vector encodes antibiotic resistance (Amp^r), a bacterial origin of replication (ori), an IPTG-regulatable promoter/operator (P/O), a ribosome binding site (RBS), a 6-histidine tag (6-His), and restriction enzyme cloning
15 sites.

 The pQE-9 vector is digested with BamHI and XbaI and the amplified fragment is ligated into the pQE-9 vector maintaining the reading frame initiated at the bacterial RBS. The ligation mixture is then used to transform the E. coli strain M15/rep4 (Qiagen, Inc.) which contains multiple copies of the plasmid pREP4, which
20 expresses the lacI repressor and also confers kanamycin resistance (Kan^r). Transformants are identified by their ability to grow on LB plates and ampicillin/kanamycin resistant colonies are selected. Plasmid DNA is isolated and confirmed by restriction analysis.

 Clones containing the desired constructs are grown overnight (O/N) in liquid
25 culture in LB media supplemented with both Amp (100 ug/ml) and Kan (25 ug/ml). The O/N culture is used to inoculate a large culture at a ratio of 1:100 to 1:250. The

cells are grown to an optical density 600 (O.D.⁶⁰⁰) of between 0.4 and 0.6. IPTG (Isopropyl-B-D-thiogalacto pyranoside) is then added to a final concentration of 1 mM. IPTG induces by inactivating the lacI repressor, clearing the P/O leading to increased gene expression.

5 Cells are grown for an extra 3 to 4 hours. Cells are then harvested by centrifugation (20 mins at 6000Xg). The cell pellet is solubilized in the chaotropic agent 6 Molar Guanidine HCl by stirring for 3-4 hours at 4 degree C. The cell debris is removed by centrifugation, and the supernatant containing the polypeptide is loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (available from
10 QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high affinity and can be purified in a simple one-step procedure (for details see: The QIAexpressionist (1995) QIAGEN, Inc., *supra*).

Briefly, the supernatant is loaded onto the column in 6 M guanidine-HCl, pH 8, the column is first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then
15 washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the polypeptide is eluted with 6 M guanidine-HCl, pH 5.

The purified protein is then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein can be successfully refolded while immobilized on the Ni-
20 NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of 1.5 hours or more. After renaturation the proteins are eluted by the addition of 250 mM imidazole. Imidazole is removed by a final dialyzing step against PBS or 50
25 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein is stored at 4 degree C or frozen at -80 degree C.

In addition to the above expression vector, the present invention further includes an expression vector comprising phage operator and promoter elements operatively linked to a polynucleotide of the present invention, called pHE4a. (ATCC Accession Number 209645, deposited on February 25, 1998.) This vector contains:

- 5 1) a neomycinphosphotransferase gene as a selection marker, 2) an *E. coli* origin of replication, 3) a T5 phage promoter sequence, 4) two lac operator sequences, 5) a Shine-Delgarno sequence, and 6) the lactose operon repressor gene (*lacIq*). The origin of replication (*oriC*) is derived from pUC19 (LTI, Gaithersburg, MD). The promoter sequence and operator sequences are made synthetically.

- 10 DNA can be inserted into the pHEa by restricting the vector with *NdeI* and *XbaI*, *BamHI*, *XhoI*, or *Asp718*, running the restricted product on a gel, and isolating the larger fragment (the stuffer fragment should be about 310 base pairs). The DNA insert is generated according to the PCR protocol described in Example 1, using PCR primers having restriction sites for *NdeI* (5' primer) and *XbaI*, *BamHI*, *XhoI*, or
15 *Asp718* (3' primer). The PCR insert is gel purified and restricted with compatible enzymes. The insert and vector are ligated according to standard protocols.

The engineered vector could easily be substituted in the above protocol to express protein in a bacterial system.

20 **Example 6: Purification of a Polypeptide from an Inclusion Body**

The following alternative method can be used to purify a polypeptide expressed in *E. coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10 degree C.

- Upon completion of the production phase of the *E. coli* fermentation, the cell
25 culture is cooled to 4-10 degree C and the cells harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield

of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

5 The cells are then lysed by passing the solution through a microfluidizer (Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 xg for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

10 The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 xg centrifugation for 15 min., the pellet is discarded and the polypeptide containing supernatant is incubated at 4 degree C overnight to allow further GuHCl extraction.

Following high speed centrifugation (30,000 xg) to remove insoluble particles,
15 the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4 degree C without mixing for 12 hours prior to further purification steps.

To clarify the refolded polypeptide solution, a previously prepared tangential
20 filtration unit equipped with 0.16 um membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a
25 stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are
5 equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A_{280} monitoring of the effluent. Fractions containing the
10 polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant polypeptide should exhibit greater than 95% purity after the above refolding and purification steps. No major contaminant bands should be observed from Commassie blue stained 16% SDS-PAGE gel when 5 ug of purified protein is loaded. The purified protein can also be tested for endotoxin/LPS
15 contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

Example 7: Cloning and Expression of a Polypeptide in a Baculovirus

Expression System

20 In this example, the plasmid shuttle vector pA2 is used to insert a polynucleotide into a baculovirus to express a polypeptide. This expression vector contains the strong polyhedrin promoter of the *Autographa californica* nuclear polyhedrosis virus (AcMNPV) followed by convenient restriction sites such as BamHI, Xba I and Asp718. The polyadenylation site of the simian virus 40 ("SV40")
25 is used for efficient polyadenylation. For easy selection of recombinant virus, the plasmid contains the beta-galactosidase gene from *E. coli* under control of a weak

Drosophila promoter in the same orientation, followed by the polyadenylation signal of the polyhedrin gene. The inserted genes are flanked on both sides by viral sequences for cell-mediated homologous recombination with wild-type viral DNA to generate a viable virus that express the cloned polynucleotide.

5 Many other baculovirus vectors can be used in place of the vector above, such as pAc373, pVL941, and pAcIM1, as one skilled in the art would readily appreciate, as long as the construct provides appropriately located signals for transcription, translation, secretion and the like, including a signal peptide and an in-frame AUG as required. Such vectors are described, for instance, in Luckow et al., Virology 170:31-
10 39 (1989).

Specifically, the cDNA sequence contained in the deposited clone, including the AUG initiation codon and the naturally associated leader sequence identified in Table 1, is amplified using the PCR protocol described in Example 1. If the naturally occurring signal sequence is used to produce the secreted protein, the pA2 vector does
15 not need a second signal peptide. Alternatively, the vector can be modified (pA2 GP) to include a baculovirus leader sequence, using the standard methods described in Summers et al., "A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures," Texas Agricultural Experimental Station Bulletin No. 1555 (1987).

20 The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("Geneclean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

The plasmid is digested with the corresponding restriction enzymes and
25 optionally, can be dephosphorylated using calf intestinal phosphatase, using routine

procedures known in the art. The DNA is then isolated from a 1% agarose gel using a commercially available kit ("GeneClean" BIO 101 Inc., La Jolla, Ca.).

- The fragment and the dephosphorylated plasmid are ligated together with T4 DNA ligase. *E. coli* HB101 or other suitable *E. coli* hosts such as XL-1 Blue
- 5 (Stratagene Cloning Systems, La Jolla, CA) cells are transformed with the ligation mixture and spread on culture plates. Bacteria containing the plasmid are identified by digesting DNA from individual colonies and analyzing the digestion product by gel electrophoresis. The sequence of the cloned fragment is confirmed by DNA sequencing.
- 10 Five ug of a plasmid containing the polynucleotide is co-transfected with 1.0 ug of a commercially available linearized baculovirus DNA ("BaculoGold™ baculovirus DNA", Pharmingen, San Diego, CA), using the lipofection method described by Felgner et al., Proc. Natl. Acad. Sci. USA 84:7413-7417 (1987). One ug of BaculoGold™ virus DNA and 5 ug of the plasmid are mixed in a sterile well of a
- 15 microtiter plate containing 50 ul of serum-free Grace's medium (Life Technologies Inc., Gaithersburg, MD). Afterwards, 10 ul Lipofectin plus 90 ul Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to Sf9 insect cells (ATCC CRL 1711) seeded in a 35 mm tissue culture plate with 1 ml Grace's medium without serum. The plate is
- 20 then incubated for 5 hours at 27 degrees C. The transfection solution is then removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. Cultivation is then continued at 27 degrees C for four days.

- After four days the supernatant is collected and a plaque assay is performed, as described by Summers and Smith, *supra*. An agarose gel with "Blue Gal" (Life
- 25 Technologies Inc., Gaithersburg) is used to allow easy identification and isolation of gal-expressing clones, which produce blue-stained plaques. (A detailed description of

a "plaque assay" of this type can also be found in the user's guide for insect cell culture and baculovirology distributed by Life Technologies Inc., Gaithersburg, page 9-10.) After appropriate incubation, blue stained plaques are picked with the tip of a micropipettor (e.g., Eppendorf). The agar containing the recombinant viruses is then
5 resuspended in a microcentrifuge tube containing 200 ul of Grace's medium and the suspension containing the recombinant baculovirus is used to infect Sf9 cells seeded in 35 mm dishes. Four days later the supernatants of these culture dishes are harvested and then they are stored at 4 degree C.

To verify the expression of the polypeptide, Sf9 cells are grown in Grace's
10 medium supplemented with 10% heat-inactivated FBS. The cells are infected with the recombinant baculovirus containing the polynucleotide at a multiplicity of infection ("MOI") of about 2. If radiolabeled proteins are desired, 6 hours later the medium is removed and is replaced with SF900 II medium minus methionine and cysteine (available from Life Technologies Inc., Rockville, MD). After 42 hours, 5
15 uCi of ^{35}S -methionine and 5 uCi ^{35}S -cysteine (available from Amersham) are added. The cells are further incubated for 16 hours and then are harvested by centrifugation. The proteins in the supernatant as well as the intracellular proteins are analyzed by SDS-PAGE followed by autoradiography (if radiolabeled).

Microsequencing of the amino acid sequence of the amino terminus of
20 purified protein may be used to determine the amino terminal sequence of the produced protein.

Example 8: Expression of a Polypeptide in Mammalian Cells

The polypeptide of the present invention can be expressed in a mammalian cell. A typical mammalian expression vector contains a promoter element, which
25 mediates the initiation of transcription of mRNA, a protein coding sequence, and

signals required for the termination of transcription and polyadenylation of the transcript. Additional elements include enhancers, Kozak sequences and intervening sequences flanked by donor and acceptor sites for RNA splicing. Highly efficient transcription is achieved with the early and late promoters from SV40, the long terminal repeats (LTRs) from Retroviruses, e.g., RSV, HTLVI, HIVI and the early promoter of the cytomegalovirus (CMV). However, cellular elements can also be used (e.g., the human actin promoter).

Suitable expression vectors for use in practicing the present invention include, for example, vectors such as pSVL and pMSG (Pharmacia, Uppsala, Sweden), pRSVcat (ATCC 37152), pSV2dhfr (ATCC 37146), pBC12MI (ATCC 67109), pCMVSPORT 2.0, and pCMVSPORT 3.0. Mammalian host cells that could be used include, human Hela, 293, H9 and Jurkat cells, mouse NIH3T3 and C127 cells, Cos 1, Cos 7 and CV1, quail QC1-3 cells, mouse L cells and Chinese hamster ovary (CHO) cells.

Alternatively, the polypeptide can be expressed in stable cell lines containing the polynucleotide integrated into a chromosome. The co-transfection with a selectable marker such as dhfr, gpt, neomycin, hygromycin allows the identification and isolation of the transfected cells.

The transfected gene can also be amplified to express large amounts of the encoded protein. The DHFR (dihydrofolate reductase) marker is useful in developing cell lines that carry several hundred or even several thousand copies of the gene of interest. (See, e.g., Alt, F. W., et al., J. Biol. Chem. 253:1357-1370 (1978); Hamlin, J. L. and Ma, C., Biochem. et Biophys. Acta, 1097:107-143 (1990); Page, M. J. and Sydenham, M. A., Biotechnology 9:64-68 (1991).) Another useful selection marker is the enzyme glutamine synthase (GS) (Murphy et al., Biochem J. 227:277-279 (1991); Bebbington et al., Bio/Technology 10:169-175 (1992). Using these markers,

the mammalian cells are grown in selective medium and the cells with the highest resistance are selected. These cell lines contain the amplified gene(s) integrated into a chromosome. Chinese hamster ovary (CHO) and NSO cells are often used for the production of proteins.

5 Derivatives of the plasmid-pSV2-dhfr (ATCC Accession No. 37146), the expression vectors pC4 (ATCC Accession No. 209646) and pC6 (ATCC Accession No. 209647) contain the strong promoter (LTR) of the Rous Sarcoma Virus (Cullen et al., Molecular and Cellular Biology, 438-447 (March, 1985)) plus a fragment of the CMV-enhancer (Boshart et al., Cell 41:521-530 (1985).) Multiple cloning sites, e.g.,
10 with the restriction enzyme cleavage sites BamHI, XbaI and Asp718, facilitate the cloning of the gene of interest. The vectors also contain the 3' intron, the polyadenylation and termination signal of the rat preproinsulin gene, and the mouse DHFR gene under control of the SV40 early promoter.

Specifically, the plasmid pC6, for example, is digested with appropriate
15 restriction enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from a 1% agarose gel.

A polynucleotide of the present invention is amplified according to the protocol outlined in Example 1. If the naturally occurring signal sequence is used to produce the secreted protein, the vector does not need a second signal peptide.
20 Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("GeneClean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1%
25 agarose gel.

The amplified fragment is then digested with the same restriction enzyme and purified on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC6 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene is used for transfection. Five μ g of the expression plasmid pC6 a pC4 is cotransfected with 0.5 μ g of the plasmid pSVneo using lipofectin (Felgner et al., *supra*). The plasmid pSV2-neo contains a dominant selectable marker, the *neo* gene from Tn5 encoding an enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 μ M, 2 μ M, 5 μ M, 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100 - 200 μ M. Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

Example 9: Protein Fusions

The polypeptides of the present invention are preferably fused to other proteins. These fusion proteins can be used for a variety of applications. For example, fusion of the present polypeptides to His-tag, HA-tag, protein A, IgG

domains, and maltose binding protein facilitates purification. (See Example 5; see also EP A 394,827; Traunecker, et al., Nature 331:84-86 (1988).) Similarly, fusion to IgG-1, IgG-3, and albumin increases the halflife time in vivo. Nuclear localization signals fused to the polypeptides of the present invention can target the protein to a specific subcellular localization, while covalent heterodimer or homodimers can increase or decrease the activity of a fusion protein. Fusion proteins can also create chimeric molecules having more than one function. Finally, fusion proteins can increase solubility and/or stability of the fused protein compared to the non-fused protein. All of the types of fusion proteins described above can be made by modifying the following protocol, which outlines the fusion of a polypeptide to an IgG molecule, or the protocol described in Example 5.

Briefly, the human Fc portion of the IgG molecule can be PCR amplified, using primers that span the 5' and 3' ends of the sequence described below. These primers also should have convenient restriction enzyme sites that will facilitate cloning into an expression vector, preferably a mammalian expression vector.

For example, if pC4 (Accession No. 209646) is used, the human Fc portion can be ligated into the BamHI cloning site. Note that the 3' BamHI site should be destroyed. Next, the vector containing the human Fc portion is re-restricted with BamHI, linearizing the vector, and a polynucleotide of the present invention, isolated by the PCR protocol described in Example 1, is ligated into this BamHI site. Note that the polynucleotide is cloned without a stop codon, otherwise a fusion protein will not be produced.

If the naturally occurring signal sequence is used to produce the secreted protein, pC4 does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

Human IgG Fc region:

GGGATCCGGAGCCCAAATCTTCTGACAAAACCTCACACATGCCCACCGTGC
CCAGCACCTGAATTCGAGGGTGCACCGTCAGTCTTCCTCTTCCCCCAAAA
5 CCAAAGGACACCCTCATGATCTCCCGGACTCCTGAGGTCACATGCGTGGT
GGTGGACGTAAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGG
ACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTA
CAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACT
GGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA
10 ACCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAC
CACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAG
GTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCAAGCGACATCGCCGT
GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCT
CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTG
15 GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCA
TGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGG
GTAAATGAGTGCGACGGCCGCGACTCTAGAGGAT (SEQ ID NO:1)

Example 10: Production of an Antibody from a Polypeptide

20 The antibodies of the present invention can be prepared by a variety of
methods. (See, Current Protocols, Chapter 2.) As one example of such methods, cells
expressing a polypeptide of the present invention is administered to an animal to
induce the production of sera containing polyclonal antibodies. In a preferred
method, a preparation of the secreted protein is prepared and purified to render it
25 substantially free of natural contaminants. Such a preparation is then introduced into
an animal in order to produce polyclonal antisera of greater specific activity.

In the most preferred method, the antibodies of the present invention are monoclonal antibodies (or protein binding fragments thereof). Such monoclonal antibodies can be prepared using hybridoma technology. (Köhler et al., *Nature* 256:495 (1975); Köhler et al., *Eur. J. Immunol.* 6:511 (1976); Köhler et al., *Eur. J. Immunol.* 6:292 (1976); Hammerling et al., in: *Monoclonal Antibodies and T-Cell Hybridomas*, Elsevier, N.Y., pp. 563-681 (1981).) In general, such procedures involve immunizing an animal (preferably a mouse) with polypeptide or, more preferably, with a secreted polypeptide-expressing cell. Such cells may be cultured in any suitable tissue culture medium; however, it is preferable to culture cells in Earle's modified Eagle's medium supplemented with 10% fetal bovine serum (inactivated at about 56 degrees C), and supplemented with about 10 g/l of nonessential amino acids, about 1,000 U/ml of penicillin, and about 100 ug/ml of streptomycin.

The splenocytes of such mice are extracted and fused with a suitable myeloma cell line. Any suitable myeloma cell line may be employed in accordance with the present invention; however, it is preferable to employ the parent myeloma cell line (SP2O), available from the ATCC. After fusion, the resulting hybridoma cells are selectively maintained in HAT medium, and then cloned by limiting dilution as described by Wands et al. (*Gastroenterology* 80:225-232 (1981).) The hybridoma cells obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding the polypeptide.

Alternatively, additional antibodies capable of binding to the polypeptide can be produced in a two-step procedure using anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, protein specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells,

and the hybridoma cells are screened to identify clones which produce an antibody whose ability to bind to the protein-specific antibody can be blocked by the polypeptide. Such antibodies comprise anti-idiotypic antibodies to the protein-specific antibody and can be used to immunize an animal to induce formation of
5 further protein-specific antibodies.

It will be appreciated that Fab and F(ab')₂ and other fragments of the antibodies of the present invention may be used according to the methods disclosed herein. Such fragments are typically produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')₂
10 fragments). Alternatively, secreted protein-binding fragments can be produced through the application of recombinant DNA technology or through synthetic chemistry.

For in vivo use of antibodies in humans, it may be preferable to use "humanized" chimeric monoclonal antibodies. Such antibodies can be produced
15 using genetic constructs derived from hybridoma cells producing the monoclonal antibodies described above. Methods for producing chimeric antibodies are known in the art. (See, for review, Morrison, Science 229:1202 (1985); Oi et al., BioTechniques 4:214 (1986); Cabilly et al., U.S. Patent No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al., EP 173494; Neuberger et al., WO 8601533; Robinson
20 et al., WO 8702671; Boulianne et al., Nature 312:643 (1984); Neuberger et al., Nature 314:268 (1985).)

Example 11: Production Of Secreted Protein For High-Throughput Screening

Assays

The following protocol produces a supernatant containing a polypeptide to be tested. This supernatant can then be used in the Screening Assays described in Examples 13-20.

- First, dilute Poly-D-Lysine (644 587 Boehringer-Mannheim) stock solution
- 5 (1mg/ml in PBS) 1:20 in PBS (w/o calcium or magnesium 17-516F Biowhittaker) for a working solution of 50ug/ml. Add 200 ul of this solution to each well (24 well plates) and incubate at RT for 20 minutes. Be sure to distribute the solution over each well (note: a 12-channel pipetter may be used with tips on every other channel). Aspirate off the Poly-D-Lysine solution and rinse with 1ml PBS (Phosphate Buffered
- 10 Saline). The PBS should remain in the well until just prior to plating the cells and plates may be poly-lysine coated in advance for up to two weeks.

- Plate 293T cells (do not carry cells past P+20) at 2×10^5 cells/well in .5ml DMEM(Dulbecco's Modified Eagle Medium)(with 4.5 G/L glucose and L-glutamine (12-604F Biowhittaker))/10% heat inactivated FBS(14-503F Biowhittaker)/1x
- 15 Penstrep(17-602E Biowhittaker). Let the cells grow overnight.

- The next day, mix together in a sterile solution basin: 300 ul Lipofectamine (18324-012 Gibco/BRL) and 5ml Optimem I (31985070 Gibco/BRL)/96-well plate. With a small volume multi-channel pipetter, aliquot approximately 2ug of an expression vector containing a polynucleotide insert, produced by the methods
- 20 described in Examples 8 or 9, into an appropriately labeled 96-well round bottom plate. With a multi-channel pipetter, add 50ul of the Lipofectamine/Optimem I mixture to each well. Pipette up and down gently to mix. Incubate at RT 15-45 minutes. After about 20 minutes, use a multi-channel pipetter to add 150ul Optimem I to each well. As a control, one plate of vector DNA lacking an insert should be
- 25 transfected with each set of transfections.

Preferably, the transfection should be performed by tag-teaming the following tasks. By tag-teaming, hands on time is cut in half, and the cells do not spend too much time on PBS. First, person A aspirates off the media from four 24-well plates of cells, and then person B rinses each well with .5-1ml PBS. Person A then aspirates
5 off PBS rinse, and person B, using a 12-channel pipetter with tips on every other channel, adds the 200ul of DNA/Lipofectamine/Optimem I complex to the odd wells first, then to the even wells, to each row on the 24-well plates. Incubate at 37 degrees C for 6 hours.

While cells are incubating, prepare appropriate media, either 1% BSA in
10 DMEM with 1x penstrep, or CHO-5 media (116.6 mg/L of CaCl_2 (anhyd); 0.00130 mg/L $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$; 0.050 mg/L of $\text{Fe}(\text{NO}_3)_3 \cdot 9\text{H}_2\text{O}$; 0.417 mg/L of $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$; 311.80 mg/L of KCl; 28.64 mg/L of MgCl_2 ; 48.84 mg/L of MgSO_4 ; 6995.50 mg/L of NaCl; 2400.0 mg/L of NaHCO_3 ; 62.50 mg/L of $\text{NaH}_2\text{PO}_4 \cdot \text{H}_2\text{O}$; 71.02 mg/L of Na_2HPO_4 ; .4320 mg/L of $\text{ZnSO}_4 \cdot 7\text{H}_2\text{O}$; .002 mg/L of Arachidonic Acid ; 1.022 mg/L
15 of Cholesterol; .070 mg/L of DL-alpha-Tocopherol-Acetate; 0.0520 mg/L of Linoleic Acid; 0.010 mg/L of Linolenic Acid; 0.010 mg/L of Myristic Acid; 0.010 mg/L of Oleic Acid; 0.010 mg/L of Palmitric Acid; 0.010 mg/L of Palmitic Acid; 100 mg/L of Pluronic F-68; 0.010 mg/L of Stearic Acid; 2.20 mg/L of Tween 80; 4551 mg/L of D-Glucose; 130.85 mg/ml of L- Alanine; 147.50 mg/ml of L-Arginine-HCL; 7.50 mg/ml
20 of L-Asparagine- H_2O ; 6.65 mg/ml of L-Aspartic Acid; 29.56 mg/ml of L-Cystine-2HCL- H_2O ; 31.29 mg/ml of L-Cystine-2HCL; 7.35 mg/ml of L-Glutamic Acid; 365.0 mg/ml of L-Glutamine; 18.75 mg/ml of Glycine; 52.48 mg/ml of L-Histidine-HCL- H_2O ; 106.97 mg/ml of L-Isoleucine; 111.45 mg/ml of L-Leucine; 163.75 mg/ml of L- Lysine HCL; 32.34 mg/ml of L-Methionine; 68.48 mg/ml of L-Phenylalanine; 40.0
25 mg/ml of L-Proline; 26.25 mg/ml of L-Serine; 101.05 mg/ml of L-Threonine; 19.22 mg/ml of L-Tryptophan; 91.79 mg/ml of L-Tyrosine-2Na- $2\text{H}_2\text{O}$; 99.65 mg/ml of L-

Valine; 0.0035 mg/L of Biotin; 3.24 mg/L of D-Ca Pantothenate; 11.78 mg/L of Choline Chloride; 4.65 mg/L of Folic Acid; 15.60 mg/L of i-Inositol; 3.02 mg/L of Niacinamide; 3.00 mg/L of Pyridoxal HCL; 0.031 mg/L of Pyridoxine HCL; 0.319 mg/L of Riboflavin; 3.17 mg/L of Thiamine HCL; 0.365 mg/L of Thymidine; and
5 0.680 mg/L of Vitamin B₁₂; 25 mM of HEPES Buffer; 2.39 mg/L of Na Hypoxanthine; 0.105 mg/L of Lipoic Acid; 0.081 mg/L of Sodium Putrescine-2HCL; 55.0 mg/L of Sodium Pyruvate; 0.0067 mg/L of Sodium Selenite; 20uM of Ethanolamine; 0.122 mg/L of Ferric Citrate; 41.70 mg/L of Methyl-B-Cyclodextrin complexed with Linoleic Acid; 33.33 mg/L of Methyl-B-Cyclodextrin complexed
10 with Oleic Acid; and 10 mg/L of Methyl-B-Cyclodextrin complexed with Retinal) with 2mm glutamine and 1x penstrep. (BSA (81-068-3 Bayer) 100gm dissolved in 1L DMEM for a 10% BSA stock solution). Filter the media and collect 50 ul for endotoxin assay in 15ml polystyrene conical.

The transfection reaction is terminated, preferably by tag-teaming, at the end
15 of the incubation period. Person A aspirates off the transfection media, while person B adds 1.5ml appropriate media to each well. Incubate at 37 degrees C for 45 or 72 hours depending on the media used: 1%BSA for 45 hours or CHO-5 for 72 hours.

On day four, using a 300ul multichannel pipetter, aliquot 600ul in one 1ml deep well plate and the remaining supernatant into a 2ml deep well. The supernatants
20 from each well can then be used in the assays described in Examples 13-20.

It is specifically understood that when activity is obtained in any of the assays described below using a supernatant, the activity originates from either the polypeptide directly (e.g., as a secreted protein) or by the polypeptide inducing expression of other proteins, which are then secreted into the supernatant. Thus, the
25 invention further provides a method of identifying the protein in the supernatant characterized by an activity in a particular assay.

Example 12: Construction of GAS Reporter Construct

One signal transduction pathway involved in the differentiation and proliferation of cells is called the Jaks-STATs pathway. Activated proteins in the
5 Jaks-STATs pathway bind to gamma activation site "GAS" elements or interferon-sensitive responsive element ("ISRE"), located in the promoter of many genes. The binding of a protein to these elements alter the expression of the associated gene.

GAS and ISRE elements are recognized by a class of transcription factors called Signal Transducers and Activators of Transcription, or "STATs." There are six
10 members of the STATs family. Stat1 and Stat3 are present in many cell types, as is Stat2 (as response to IFN-alpha is widespread). Stat4 is more restricted and is not in many cell types though it has been found in T helper class 1, cells after treatment with IL-12. Stat5 was originally called mammary growth factor, but has been found at higher concentrations in other cells including myeloid cells. It can be activated in
15 tissue culture cells by many cytokines.

The STATs are activated to translocate from the cytoplasm to the nucleus upon tyrosine phosphorylation by a set of kinases known as the Janus Kinase ("Jaks") family. Jaks represent a distinct family of soluble tyrosine kinases and include Tyk2, Jak1, Jak2, and Jak3. These kinases display significant sequence similarity and are
20 generally catalytically inactive in resting cells.

The Jaks are activated by a wide range of receptors summarized in the Table below. (Adapted from review by Schidler and Darnell, Ann. Rev. Biochem. 64:621-51 (1995).) A cytokine receptor family, capable of activating Jaks, is divided into two groups: (a) Class 1 includes receptors for IL-2, IL-3, IL-4, IL-6, IL-7, IL-9, IL-11, IL-
25 12, IL-15, Epo, PRL, GH, G-CSF, GM-CSF, LIF, CNTF, and thrombopoietin; and (b)

Class 2 includes IFN-a, IFN-g, and IL-10. The Class 1 receptors share a conserved cysteine motif (a set of four conserved cysteines and one tryptophan) and a WSXWS motif (a membrane proximal region encoding Trp-Ser-Xxx-Trp-Ser (SEQ ID NO:2)).

Thus, on binding of a ligand to a receptor, Jaks are activated, which in turn
5 activate STATs, which then translocate and bind to GAS elements. This entire
process is encompassed in the Jaks-STATs signal transduction pathway.

Therefore, activation of the Jaks-STATs pathway, reflected by the binding of
the GAS or the ISRE element, can be used to indicate proteins involved in the
proliferation and differentiation of cells. For example, growth factors and cytokines
10 are known to activate the Jaks-STATs pathway. (See Table below.) Thus, by using
GAS elements linked to reporter molecules, activators of the Jaks-STATs pathway
can be identified.

			<u>JAKs</u>		<u>STATS</u>	<u>GAS(elements) or ISRE</u>
	<u>Ligand</u>	<u>tyk2</u>	<u>Jak1</u>	<u>Jak2</u>	<u>Jak3</u>	
	<u>IFN family</u>					
5	IFN-a/B	+	+	-	-	1,2,3 ISRE
	IFN-g		+	+	-	1 GAS (IRF1>Lys6>IFP)
	Il-10	+	?	?	-	1,3
	<u>gp130 family</u>					
10	IL-6 (Pleiotrophic)	+	+	+	?	1,3 GAS (IRF1>Lys6>IFP)
	Il-11(Pleiotrophic)	?	+	?	?	1,3
	OnM(Pleiotrophic)	?	+	+	?	1,3
	LIF(Pleiotrophic)	?	+	+	?	1,3
	CNTF(Pleiotrophic)	-/+	+	+	?	1,3
15	G-CSF(Pleiotrophic)	?	+	?	?	1,3
	IL-12(Pleiotrophic)	+	-	+	+	1,3
	<u>g-C family</u>					
	IL-2 (lymphocytes)	-	+	-	+	1,3,5 GAS
20	IL-4 (lymph/myeloid)	-	+	-	+	6 GAS (IRF1 = IFP >>Ly6)(IgH)
	IL-7 (lymphocytes)	-	+	-	+	5 GAS
	IL-9 (lymphocytes)	-	+	-	+	5 GAS
	IL-13 (lymphocyte)	-	+	?	?	6 GAS
	IL-15	?	+	?	+	5 GAS
25	<u>gp140 family</u>					
	IL-3 (myeloid)	-	-	+	-	5 GAS (IRF1>IFP>>Ly6)
	IL-5 (myeloid)	-	-	+	-	5 GAS
	GM-CSF (myeloid)	-	-	+	-	5 GAS
30	<u>Growth hormone family</u>					
	GH	?	-	+	-	5
	PRL	?	+/-	+	-	1,3,5
	EPO	?	-	+	-	5 GAS(B-CAS>IRF1=IFP>>Ly6)
35	<u>Receptor Tyrosine Kinases</u>					
	EGF	?	+	+	-	1,3 GAS (IRF1)
	PDGF	?	+	+	-	1,3

CSF-1

?

+

+

-

1,3

GAS (not IRF1)

To construct a synthetic GAS containing promoter element, which is used in the Biological Assays described in Examples 13-14, a PCR based strategy is employed to generate a GAS-SV40 promoter sequence. The 5' primer contains four tandem copies of the GAS binding site found in the IRF1 promoter and previously demonstrated to bind STATs upon induction with a range of cytokines (Rothman et al., Immunity 1:457-468 (1994).), although other GAS or ISRE elements can be used instead. The 5' primer also contains 18bp of sequence complementary to the SV40 early promoter sequence and is flanked with an XhoI site. The sequence of the 5' primer is:

10 5':GCGCCTCGAGATTTCCCCGAAATCTAGATTTCCCCGAAATGATTTCCCC
GAAATGATTTCCCCGAAATATCTGCCATCTCAATTAG:3' (SEQ ID NO:3)

The downstream primer is complementary to the SV40 promoter and is flanked with a Hind III site: 5':GCGGCAAGCTTTTTGCAAAGCCTAGGC:3' (SEQ ID NO:4)

15 PCR amplification is performed using the SV40 promoter template present in the B-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI/Hind III and subcloned into BLSK2-. (Stratagene.) Sequencing with forward and reverse primers confirms that the insert contains the following sequence:

20 5':CTCGAGATTTCCCCGAAATCTAGATTTCCCCGAAATGATTTCCCCGAAA
TGATTTCCCCGAAATATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCG
CCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCT
CCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCC
TCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCT
25 AGGCTTTTGCAAAAAGCTT:3' (SEQ ID NO:5)

With this GAS promoter element linked to the SV40 promoter, a GAS:SEAP2 reporter construct is next engineered. Here, the reporter molecule is a secreted alkaline phosphatase, or "SEAP." Clearly, however, any reporter molecule can be instead of SEAP, in this or in any of the other Examples. Well known reporter molecules that can be used instead of SEAP include chloramphenicol- acetyltransferase (CAT), luciferase, alkaline phosphatase, B-galactosidase, green fluorescent protein (GFP), or any protein detectable by an antibody.

The above sequence confirmed synthetic GAS-SV40 promoter element is subcloned into the pSEAP-Promoter vector obtained from Clontech using HindIII and XhoI, effectively replacing the SV40 promoter with the amplified GAS:SV40 promoter element, to create the GAS-SEAP vector. However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

Thus, in order to generate mammalian stable cell lines expressing the GAS-SEAP reporter, the GAS-SEAP cassette is removed from the GAS-SEAP vector using SalI and NotI, and inserted into a backbone vector containing the neomycin resistance gene, such as pGFP-1 (Clontech), using these restriction sites in the multiple cloning site, to create the GAS-SEAP/Neo vector. Once this vector is transfected into mammalian cells, this vector can then be used as a reporter molecule for GAS binding as described in Examples 13-14.

Other constructs can be made using the above description and replacing GAS with a different promoter sequence. For example, construction of reporter molecules containing NFK-B and EGR promoter sequences are described in Examples 15 and 16. However, many other promoters can be substituted using the protocols described in these Examples. For instance, SRE, IL-2, NFAT, or Osteocalcin promoters can be substituted, alone or in combination (e.g., GAS/NF-KB/EGR, GAS/NF-KB, IL-

2/NFAT, or NF-KB/GAS). Similarly, other cell lines can be used to test reporter construct activity, such as HELA (epithelial), HUVEC (endothelial), Reh (B-cell), Saos-2 (osteoblast), HUVAC (aortic), or Cardiomyocyte.

5 **Example 13: High-Throughput Screening Assay for T-cell Activity.**

 The following protocol is used to assess T-cell activity by identifying factors, and determining whether supernate containing a polypeptide of the invention proliferates and/or differentiates T-cells. T-cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP
10 activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The T-cell used in this assay is Jurkat T-cells (ATCC Accession No. TIB-152), although Molt-3 cells (ATCC Accession No. CRL-1552) and Molt-4 cells (ATCC Accession No. CRL-1582) cells can also be used.

 Jurkat T-cells are lymphoblastic CD4+ Th1 helper cells. In order to generate
15 stable cell lines, approximately 2 million Jurkat cells are transfected with the GAS-SEAP/neo vector using DMRIE-C (Life Technologies)(transfection procedure described below). The transfected cells are seeded to a density of approximately 20,000 cells per well and transfectants resistant to 1 mg/ml gentamicin selected. Resistant colonies are expanded and then tested for their response to increasing
20 concentrations of interferon gamma. The dose response of a selected clone is demonstrated.

 Specifically, the following protocol will yield sufficient cells for 75 wells containing 200 ul of cells. Thus, it is either scaled up, or performed in multiple to generate sufficient cells for multiple 96 well plates. Jurkat cells are maintained in
25 RPMI + 10% serum with 1% Pen-Strep. Combine 2.5 mls of OPTI-MEM (Life

Technologies) with 10 ug of plasmid DNA in a T25 flask. Add 2.5 ml OPTI-MEM containing 50 ul of DMRIE-C and incubate at room temperature for 15-45 mins.

During the incubation period, count cell concentration, spin down the required number of cells (10^7 per transfection), and resuspend in OPTI-MEM to a final
5 concentration of 10^7 cells/ml. Then add 1 ml of 1×10^7 cells in OPTI-MEM to T25 flask and incubate at 37 degrees C for 6 hrs. After the incubation, add 10 ml of RPMI + 15% serum.

The Jurkat:GAS-SEAP stable reporter lines are maintained in RPMI + 10% serum, 1 mg/ml Genticin, and 1% Pen-Strep. These cells are treated with
10 supernatants containing polypeptides of the invention and/or induced polypeptides of the invention as produced by the protocol described in Example 11.

On the day of treatment with the supernatant, the cells should be washed and resuspended in fresh RPMI + 10% serum to a density of 500,000 cells per ml. The exact number of cells required will depend on the number of supernatants being
15 screened. For one 96 well plate, approximately 10 million cells (for 10 plates, 100 million cells) are required.

Transfer the cells to a triangular reservoir boat, in order to dispense the cells into a 96 well dish, using a 12 channel pipette. Using a 12 channel pipette, transfer 200 ul of cells into each well (therefore adding 100, 000 cells per well).

20 After all the plates have been seeded, 50 ul of the supernatants are transferred directly from the 96 well plate containing the supernatants into each well using a 12 channel pipette. In addition, a dose of exogenous interferon gamma (0.1, 1.0, 10 ng) is added to wells H9, H10, and H11 to serve as additional positive controls for the assay.

25 The 96 well dishes containing Jurkat cells treated with supernatants are placed in an incubator for 48 hrs (note: this time is variable between 48-72 hrs). 35 ul

samples from each well are then transferred to an opaque 96 well plate using a 12 channel pipette. The opaque plates should be covered (using sellophene covers) and stored at -20 degrees C until SEAP assays are performed according to Example 17. The plates containing the remaining treated cells are placed at 4 degrees C and serve
5 as a source of material for repeating the assay on a specific well if desired.

As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate Jurkat T cells. Over 30 fold induction is typically observed in the positive control wells.

The above protocol may be used in the generation of both transient, as well as,
10 stable transfected cells, which would be apparent to those of skill in the art.

Example 14: High-Throughput Screening Assay Identifying Myeloid Activity

The following protocol is used to assess myeloid activity by determining whether polypeptides of the invention proliferates and/or differentiates myeloid cells.
15 Myeloid cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The myeloid cell used in this assay is U937, a pre-monocyte cell line, although TF-1, HL60, or KG1 can be used.

To transiently transfect U937 cells with the GAS/SEAP/Neo construct
20 produced in Example 12, a DEAE-Dextran method (Kharbanda et. al., 1994, Cell Growth & Differentiation, 5:259-265) is used. First, harvest 2×10^7 U937 cells and wash with PBS. The U937 cells are usually grown in RPMI 1640 medium containing 10% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 mg/ml streptomycin.

25 Next, suspend the cells in 1 ml of 20 mM Tris-HCl (pH 7.4) buffer containing 0.5 mg/ml DEAE-Dextran, 8 ug GAS-SEAP2 plasmid DNA, 140 mM NaCl, 5 mM

KCl, 375 μ M $\text{Na}_2\text{HPO}_4 \cdot 7\text{H}_2\text{O}$, 1 mM MgCl_2 , and 675 μ M CaCl_2 . Incubate at 37 degrees C for 45 min.

Wash the cells with RPMI 1640 medium containing 10% FBS and then resuspend in 10 ml complete medium and incubate at 37 degrees C for 36 hr.

5 The GAS-SEAP/U937 stable cells are obtained by growing the cells in 400 μ g/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 400 μ g/ml G418 for couple of passages.

These cells are tested by harvesting 1×10^8 cells (this is enough for ten 96-well plates assay) and wash with PBS. Suspend the cells in 200 ml above described growth medium, with a final density of 5×10^5 cells/ml. Plate 200 μ l cells per well in the 96-well plate (or 1×10^5 cells/well).

Add 50 μ l of the supernatant prepared by the protocol described in Example 11. Incubate at 37 degrees C for 48 to 72 hr. As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate U937 cells. Over 30 fold induction is typically observed in the positive control wells. SEAP assay the supernatant according to the protocol described in Example 17.

Example 15: High-Throughput Screening Assay Identifying Neuronal Activity.

When cells undergo differentiation and proliferation, a group of genes are activated through many different signal transduction pathways. One of these genes, EGR1 (early growth response gene 1), is induced in various tissues and cell types upon activation. The promoter of EGR1 is responsible for such induction. Using the EGR1 promoter linked to reporter molecules, activation of cells can be assessed.

Particularly, the following protocol is used to assess neuronal activity in PC12 cell lines. PC12 cells (rat pheochromocytoma cells) are known to proliferate and/or differentiate by activation with a number of mitogens, such as TPA (tetradecanoyl

phorbol acetate), NGF (nerve growth factor), and EGF (epidermal growth factor).

The EGR1 gene expression is activated during this treatment. Thus, by stably transfecting PC12 cells with a construct containing an EGR promoter linked to SEAP reporter, activation of PC12 cells can be assessed.

- 5 The EGR/SEAP reporter construct can be assembled by the following protocol. The EGR-1 promoter sequence (-633 to +1)(Sakamoto K et al., Oncogene 6:867-871 (1991)) can be PCR amplified from human genomic DNA using the following primers:

5' GCGCTCGAGGGATGACAGCGATAGAACCCCGG -3' (SEQ ID NO:6)

- 10 5' GCGAAGCTTCGCGACTCCCCGGATCCGCCTC-3' (SEQ ID NO:7)

- Using the GAS:SEAP/Neo vector produced in Example 12, EGR1 amplified product can then be inserted into this vector. Linearize the GAS:SEAP/Neo vector using restriction enzymes XhoI/HindIII, removing the GAS/SV40 stuffer. Restrict the EGR1 amplified product with these same enzymes. Ligate the vector and the EGR1
15 promoter.

To prepare 96 well-plates for cell culture, two mls of a coating solution (1:30 dilution of collagen type I (Upstate Biotech Inc. Cat#08-115) in 30% ethanol (filter sterilized)) is added per one 10 cm plate or 50 ml per well of the 96-well plate, and allowed to air dry for 2 hr.

- 20 PC12 cells are routinely grown in RPMI-1640 medium (Bio Whittaker) containing 10% horse serum (JRH BIOSCIENCES, Cat. # 12449-78P), 5% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 ug/ml streptomycin on a precoated 10 cm tissue culture dish. One to four split is done every three to four days. Cells are removed from the plates by scraping and
25 resuspended with pipetting up and down for more than 15 times.

Transfect the EGR/SEAP/Neo construct into PC12 using the Lipofectamine protocol described in Example 11. EGR-SEAP/PC12 stable cells are obtained by growing the cells in 300 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 300 ug/ml G418 for couple of passages.

To assay for neuronal activity, a 10 cm plate with cells around 70 to 80% confluent is screened by removing the old medium. Wash the cells once with PBS (Phosphate buffered saline). Then starve the cells in low serum medium (RPMI-1640 containing 1% horse serum and 0.5% FBS with antibiotics) overnight.

10 The next morning, remove the medium and wash the cells with PBS. Scrape off the cells from the plate, suspend the cells well in 2 ml low serum medium. Count the cell number and add more low serum medium to reach final cell density as 5×10^5 cells/ml.

Add 200 ul of the cell suspension to each well of 96-well plate (equivalent to 1×10^5 cells/well). Add 50 ul supernatant produced by Example 11, 37°C for 48 to 72 hr. As a positive control, a growth factor known to activate PC12 cells through EGR can be used, such as 50 ng/ul of Neuronal Growth Factor (NGF). Over fifty-fold induction of SEAP is typically seen in the positive control wells. SEAP assay the supernatant according to Example 17.

20

Example 16: High-Throughput Screening Assay for T-cell Activity

NF-KB (Nuclear Factor KB) is a transcription factor activated by a wide variety of agents including the inflammatory cytokines IL-1 and TNF, CD30 and CD40, lymphotoxin-alpha and lymphotoxin-beta, by exposure to LPS or thrombin, and by expression of certain viral gene products. As a transcription factor, NF-KB regulates the expression of genes involved in immune cell activation, control of

apoptosis (NF- KB appears to shield cells from apoptosis), B and T-cell development, anti-viral and antimicrobial responses, and multiple stress responses.

In non-stimulated conditions, NF- KB is retained in the cytoplasm with I-KB (Inhibitor KB). However, upon stimulation, I- KB is phosphorylated and degraded,
5 causing NF- KB to shuttle to the nucleus, thereby activating transcription of target genes. Target genes activated by NF- KB include IL-2, IL-6, GM-CSF, ICAM-1 and class I MHC.

Due to its central role and ability to respond to a range of stimuli, reporter constructs utilizing the NF-KB promoter element are used to screen the supernatants
10 produced in Example 11. Activators or inhibitors of NF-KB would be useful in treating diseases. For example, inhibitors of NF-KB could be used to treat those diseases related to the acute or chronic activation of NF-KB, such as rheumatoid arthritis.

To construct a vector containing the NF-KB promoter element, a PCR based
15 strategy is employed. The upstream primer contains four tandem copies of the NF-KB binding site (GGGGACTTTCCC) (SEQ ID NO:8), 18 bp of sequence complementary to the 5' end of the SV40 early promoter sequence, and is flanked with an XhoI site:

5':GCGGCCTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGAC
20 TTTCCATCCTGCCATCTCAATTAG:3' (SEQ ID NO:9)

The downstream primer is complementary to the 3' end of the SV40 promoter and is flanked with a Hind III site:

5':GCGGCAAGCTTTTTGCAAAGCCTAGGC:3' (SEQ ID NO:4)

PCR amplification is performed using the SV40 promoter template present in
25 the pB-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI and Hind III and subcloned into BLSK2-. (Stratagene)

Sequencing with the T7 and T3 primers confirms the insert contains the following sequence:

5' : CTCGAGGGGACTTTCCCGGGGACTTTCCGGGACTTTCCGGGACTTTCCATCTGCCATCTCAATTA
 5 GTCAGCAACCATAGTCCCGCCCCCTAACTCCGCCCATCCCGCCCCCTAACTCCGCCCAGTTCCGCCCATTC
 TCCGCCCATGGCTGACTAATTTTTTTTATTTATGTCAGAGGCCGAGGCCGCTCGGCCTCTGAGCTATT
 CCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAAAGCTT:3' (SEQ ID
 NO:10)

10 Next, replace the SV40 minimal promoter element present in the pSEAP2-
 promoter plasmid (Clontech) with this NF-KB/SV40 fragment using XhoI and
 HindIII. However, this vector does not contain a neomycin resistance gene, and
 therefore, is not preferred for mammalian expression systems.

In order to generate stable mammalian cell lines, the NF-KB/SV40/SEAP
 15 cassette is removed from the above NF-KB/SEAP vector using restriction enzymes
 Sall and NotI, and inserted into a vector containing neomycin resistance. Particularly,
 the NF-KB/SV40/SEAP cassette was inserted into pGFP-1 (Clontech), replacing the
 GFP gene, after restricting pGFP-1 with Sall and NotI.

Once NF-KB/SV40/SEAP/Neo vector is created, stable Jurkat T-cells are
 20 created and maintained according to the protocol described in Example 13. Similarly,
 the method for assaying supernatants with these stable Jurkat T-cells is also described
 in Example 13. As a positive control, exogenous TNF alpha (0.1, 1, 10 ng) is added to
 wells H9, H10, and H11, with a 5-10 fold activation typically observed.

25 **Example 17: Assay for SEAP Activity**

As a reporter molecule for the assays described in Examples 13-16, SEAP
 activity is assayed using the Tropix Phospho-light Kit (Cat. BP-400) according to the

following general procedure. The Tropix Phospho-light Kit supplies the Dilution, Assay, and Reaction Buffers used below.

Prime a dispenser with the 2.5x Dilution Buffer and dispense 15 ul of 2.5x dilution buffer into Optiplates containing 35 ul of a supernatant. Seal the plates with a plastic sealer and incubate at 65 degree C for 30 min. Separate the Optiplates to avoid uneven heating.

Cool the samples to room temperature for 15 minutes. Empty the dispenser and prime with the Assay Buffer. Add 50 ml Assay Buffer and incubate at room temperature 5 min. Empty the dispenser and prime with the Reaction Buffer (see the table below). Add 50 ul Reaction Buffer and incubate at room temperature for 20 minutes. Since the intensity of the chemiluminescent signal is time dependent, and it takes about 10 minutes to read 5 plates on luminometer, one should treat 5 plates at each time and start the second set 10 minutes later.

Read the relative light unit in the luminometer. Set H12 as blank, and print the results. An increase in chemiluminescence indicates reporter activity.

Reaction Buffer Formulation:

# of plates	Rxn buffer diluent (ml)	CSPD (ml)
10	60	3
11	65	3.25
12	70	3.5
13	75	3.75
14	80	4
15	85	4.25
16	90	4.5
17	95	4.75
18	100	5
19	105	5.25
20	110	5.5
21	115	5.75
22	120	6
23	125	6.25
24	130	6.5

25	135	6.75
26	140	7
27	145	7.25
28	150	7.5
29	155	7.75
30	160	8
31	165	8.25
32	170	8.5
33	175	8.75
34	180	9
35	185	9.25
36	190	9.5
37	195	9.75
38	200	10
39	205	10.25
40	210	10.5
41	215	10.75
42	220	11
43	225	11.25
44	230	11.5
45	235	11.75
46	240	12
47	245	12.25
48	250	12.5
49	255	12.75
50	260	13

Example 18: High-Throughput Screening Assay Identifying Changes in Small Molecule Concentration and Membrane Permeability

Binding of a ligand to a receptor is known to alter intracellular levels of small molecules, such as calcium, potassium, sodium, and pH, as well as alter membrane potential. These alterations can be measured in an assay to identify supernatants which bind to receptors of a particular cell. Although the following protocol describes an assay for calcium, this protocol can easily be modified to detect changes in potassium, sodium, pH, membrane potential, or any other small molecule which is detectable by a fluorescent probe.

The following assay uses Fluorometric Imaging Plate Reader ("FLIPR") to measure changes in fluorescent molecules (Molecular Probes) that bind small molecules. Clearly, any fluorescent molecule detecting a small molecule can be used instead of the calcium fluorescent molecule, fluo-4 (Molecular Probes, Inc.; catalog no. F-14202), used here.

For adherent cells, seed the cells at 10,000 -20,000 cells/well in a Co-star black 96-well plate with clear bottom. The plate is incubated in a CO₂ incubator for 20 hours. The adherent cells are washed two times in Biotek washer with 200 ul of HBSS (Hank's Balanced Salt Solution) leaving 100 ul of buffer after the final wash.

10 A stock solution of 1 mg/ml fluo-4 is made in 10% pluronic acid DMSO. To load the cells with fluo-4, 50 ul of 12 ug/ml fluo-4 is added to each well. The plate is incubated at 37 degrees C in a CO₂ incubator for 60 min. The plate is washed four times in the Biotek washer with HBSS leaving 100 ul of buffer.

For non-adherent cells, the cells are spun down from culture media. Cells are re-suspended to 2.5×10^6 cells/ml with HBSS in a 50-ml conical tube. 4 ul of 1 mg/ml fluo-4 solution in 10% pluronic acid DMSO is added to each ml of cell suspension. The tube is then placed in a 37 degrees C water bath for 30-60 min. The cells are washed twice with HBSS, resuspended to 1×10^6 cells/ml, and dispensed into a microplate, 100 ul/well. The plate is centrifuged at 1000 rpm for 5 min. The plate is

15 20 then washed once in Denley CellWash with 200 ul, followed by an aspiration step to 100 ul final volume.

For a non-cell based assay, each well contains a fluorescent molecule, such as fluo-4. The supernatant is added to the well, and a change in fluorescence is detected.

25 To measure the fluorescence of intracellular calcium, the FLIPR is set for the following parameters: (1) System gain is 300-800 mW; (2) Exposure time is 0.4

second; (3) Camera F/stop is F/2; (4) Excitation is 488 nm; (5) Emission is 530 nm; and (6) Sample addition is 50 ul. Increased emission at 530 nm indicates an extracellular signaling event which has resulted in an increase in the intracellular Ca^{++} concentration.

5

Example 19: High-Throughput Screening Assay Identifying Tyrosine Kinase Activity

The Protein Tyrosine Kinases (PTK) represent a diverse group of transmembrane and cytoplasmic kinases. Within the Receptor Protein Tyrosine Kinase (RPTK) group are receptors for a range of mitogenic and metabolic growth factors including the PDGF, FGF, EGF, NGF, HGF and Insulin receptor subfamilies. In addition there are a large family of RPTKs for which the corresponding ligand is unknown. Ligands for RPTKs include mainly secreted small proteins, but also membrane-bound and extracellular matrix proteins.

15 Activation of RPTK by ligands involves ligand-mediated receptor dimerization, resulting in transphosphorylation of the receptor subunits and activation of the cytoplasmic tyrosine kinases. The cytoplasmic tyrosine kinases include receptor associated tyrosine kinases of the src-family (e.g., src, yes, lck, lyn, fyn) and non-receptor linked and cytosolic protein tyrosine kinases, such as the Jak family, 20 members of which mediate signal transduction triggered by the cytokine superfamily of receptors (e.g., the Interleukins, Interferons, GM-CSF, and Leptin).

Because of the wide range of known factors capable of stimulating tyrosine kinase activity, the identification of novel human secreted proteins capable of activating tyrosine kinase signal transduction pathways are of interest. Therefore, the 25 following protocol is designed to identify those novel human secreted proteins capable of activating the tyrosine kinase signal transduction pathways.

Seed target cells (e.g., primary keratinocytes) at a density of approximately 25,000 cells per well in a 96 well Loprodyne Silent Screen Plates purchased from Nalge Nunc (Naperville, IL). The plates are sterilized with two 30 minute rinses with 100% ethanol, rinsed with water and dried overnight. Some plates are coated for 2 hr

5 with 100 ml of cell culture grade type I collagen (50 mg/ml), gelatin (2%) or polylysine (50 mg/ml), all of which can be purchased from Sigma Chemicals (St. Louis, MO) or 10% Matrigel purchased from Becton Dickinson (Bedford, MA), or calf serum, rinsed with PBS and stored at 4 degree C. Cell growth on these plates is assayed by seeding 5,000 cells/well in growth medium and indirect quantitation of

10 cell number through use of alamarBlue as described by the manufacturer Alamar Biosciences, Inc. (Sacramento, CA) after 48 hr. Falcon plate covers #3071 from Becton Dickinson (Bedford, MA) are used to cover the Loprodyne Silent Screen Plates. Falcon Microtest III cell culture plates can also be used in some proliferation experiments.

15 To prepare extracts, A431 cells are seeded onto the nylon membranes of Loprodyne plates (20,000/200ml/well) and cultured overnight in complete medium. Cells are quiesced by incubation in serum-free basal medium for 24 hr. After 5-20 minutes treatment with EGF (60ng/ml) or 50 ul of the supernatant produced in

Example 11, the medium was removed and 100 ml of extraction buffer ((20 mM

20 HEPES pH 7.5, 0.15 M NaCl, 1% Triton X-100, 0.1% SDS, 2 mM Na₃VO₄, 2 mM Na₄P₂O₇ and a cocktail of protease inhibitors (# 1836170) obtained from Boehringer Mannheim (Indianapolis, IN) is added to each well and the plate is shaken on a rotating shaker for 5 minutes at 4 degrees C. The plate is then placed in a vacuum transfer manifold and the extract filtered through the 0.45 mm membrane

25 bottoms of each well using house vacuum. Extracts are collected in a 96-well catch/assay plate in the bottom of the vacuum manifold and immediately placed on

ice. To obtain extracts clarified by centrifugation, the content of each well, after detergent solubilization for 5 minutes, is removed and centrifuged for 15 minutes at 4 degrees C at 16,000 x g.

Test the filtered extracts for levels of tyrosine kinase activity. Although many
5 methods of detecting tyrosine kinase activity are known, one method is described here.

Generally, the tyrosine kinase activity of a supernatant is evaluated by determining its ability to phosphorylate a tyrosine residue on a specific substrate (a biotinylated peptide). Biotinylated peptides that can be used for this purpose include
10 PSK1 (corresponding to amino acids 6-20 of the cell division kinase cdc2-p34) and PSK2 (corresponding to amino acids 1-17 of gastrin). Both peptides are substrates for a range of tyrosine kinases and are available from Boehringer Mannheim.

The tyrosine kinase reaction is set up by adding the following components in order. First, add 10ul of 5uM Biotinylated Peptide, then 10ul ATP/Mg₂₊ (5mM
15 ATP/50mM MgCl₂), then 10ul of 5x Assay Buffer (40mM imidazole hydrochloride, pH7.3, 40 mM beta-glycerophosphate, 1mM EGTA, 100mM MgCl₂, 5 mM MnCl₂, 0.5 mg/ml BSA), then 5ul of Sodium Vanadate(1mM), and then 5ul of water. Mix the components gently and preincubate the reaction mix at 30 degrees C for 2 min. Initial the reaction by adding 10ul of the control enzyme or the filtered supernatant.

20 The tyrosine kinase assay reaction is then terminated by adding 10 ul of 120mM EDTA and place the reactions on ice.

Tyrosine kinase activity is determined by transferring 50 ul aliquot of reaction mixture to a microtiter plate (MTP) module and incubating at 37 degrees C for 20 min. This allows the streptavidin coated 96 well plate to associate with the
25 biotinylated peptide. Wash the MTP module with 300ul/well of PBS four times.

Next add 75 ul of anti-phosphotyrosine antibody conjugated to horse radish peroxidase(anti-P-Tyr-POD(0.5u/ml)) to each well and incubate at 37 degrees C for one hour. Wash the well as above.

- Next add 100ul of peroxidase substrate solution (Boehringer Mannheim) and
- 5 incubate at room temperature for at least 5 mins (up to 30 min). Measure the absorbance of the sample at 405 nm by using ELISA reader. The level of bound peroxidase activity is quantitated using an ELISA reader and reflects the level of tyrosine kinase activity.

10 **Example 20: High-Throughput Screening Assay Identifying Phosphorylation Activity**

- As a potential alternative and/or compliment to the assay of protein tyrosine kinase activity described in Example 19, an assay which detects activation (phosphorylation) of major intracellular signal transduction intermediates can also be
- 15 used. For example, as described below one particular assay can detect tyrosine phosphorylation of the Erk-1 and Erk-2 kinases. However, phosphorylation of other molecules, such as Raf, JNK, p38 MAP, Map kinase kinase (MEK), MEK kinase, Src, Muscle specific kinase (MuSK), IRAK, Tec, and Janus, as well as any other phosphoserine, phosphotyrosine, or phosphothreonine molecule, can be detected by
- 20 substituting these molecules for Erk-1 or Erk-2 in the following assay.

- Specifically, assay plates are made by coating the wells of a 96-well ELISA plate with 0.1ml of protein G (1ug/ml) for 2 hr at room temp, (RT). The plates are then rinsed with PBS and blocked with 3% BSA/PBS for 1 hr at RT. The protein G plates are then treated with 2 commercial monoclonal antibodies (100ng/well) against
- 25 Erk-1 and Erk-2 (1 hr at RT) (Santa Cruz Biotechnology). (To detect other molecules, this step can easily be modified by substituting a monoclonal antibody detecting any

of the above described molecules.) After 3-5 rinses with PBS, the plates are stored at 4 degrees C until use.

A431 cells are seeded at 20,000/well in a 96-well Loprodyn filterplate and cultured overnight in growth medium. The cells are then starved for 48 hr in basal medium (DMEM) and then treated with EGF (6ng/well) or 50 ul of the supernatants obtained in Example 11 for 5-20 minutes. The cells are then solubilized and extracts filtered directly into the assay plate.

After incubation with the extract for 1 hr at RT, the wells are again rinsed. As a positive control, a commercial preparation of MAP kinase (10ng/well) is used in place of A431 extract. Plates are then treated with a commercial polyclonal (rabbit) antibody (1ug/ml) which specifically recognizes the phosphorylated epitope of the Erk-1 and Erk-2 kinases (1 hr at RT). This antibody is biotinylated by standard procedures. The bound polyclonal antibody is then quantitated by successive incubations with Europium-streptavidin and Europium fluorescence enhancing reagent in the Wallac DELFIA instrument (time-resolved fluorescence). An increased fluorescent signal over background indicates a phosphorylation.

Example 21: Method of Determining Alterations in a Gene Corresponding to a Polynucleotide

RNA isolated from entire families or individual patients presenting with a phenotype of interest (such as a disease) is be isolated. cDNA is then generated from these RNA samples using protocols known in the art. (See, Sambrook.) The cDNA is then used as a template for PCR, employing primers surrounding regions of interest in SEQ ID NO:X. Suggested PCR conditions consist of 35 cycles at 95 degrees C for 30 seconds; 60-120 seconds at 52-58 degrees C; and 60-120 seconds at 70 degrees C, using buffer solutions described in Sidransky et al., Science 252:706 (1991).

PCR products are then sequenced using primers labeled at their 5' end with T4 polynucleotide kinase, employing SequiTherm Polymerase. (Epicentre Technologies). The intron-exon borders of selected exons is also determined and genomic PCR products analyzed to confirm the results. PCR products harboring
5 suspected mutations is then cloned and sequenced to validate the results of the direct sequencing.

PCR products is cloned into T-tailed vectors as described in Holton et al., Nucleic Acids Research, 19:1156 (1991) and sequenced with T7 polymerase (United States Biochemical). Affected individuals are identified by mutations not present in
10 unaffected individuals.

Genomic rearrangements are also observed as a method of determining alterations in a gene corresponding to a polynucleotide. Genomic clones isolated according to Example 2 are nick-translated with digoxigenindeoxy-uridine 5'-triphosphate (Boehringer Mannheim), and FISH performed as described in Johnson et
15 al., Methods Cell Biol. 35:73-99 (1991). Hybridization with the labeled probe is carried out using a vast excess of human cot-1 DNA for specific hybridization to the corresponding genomic locus.

Chromosomes are counterstained with 4,6-diamino-2-phenylidole and propidium iodide, producing a combination of C- and R-bands. Aligned images for
20 precise mapping are obtained using a triple-band filter set (Chroma Technology, Brattleboro, VT) in combination with a cooled charge-coupled device camera (Photometrics, Tucson, AZ) and variable excitation wavelength filters. (Johnson et al., Genet. Anal. Tech. Appl., 8:75 (1991).) Image collection, analysis and chromosomal fractional length measurements are performed using the ISee Graphical
25 Program System. (Inovision Corporation, Durham, NC.) Chromosome alterations of the genomic region hybridized by the probe are identified as insertions, deletions, and

translocations. These alterations are used as a diagnostic marker for an associated disease.

Example 22: Method of Detecting Abnormal Levels of a Polypeptide in a

5 **Biological Sample**

A polypeptide of the present invention can be detected in a biological sample, and if an increased or decreased level of the polypeptide is detected, this polypeptide is a marker for a particular phenotype. Methods of detection are numerous, and thus, it is understood that one skilled in the art can modify the following assay to fit their particular needs.

For example, antibody-sandwich ELISAs are used to detect polypeptides in a sample, preferably a biological sample. Wells of a microtiter plate are coated with specific antibodies, at a final concentration of 0.2 to 10 ug/ml. The antibodies are either monoclonal or polyclonal and are produced by the method described in Example 10. The wells are blocked so that non-specific binding of the polypeptide to the well is reduced.

The coated wells are then incubated for > 2 hours at RT with a sample containing the polypeptide. Preferably, serial dilutions of the sample should be used to validate results. The plates are then washed three times with deionized or distilled water to remove unbounded polypeptide.

Next, 50 ul of specific antibody-alkaline phosphatase conjugate, at a concentration of 25-400 ng, is added and incubated for 2 hours at room temperature. The plates are again washed three times with deionized or distilled water to remove unbounded conjugate.

25 Add 75 ul of 4-methylumbelliferyl phosphate (MUP) or p-nitrophenyl phosphate (NPP) substrate solution to each well and incubate 1 hour at room

temperature. Measure the reaction by a microtiter plate reader. Prepare a standard curve, using serial dilutions of a control sample, and plot polypeptide concentration on the X-axis (log scale) and fluorescence or absorbance of the Y-axis (linear scale). Interpolate the concentration of the polypeptide in the sample using the standard
5 curve.

Example 23: Formulation

The invention also provides methods of treatment and/or prevention diseases, disorders, and/or conditions (such as, for example, any one or more of the diseases or
10 disorders disclosed herein) by administration to a subject of an effective amount of a Therapeutic. By therapeutic is meant a polynucleotides or polypeptides of the invention (including fragments and variants), agonists or antagonists thereof, and/or antibodies thereto, in combination with a pharmaceutically acceptable carrier type (e.g., a sterile carrier).

15 The Therapeutic will be formulated and dosed in a fashion consistent with good medical practice, taking into account the clinical condition of the individual patient (especially the side effects of treatment with the Therapeutic alone), the site of delivery, the method of administration, the scheduling of administration, and other factors known to practitioners. The "effective amount" for purposes herein is thus
20 determined by such considerations.

As a general proposition, the total pharmaceutically effective amount of the Therapeutic administered parenterally per dose will be in the range of about 1 µg/kg/day to 10 mg/kg/day of patient body weight, although, as noted above, this will be subject to therapeutic discretion. More preferably, this dose is at least 0.01
25 mg/kg/day, and most preferably for humans between about 0.01 and 1 mg/kg/day for the hormone. If given continuously, the Therapeutic is typically administered at a

dose rate of about 1 ug/kg/hour to about 50 ug/kg/hour, either by 1-4 injections per day or by continuous subcutaneous infusions, for example, using a mini-pump. An intravenous bag solution may also be employed. The length of treatment needed to observe changes and the interval following treatment for responses to occur appears to vary depending on the desired effect.

Therapeutics can be administered orally, rectally, parenterally, intracisternally, intravaginally, intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal patch), buccally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material or formulation auxiliary of any. The term "parenteral" as used herein refers to modes of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

Therapeutics of the invention are also suitably administered by sustained-release systems. Suitable examples of sustained-release Therapeutics are administered orally, rectally, parenterally, intracisternally, intravaginally, intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal patch), buccally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material or formulation auxiliary of any type. The term "parenteral" as used herein refers to modes of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

Therapeutics of the invention are also suitably administered by sustained-release systems. Suitable examples of sustained-release Therapeutics include suitable polymeric materials (such as, for example, semi-permeable polymer matrices in the form of shaped articles, e.g., films, or microcapsules), suitable hydrophobic materials

(for example as an emulsion in an acceptable oil) or ion exchange resins, and sparingly soluble derivatives (such as, for example, a sparingly soluble salt).

Sustained-release matrices include polylactides (U.S. Pat. No. 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma-ethyl-L-glutamate (Sidman et al.,
5 Biopolymers 22:547-556 (1983)), poly (2- hydroxyethyl methacrylate) (Langer et al., J. Biomed. Mater. Res. 15:167-277 (1981), and Langer, Chem. Tech. 12:98-105 (1982)), ethylene vinyl acetate (Langer et al., Id.) or poly-D- (-)-3-hydroxybutyric acid (EP 133,988).

Sustained-release Therapeutics also include liposomally entrapped
10 Therapeutics of the invention (*see* generally, Langer, *Science* 249:1527-1533 (1990); Treat et al., in *Liposomes in the Therapy of Infectious Disease and Cancer*, Lopez-Berestein and Fidler (eds.), Liss, New York, pp. 317 -327 and 353-365 (1989)). Liposomes containing the Therapeutic are prepared by methods known per se: DE 3,218,121; Epstein et al., Proc. Natl. Acad. Sci. (USA) 82:3688-3692 (1985); Hwang
15 et al., Proc. Natl. Acad. Sci.(USA) 77:4030-4034 (1980); EP 52,322; EP 36,676; EP 88,046; EP 143,949; EP 142,641; Japanese Pat. Appl. 83-118008; U.S. Pat. Nos. 4,485,045 and 4,544,545; and EP 102,324. Ordinarily, the liposomes are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mol. percent cholesterol, the selected proportion being adjusted for the
20 optimal Therapeutic.

In yet an additional embodiment, the Therapeutics of the invention are delivered by way of a pump (*see* Langer, *supra*; Sefton, CRC Crit. Ref. Biomed. Eng. 14:201 (1987); Buchwald et al., Surgery 88:507 (1980); Saudek et al., N. Engl. J. Med. 321:574 (1989)).

25 Other controlled release systems are discussed in the review by Langer (*Science* 249:1527-1533 (1990)).

For parenteral administration, in one embodiment, the Therapeutic is formulated generally by mixing it at the desired degree of purity, in a unit dosage injectable form (solution, suspension, or emulsion), with a pharmaceutically acceptable carrier, i.e., one that is non-toxic to recipients at the dosages and concentrations employed and is compatible with other ingredients of the formulation. For example, the formulation preferably does not include oxidizing agents and other compounds that are known to be deleterious to the Therapeutic.

Generally, the formulations are prepared by contacting the Therapeutic uniformly and intimately with liquid carriers or finely divided solid carriers or both. Then, if necessary, the product is shaped into the desired formulation. Preferably the carrier is a parenteral carrier, more preferably a solution that is isotonic with the blood of the recipient. Examples of such carrier vehicles include water, saline, Ringer's solution, and dextrose solution. Non-aqueous vehicles such as fixed oils and ethyl oleate are also useful herein, as well as liposomes.

The carrier suitably contains minor amounts of additives such as substances that enhance isotonicity and chemical stability. Such materials are non-toxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, succinate, acetic acid, and other organic acids or their salts; antioxidants such as ascorbic acid; low molecular weight (less than about ten residues) polypeptides, e.g., polyarginine or tripeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids, such as glycine, glutamic acid, aspartic acid, or arginine; monosaccharides, disaccharides, and other carbohydrates including cellulose or its derivatives, glucose, manose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; counterions such as sodium; and/or nonionic surfactants such as polysorbates, poloxamers, or PEG.

The Therapeutic is typically formulated in such vehicles at a concentration of about 0.1 mg/ml to 100 mg/ml, preferably 1-10 mg/ml, at a pH of about 3 to 8. It will be understood that the use of certain of the foregoing excipients, carriers, or stabilizers will result in the formation of polypeptide salts.

5 Any pharmaceutical used for therapeutic administration can be sterile. Sterility is readily accomplished by filtration through sterile filtration membranes (e.g., 0.2 micron membranes). Therapeutics generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

10 Therapeutics ordinarily will be stored in unit or multi-dose containers, for example, sealed ampoules or vials, as an aqueous solution or as a lyophilized formulation for reconstitution. As an example of a lyophilized formulation, 10-ml vials are filled with 5 ml of sterile-filtered 1% (w/v) aqueous Therapeutic solution, and the resulting mixture is lyophilized. The infusion solution is prepared by
15 reconstituting the lyophilized Therapeutic using bacteriostatic Water-for-Injection.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the Therapeutics of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or
20 biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. In addition, the Therapeutics may be employed in conjunction with other therapeutic compounds.

The Therapeutics of the invention may be administered alone or in combination with adjuvants. Adjuvants that may be administered with the
25 Therapeutics of the invention include, but are not limited to, alum, alum plus deoxycholate (ImmunoAg), MTP-PE (Biocine Corp.), QS21 (Genentech, Inc.), BCG,

and MPL. In a specific embodiment, Therapeutics of the invention are administered in combination with alum. In another specific embodiment, Therapeutics of the invention are administered in combination with QS-21. Further adjuvants that may be administered with the Therapeutics of the invention include, but are not limited to,

5 Monophosphoryl lipid immunomodulator, AdjuVax 100a, QS-21, QS-18, CRL1005, Aluminum salts, MF-59, and Virosomal adjuvant technology. Vaccines that may be administered with the Therapeutics of the invention include, but are not limited to, vaccines directed toward protection against MMR (measles, mumps, rubella), polio, varicella, tetanus/diphtheria, hepatitis A, hepatitis B, haemophilus influenzae B,

10 whooping cough, pneumonia, influenza, Lyme's Disease, rotavirus, cholera, yellow fever, Japanese encephalitis, poliomyelitis, rabies, typhoid fever, and pertussis. Combinations may be administered either concomitantly, e.g., as an admixture, separately but simultaneously or concurrently; or sequentially. This includes presentations in which the combined agents are administered together as a therapeutic

15 mixture, and also procedures in which the combined agents are administered separately but simultaneously, e.g., as through separate intravenous lines into the same individual. Administration "in combination" further includes the separate administration of one of the compounds or agents given first, followed by the second.

The Therapeutics of the invention may be administered alone or in

20 combination with other therapeutic agents. Therapeutic agents that may be administered in combination with the Therapeutics of the invention, include but not limited to, other members of the TNF family, chemotherapeutic agents, antibiotics, steroidal and non-steroidal anti-inflammatories, conventional immunotherapeutic agents, cytokines and/or growth factors. Combinations may be administered either

25 concomitantly, e.g., as an admixture, separately but simultaneously or concurrently; or sequentially. This includes presentations in which the combined agents are

administered together as a therapeutic mixture, and also procedures in which the combined agents are administered separately but simultaneously, e.g., as through separate intravenous lines into the same individual. Administration "in combination" further includes the separate administration of one of the compounds or agents given
5 first, followed by the second.

In one embodiment, the Therapeutics of the invention are administered in combination with members of the TNF family. TNF, TNF-related or TNF-like molecules that may be administered with the Therapeutics of the invention include, but are not limited to, soluble forms of TNF-alpha, lymphotoxin-alpha (LT-alpha,
10 also known as TNF-beta), LT-beta (found in complex heterotrimer LT-alpha2-beta), OPGL, FasL, CD27L, CD30L, CD40L, 4-1BBL, DcR3, OX40L, TNF-gamma (International Publication No. WO 96/14328), AIM-I (International Publication No. WO 97/33899), endokine-alpha (International Publication No. WO 98/07880), TR6 (International Publication No. WO 98/30694), OPG, and neutrokin-alpha
15 (International Publication No. WO 98/18921, OX40, and nerve growth factor (NGF), and soluble forms of Fas, CD30, CD27, CD40 and 4-1BB, TR2 (International Publication No. WO 96/34095), DR3 (International Publication No. WO 97/33904), DR4 (International Publication No. WO 98/32856), TR5 (International Publication No. WO 98/30693), TR6 (International Publication No. WO 98/30694), TR7
20 (International Publication No. WO 98/41629), TRANK, TR9 (International Publication No. WO 98/56892), TR10 (International Publication No. WO 98/54202), 312C2 (International Publication No. WO 98/06842), and TR12, and soluble forms CD154, CD70, and CD153.

In certain embodiments, Therapeutics of the invention are administered in
25 combination with antiretroviral agents, nucleoside reverse transcriptase inhibitors, non-nucleoside reverse transcriptase inhibitors, and/or protease inhibitors.

Nucleoside reverse transcriptase inhibitors that may be administered in combination with the Therapeutics of the invention, include, but are not limited to, RETROVIR™ (zidovudine/AZT), VIDEX™ (didanosine/ddI), HIVID™ (zalcitabine/ddC), ZERIT™ (stavudine/d4T), EPIVIR™ (lamivudine/3TC), and COMBIVIR™

5 (zidovudine/lamivudine). Non-nucleoside reverse transcriptase inhibitors that may be administered in combination with the Therapeutics of the invention, include, but are not limited to, VIRAMUNE™ (nevirapine), RESCRIPTOR™ (delavirdine), and SUSTIVA™ (efavirenz). Protease inhibitors that may be administered in combination with the Therapeutics of the invention, include, but are not limited to,
10 CRIXIVAN™ (indinavir), NORVIR™ (ritonavir), INVIRASE™ (saquinavir), and VIRACEPT™ (nelfinavir). In a specific embodiment, antiretroviral agents, nucleoside reverse transcriptase inhibitors, non-nucleoside reverse transcriptase inhibitors, and/or protease inhibitors may be used in any combination with Therapeutics of the invention to treat AIDS and/or to prevent or treat HIV infection.

15 In other embodiments, Therapeutics of the invention may be administered in combination with anti-opportunistic infection agents. Anti-opportunistic agents that may be administered in combination with the Therapeutics of the invention, include, but are not limited to, TRIMETHOPRIM-SULFAMETHOXAZOLE™, DAPSONE™, PENTAMIDINE™, ATOVAQUONE™, ISONIAZID™,
20 RIFAMPIN™, PYRAZINAMIDE™, ETHAMBUTOL™, RIFABUTIN™, CLARITHROMYCIN™, AZITHROMYCIN™, GANCICLOVIR™, FOSCARNET™, CIDOFOVIR™, FLUCONAZOLE™, ITRACONAZOLE™, KETOCONAZOLE™, ACYCLOVIR™, FAMCICOLVIR™, PYRIMETHAMINE™, LEUCOVORIN™, NEUPOGEN™ (filgrastim/G-CSF), and LEUKINE™
25 (sargramostim/GM-CSF). In a specific embodiment, Therapeutics of the invention

are used in any combination with TRIMETHOPRIM-SULFAMETHOXAZOLE™, DAPSONE™, PENTAMIDINE™, and/or ATOVAQUONE™ to prophylactically treat or prevent an opportunistic *Pneumocystis carinii* pneumonia infection. In another specific embodiment, Therapeutics of the invention are used in any combination with ISONIAZID™, RIFAMPIN™, PYRAZINAMIDE™, and/or ETHAMBUTOL™ to prophylactically treat or prevent an opportunistic *Mycobacterium avium* complex infection. In another specific embodiment, Therapeutics of the invention are used in any combination with RIFABUTIN™, CLARITHROMYCIN™, and/or AZITHROMYCIN™ to prophylactically treat or prevent an opportunistic *Mycobacterium tuberculosis* infection. In another specific embodiment, Therapeutics of the invention are used in any combination with GANCICLOVIR™, FOSCARNET™, and/or CIDOFOVIR™ to prophylactically treat or prevent an opportunistic cytomegalovirus infection. In another specific embodiment, Therapeutics of the invention are used in any combination with FLUCONAZOLE™, ITRACONAZOLE™, and/or KETOCONAZOLE™ to prophylactically treat or prevent an opportunistic fungal infection. In another specific embodiment, Therapeutics of the invention are used in any combination with ACYCLOVIR™ and/or FAMCICOLVIR™ to prophylactically treat or prevent an opportunistic herpes simplex virus type I and/or type II infection. In another specific embodiment, Therapeutics of the invention are used in any combination with PYRIMETHAMINE™ and/or LEUCOVORIN™ to prophylactically treat or prevent an opportunistic *Toxoplasma gondii* infection. In another specific embodiment, Therapeutics of the invention are used in any combination with LEUCOVORIN™ and/or NEUPOGEN™ to prophylactically treat or prevent an opportunistic bacterial infection.

In a further embodiment, the Therapeutics of the invention are administered in combination with an antiviral agent. Antiviral agents that may be administered with the Therapeutics of the invention include, but are not limited to, acyclovir, ribavirin, amantadine, and remantidine.

5 In a further embodiment, the Therapeutics of the invention are administered in combination with an antibiotic agent. Antibiotic agents that may be administered with the Therapeutics of the invention include, but are not limited to, amoxicillin, beta-lactamases, aminoglycosides, beta-lactam (glycopeptide), beta-lactamases, Clindamycin, chloramphenicol, cephalosporins, ciprofloxacin, ciprofloxacin,
10 erythromycin, fluoroquinolones, macrolides, metronidazole, penicillins, quinolones, rifampin, streptomycin, sulfonamide, tetracyclines, trimethoprim, trimethoprim-sulfamthoxazole, and vancomycin.

Conventional nonspecific immunosuppressive agents, that may be administered in combination with the Therapeutics of the invention include, but are
15 not limited to, steroids, cyclosporine, cyclosporine analogs, cyclophosphamide methylprednisone, prednisone, azathioprine, FK-506, 15-deoxyspergualin, and other immunosuppressive agents that act by suppressing the function of responding T cells.

In specific embodiments, Therapeutics of the invention are administered in combination with immunosuppressants. Immunosuppressants preparations that may
20 be administered with the Therapeutics of the invention include, but are not limited to, ORTHOCLONE™ (OKT3), SANDIMMUNE™/NEORAL™/SANGDYA™ (cyclosporin), PROGRAF™ (tacrolimus), CELLCEPT™ (mycophenolate), Azathioprine, glucocorticosteroids, and RAPAMUNE™ (sirolimus). In a specific embodiment, immunosuppressants may be used to prevent rejection of organ or bone
25 marrow transplantation.

In an additional embodiment, Therapeutics of the invention are administered alone or in combination with one or more intravenous immune globulin preparations. Intravenous immune globulin preparations that may be administered with the Therapeutics of the invention include, but not limited to, GAMMAR™,

5 IVEEGAM™, SANDOGLOBULIN™, GAMMAGARD S/D™, and GAMIMUNE™.

In a specific embodiment, Therapeutics of the invention are administered in combination with intravenous immune globulin preparations in transplantation therapy (e.g., bone marrow transplant).

In an additional embodiment, the Therapeutics of the invention are
10 administered alone or in combination with an anti-inflammatory agent. Anti-inflammatory agents that may be administered with the Therapeutics of the invention include, but are not limited to, glucocorticoids and the nonsteroidal anti-inflammatories, aminoarylcarboxylic acid derivatives, arylacetic acid derivatives, arylbutyric acid derivatives, arylcarboxylic acids, arylpropionic acid derivatives,
15 pyrazoles, pyrazolones, salicylic acid derivatives, thiazinecarboxamides, e-acetamidocaproic acid, S-adenosylmethionine, 3-amino-4-hydroxybutyric acid, amixetrine, bendazac, benzydamine, bucolome, difenpiramide, ditazol, emorfazone, guaiazulene, nabumetone, nimesulide, orgotein, oxaceprol, paranyline, perisoxal, pifoxime, proquazone, proxazole, and tenidap.

20 In another embodiment, compositions of the invention are administered in combination with a chemotherapeutic agent. Chemotherapeutic agents that may be administered with the Therapeutics of the invention include, but are not limited to, antibiotic derivatives (e.g., doxorubicin, bleomycin, daunorubicin, and dactinomycin); antiestrogens (e.g., tamoxifen); antimetabolites (e.g., fluorouracil, 5-
25 FU, methotrexate, floxuridine, interferon alpha-2b, glutamic acid, plicamycin, mercaptopurine, and 6-thioguanine); cytotoxic agents (e.g., carmustine, BCNU,

lomustine, CCNU, cytosine arabinoside, cyclophosphamide, estramustine, hydroxyurea, procarbazine, mitomycin, busulfan, cis-platin, and vincristine sulfate); hormones (e.g., medroxyprogesterone, estramustine phosphate sodium, ethinyl estradiol, estradiol, megestrol acetate, methyltestosterone, diethylstilbestrol
5 - diphosphate, chlorotrianisene, and testolactone); nitrogen mustard derivatives (e.g., mephallen, chorambucil, mechlorethamine (nitrogen mustard) and thiotepa); steroids and combinations (e.g., bethamethasone sodium phosphate); and others (e.g., dicarbazine, asparaginase, mitotane, vincristine sulfate, vinblastine sulfate, and etoposide).

10 In a specific embodiment, Therapeutics of the invention are administered in combination with CHOP (cyclophosphamide, doxorubicin, vincristine, and prednisone) or any combination of the components of CHOP. In another embodiment, Therapeutics of the invention are administered in combination with Rituximab. In a further embodiment, Therapeutics of the invention are administered
15 with Rituxmab and CHOP, or Rituxmab and any combination of the components of CHOP.

 In an additional embodiment, the Therapeutics of the invention are administered in combination with cytokines. Cytokines that may be administered with the Therapeutics of the invention include, but are not limited to, IL2, IL3, IL4,
20 IL5, IL6, IL7, IL10, IL12, IL13, IL15, anti-CD40, CD40L, IFN-gamma and TNF-alpha. In another embodiment, Therapeutics of the invention may be administered with any interleukin, including, but not limited to, IL-1alpha, IL-1beta, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IL-16, IL-17, IL-18, IL-19, IL-20, and IL-21.

25 In an additional embodiment, the Therapeutics of the invention are administered in combination with angiogenic proteins. Angiogenic proteins that may

be administered with the Therapeutics of the invention include, but are not limited to, Glioma Derived Growth Factor (GDGF), as disclosed in European Patent Number EP-399816; Platelet Derived Growth Factor-A (PDGF-A), as disclosed in European Patent Number EP-682110; Platelet Derived Growth Factor-B (PDGF-B), as
5 disclosed in European Patent Number EP-282317; Placental Growth Factor (PIGF), as disclosed in International Publication Number WO 92/06194; Placental Growth Factor-2 (PIGF-2), as disclosed in Hauser et al., Growth Factors, 4:259-268 (1993); Vascular Endothelial Growth Factor (VEGF), as disclosed in International Publication Number WO 90/13649; Vascular Endothelial Growth Factor-A (VEGF-A), as
10 disclosed in European Patent Number EP-506477; Vascular Endothelial Growth Factor-2 (VEGF-2), as disclosed in International Publication Number WO 96/39515; Vascular Endothelial Growth Factor B (VEGF-3); Vascular Endothelial Growth Factor B-186 (VEGF-B186), as disclosed in International Publication Number WO 96/26736; Vascular Endothelial Growth Factor-D (VEGF-D), as disclosed in
15 International Publication Number WO 98/02543; Vascular Endothelial Growth Factor-D (VEGF-D), as disclosed in International Publication Number WO 98/07832; and Vascular Endothelial Growth Factor-E (VEGF-E), as disclosed in German Patent Number DE19639601. The above mentioned references are incorporated herein by reference herein.

20 In an additional embodiment, the Therapeutics of the invention are administered in combination with hematopoietic growth factors. Hematopoietic growth factors that may be administered with the Therapeutics of the invention include, but are not limited to, LEUKINE™ (SARGRAMOSTIM™) and NEUPOGEN™ (FILGRASTIM™).

25 In an additional embodiment, the Therapeutics of the invention are administered in combination with Fibroblast Growth Factors. Fibroblast Growth

Factors that may be administered with the Therapeutics of the invention include, but are not limited to, FGF-1, FGF-2, FGF-3, FGF-4, FGF-5, FGF-6, FGF-7, FGF-8, FGF-9, FGF-10, FGF-11, FGF-12, FGF-13, FGF-14, and FGF-15.

In additional embodiments, the Therapeutics of the invention are administered in

5 combination with other therapeutic or prophylactic regimens, such as, for example, radiation therapy.

Example 24: Method of Treating Decreased Levels of the Polypeptide

The present invention relates to a method for treating an individual in need of
10 an increased level of a polypeptide of the invention in the body comprising administering to such an individual a composition comprising a therapeutically effective amount of an agonist of the invention (including polypeptides of the invention). Moreover, it will be appreciated that conditions caused by a decrease in the standard or normal expression level of a secreted protein in an individual can be
15 treated by administering the polypeptide of the present invention, preferably in the secreted form. Thus, the invention also provides a method of treatment of an individual in need of an increased level of the polypeptide comprising administering to such an individual a Therapeutic comprising an amount of the polypeptide to increase the activity level of the polypeptide in such an individual.

20 For example, a patient with decreased levels of a polypeptide receives a daily dose 0.1-100 ug/kg of the polypeptide for six consecutive days. Preferably, the polypeptide is in the secreted form. The exact details of the dosing scheme, based on administration and formulation, are provided in Example 23.

25 **Example 25: Method of Treating Increased Levels of the Polypeptide**

The present invention also relates to a method of treating an individual in need of a decreased level of a polypeptide of the invention in the body comprising administering to such an individual a composition comprising a therapeutically effective amount of an antagonist of the invention (including polypeptides and
5 antibodies of the invention).

In one example, antisense technology is used to inhibit production of a polypeptide of the present invention. This technology is one example of a method of decreasing levels of a polypeptide, preferably a secreted form, due to a variety of etiologies, such as cancer. For example, a patient diagnosed with abnormally
10 increased levels of a polypeptide is administered intravenously antisense polynucleotides at 0.5, 1.0, 1.5, 2.0 and 3.0 mg/kg day for 21 days. This treatment is repeated after a 7-day rest period if the treatment was well tolerated. The formulation of the antisense polynucleotide is provided in Example 23.

15 **Example 26: Method of Treatment Using Gene Therapy-Ex Vivo**

One method of gene therapy transplants fibroblasts, which are capable of expressing a polypeptide, onto a patient. Generally, fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in tissue-culture medium and separated into small pieces. Small chunks of the tissue are placed on a wet surface of
20 a tissue culture flask, approximately ten pieces are placed in each flask. The flask is turned upside down, closed tight and left at room temperature over night. After 24 hours at room temperature, the flask is inverted and the chunks of tissue remain fixed to the bottom of the flask and fresh media (e.g., Ham's F12 media, with 10% FBS, penicillin and streptomycin) is added. The flasks are then incubated at 37 degree C
25 for approximately one week.

At this time, fresh media is added and subsequently changed every several days. After an additional two weeks in culture, a monolayer of fibroblasts emerge. The monolayer is trypsinized and scaled into larger flasks.

pMV-7 (Kirschmeier, P.T. et al., DNA, 7:219-25 (1988)), flanked by the long
5 terminal repeats of the Moloney murine sarcoma virus, is digested with EcoRI and HindIII and subsequently treated with calf intestinal phosphatase. The linear vector is fractionated on agarose gel and purified, using glass beads.

The cDNA encoding a polypeptide of the present invention can be amplified using PCR primers which correspond to the 5' and 3' end sequences respectively as set
10 forth in Example 1 using primers and having appropriate restriction sites and initiation/stop codons, if necessary. Preferably, the 5' primer contains an EcoRI site and the 3' primer includes a HindIII site. Equal quantities of the Moloney murine sarcoma virus linear backbone and the amplified EcoRI and HindIII fragment are added together, in the presence of T4 DNA ligase. The resulting mixture is
15 maintained under conditions appropriate for ligation of the two fragments. The ligation mixture is then used to transform bacteria HB101, which are then plated onto agar containing kanamycin for the purpose of confirming that the vector has the gene of interest properly inserted.

The amphotropic pA317 or GP+am12 packaging cells are grown in tissue
20 culture to confluent density in Dulbecco's Modified Eagles Medium (DMEM) with 10% calf serum (CS), penicillin and streptomycin. The MSV vector containing the gene is then added to the media and the packaging cells transduced with the vector. The packaging cells now produce infectious viral particles containing the gene (the packaging cells are now referred to as producer cells).

25 Fresh media is added to the transduced producer cells, and subsequently, the media is harvested from a 10 cm plate of confluent producer cells. The spent media,

containing the infectious viral particles, is filtered through a millipore filter to remove detached producer cells and this media is then used to infect fibroblast cells. Media is removed from a sub-confluent plate of fibroblasts and quickly replaced with the media from the producer cells. This media is removed and replaced with fresh media.

5 If the titer of virus is high, then virtually all fibroblasts will be infected and no selection is required. If the titer is very low, then it is necessary to use a retroviral vector that has a selectable marker, such as neo or his. Once the fibroblasts have been efficiently infected, the fibroblasts are analyzed to determine whether protein is produced.

10 The engineered fibroblasts are then transplanted onto the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads.

**Example 27: Gene Therapy Using Endogenous Genes Corresponding To
Polynucleotides of the Invention**

15 Another method of gene therapy according to the present invention involves operably associating the endogenous polynucleotide sequence of the invention with a promoter via homologous recombination as described, for example, in U.S. Patent NO: 5,641,670, issued June 24, 1997; International Publication NO: WO 96/29411, published September 26, 1996; International Publication NO: WO 94/12650,
20 published August 4, 1994; Koller et al., *Proc. Natl. Acad. Sci. USA*, 86:8932-8935 (1989); and Zijlstra et al., *Nature*, 342:435-438 (1989). This method involves the activation of a gene which is present in the target cells, but which is not expressed in the cells, or is expressed at a lower level than desired.

Polynucleotide constructs are made which contain a promoter and targeting
25 sequences, which are homologous to the 5' non-coding sequence of endogenous polynucleotide sequence, flanking the promoter. The targeting sequence will be

sufficiently near the 5' end of the polynucleotide sequence so the promoter will be operably linked to the endogenous sequence upon homologous recombination. The promoter and the targeting sequences can be amplified using PCR. Preferably, the amplified promoter contains distinct restriction enzyme sites on the 5' and 3' ends.

5 Preferably, the 3' end of the first targeting sequence contains the same restriction enzyme site as the 5' end of the amplified promoter and the 5' end of the second targeting sequence contains the same restriction site as the 3' end of the amplified promoter.

The amplified promoter and the amplified targeting sequences are digested
10 with the appropriate restriction enzymes and subsequently treated with calf intestinal phosphatase. The digested promoter and digested targeting sequences are added together in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions appropriate for ligation of the two fragments. The construct is size fractionated on an agarose gel then purified by phenol extraction and ethanol
15 precipitation.

In this Example, the polynucleotide constructs are administered as naked polynucleotides via electroporation. However, the polynucleotide constructs may also be administered with transfection-facilitating agents, such as liposomes, viral sequences, viral particles, precipitating agents, etc. Such methods of delivery are
20 known in the art.

Once the cells are transfected, homologous recombination will take place which results in the promoter being operably linked to the endogenous polynucleotide sequence. This results in the expression of polynucleotide corresponding to the polynucleotide in the cell. Expression may be detected by immunological staining, or
25 any other method known in the art.

Fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in DMEM + 10% fetal calf serum. Exponentially growing or early stationary phase fibroblasts are trypsinized and rinsed from the plastic surface with nutrient medium. An aliquot of the cell suspension is removed for counting, and the remaining
5 cells are subjected to centrifugation. The supernatant is aspirated and the pellet is resuspended in 5 ml of electroporation buffer (20 mM HEPES pH 7.3, 137 mM NaCl, 5 mM KCl, 0.7 mM Na₂ HPO₄, 6 mM dextrose). The cells are recentrifuged, the supernatant aspirated, and the cells resuspended in electroporation buffer containing 1 mg/ml acetylated bovine serum albumin. The final cell suspension contains
10 approximately 3×10^6 cells/ml. Electroporation should be performed immediately following resuspension.

Plasmid DNA is prepared according to standard techniques. For example, to construct a plasmid for targeting to the locus corresponding to the polynucleotide of the invention, plasmid pUC18 (MBI Fermentas, Amherst, NY) is digested with
15 HindIII. The CMV promoter is amplified by PCR with an XbaI site on the 5' end and a BamHI site on the 3' end. Two non-coding sequences are amplified via PCR: one non-coding sequence (fragment 1) is amplified with a HindIII site at the 5' end and an Xba site at the 3' end; the other non-coding sequence (fragment 2) is amplified with a BamHI site at the 5' end and a HindIII site at the 3' end. The CMV promoter and the
20 fragments (1 and 2) are digested with the appropriate enzymes (CMV promoter - XbaI and BamHI; fragment 1 - XbaI; fragment 2 - BamHI) and ligated together. The resulting ligation product is digested with HindIII, and ligated with the HindIII-digested pUC18 plasmid.

Plasmid DNA is added to a sterile cuvette with a 0.4 cm electrode gap
25 (Bio-Rad). The final DNA concentration is generally at least 120 $\mu\text{g/ml}$. 0.5 ml of the cell suspension (containing approximately 1.5×10^6 cells) is then added to the cuvette,

and the cell suspension and DNA solutions are gently mixed. Electroporation is performed with a Gene-Pulser apparatus (Bio-Rad). Capacitance and voltage are set at 960 μ F and 250-300 V, respectively. As voltage increases, cell survival decreases, but the percentage of surviving cells that stably incorporate the introduced DNA into their genome increases dramatically. Given these parameters, a pulse time of approximately 14-20 mSec should be observed.

Electroporated cells are maintained at room temperature for approximately 5 min, and the contents of the cuvette are then gently removed with a sterile transfer pipette. The cells are added directly to 10 ml of prewarmed nutrient media (DMEM with 15% calf serum) in a 10 cm dish and incubated at 37 degree C. The following day, the media is aspirated and replaced with 10 ml of fresh media and incubated for a further 16-24 hours.

The engineered fibroblasts are then injected into the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads. The fibroblasts now produce the protein product. The fibroblasts can then be introduced into a patient as described above.

Example 28: Method of Treatment Using Gene Therapy - In Vivo

Another aspect of the present invention is using *in vivo* gene therapy methods to treat disorders, diseases and conditions. The gene therapy method relates to the introduction of naked nucleic acid (DNA, RNA, and antisense DNA or RNA) sequences into an animal to increase or decrease the expression of the polypeptide. The polynucleotide of the present invention may be operatively linked to a promoter or any other genetic elements necessary for the expression of the polypeptide by the target tissue. Such gene therapy and delivery techniques and methods are known in the art, see, for example, WO90/11092, WO98/11779; U.S. Patent NO. 5693622,

5705151, 5580859; Tabata et al., *Cardiovasc. Res.* 35(3):470-479 (1997); Chao et al., *Pharmacol. Res.* 35(6):517-522 (1997); Wolff, *Neuromuscul. Disord.* 7(5):314-318 (1997); Schwartz et al., *Gene Ther.* 3(5):405-411 (1996); Tsurumi et al., *Circulation* 94(12):3281-3290 (1996) (incorporated herein by reference).

5 The polynucleotide constructs may be delivered by any method that delivers injectable materials to the cells of an animal, such as, injection into the interstitial space of tissues (heart, muscle, skin, lung, liver, intestine and the like). The polynucleotide constructs can be delivered in a pharmaceutically acceptable liquid or aqueous carrier.

10 The term "naked" polynucleotide, DNA or RNA, refers to sequences that are free from any delivery vehicle that acts to assist, promote, or facilitate entry into the cell, including viral sequences, viral particles, liposome formulations, lipofectin or precipitating agents and the like. However, the polynucleotides of the present invention may also be delivered in liposome formulations (such as those taught in
15 Felgner P.L. et al. (1995) *Ann. NY Acad. Sci.* 772:126-139 and Abdallah B. et al. (1995) *Biol. Cell* 85(1):1-7) which can be prepared by methods well known to those skilled in the art.

 The polynucleotide vector constructs used in the gene therapy method are preferably constructs that will not integrate into the host genome nor will they contain
20 sequences that allow for replication. Any strong promoter known to those skilled in the art can be used for driving the expression of DNA. Unlike other gene therapies techniques, one major advantage of introducing naked nucleic acid sequences into target cells is the transitory nature of the polynucleotide synthesis in the cells. Studies have shown that non-replicating DNA sequences can be introduced into cells to
25 provide production of the desired polypeptide for periods of up to six months.

 The polynucleotide construct can be delivered to the interstitial space of

tissues within the an animal, including of muscle, skin, brain, lung, liver, spleen, bone marrow, thymus, heart, lymph, blood, bone, cartilage, pancreas, kidney, gall bladder, stomach, intestine, testis, ovary, uterus, rectum, nervous system, eye, gland, and connective tissue. Interstitial space of the tissues comprises the intercellular fluid, mucopolysaccharide matrix among the reticular fibers of organ tissues, elastic fibers in the walls of vessels or chambers, collagen fibers of fibrous tissues, or that same matrix within connective tissue ensheathing muscle cells or in the lacunae of bone. It is similarly the space occupied by the plasma of the circulation and the lymph fluid of the lymphatic channels. Delivery to the interstitial space of muscle tissue is preferred for the reasons discussed below. They may be conveniently delivered by injection into the tissues comprising these cells. They are preferably delivered to and expressed in persistent, non-dividing cells which are differentiated, although delivery and expression may be achieved in non-differentiated or less completely differentiated cells, such as, for example, stem cells of blood or skin fibroblasts. *In vivo* muscle cells are particularly competent in their ability to take up and express polynucleotides.

For the naked polynucleotide injection, an effective dosage amount of DNA or RNA will be in the range of from about 0.05 g/kg body weight to about 50 mg/kg body weight. Preferably the dosage will be from about 0.005 mg/kg to about 20 mg/kg and more preferably from about 0.05 mg/kg to about 5 mg/kg. Of course, as the artisan of ordinary skill will appreciate, this dosage will vary according to the tissue site of injection. The appropriate and effective dosage of nucleic acid sequence can readily be determined by those of ordinary skill in the art and may depend on the condition being treated and the route of administration. The preferred route of administration is by the parenteral route of injection into the interstitial space of tissues. However, other parenteral routes may also be used, such as, inhalation of an

aerosol formulation particularly for delivery to lungs or bronchial tissues, throat or mucous membranes of the nose. In addition, naked polynucleotide constructs can be delivered to arteries during angioplasty by the catheter used in the procedure.

The dose response effects of injected polynucleotide in muscle *in vivo* is
5 determined as follows. Suitable template DNA for production of mRNA coding for polypeptide of the present invention is prepared in accordance with a standard recombinant DNA methodology. The template DNA, which may be either circular or linear, is either used as naked DNA or complexed with liposomes. The quadriceps muscles of mice are then injected with various amounts of the template DNA.

10 Five to six week old female and male Balb/C mice are anesthetized by intraperitoneal injection with 0.3 ml of 2.5% Avertin. A 1.5 cm incision is made on the anterior thigh, and the quadriceps muscle is directly visualized. The template DNA is injected in 0.1 ml of carrier in a 1 cc syringe through a 27 gauge needle over one minute, approximately 0.5 cm from the distal insertion site of the muscle into the
15 knee and about 0.2 cm deep. A suture is placed over the injection site for future localization, and the skin is closed with stainless steel clips.

After an appropriate incubation time (e.g., 7 days) muscle extracts are prepared by excising the entire quadriceps. Every fifth 15 um cross-section of the individual quadriceps muscles is histochemically stained for protein expression. A
20 time course for protein expression may be done in a similar fashion except that quadriceps from different mice are harvested at different times. Persistence of DNA in muscle following injection may be determined by Southern blot analysis after preparing total cellular DNA and HIRT supernatants from injected and control mice. The results of the above experimentation in mice can be use to extrapolate proper
25 dosages and other treatment parameters in humans and other animals using naked DNA.

Example 29: Transgenic Animals.

The polypeptides of the invention can also be expressed in transgenic animals. Animals of any species, including, but not limited to, mice, rats, rabbits, hamsters, guinea pigs, pigs, micro-pigs, goats, sheep, cows and non-human primates, *e.g.*, baboons, monkeys, and chimpanzees may be used to generate transgenic animals. In a specific embodiment, techniques described herein or otherwise known in the art, are used to express polypeptides of the invention in humans, as part of a gene therapy protocol.

Any technique known in the art may be used to introduce the transgene (*i.e.*, polynucleotides of the invention) into animals to produce the founder lines of transgenic animals. Such techniques include, but are not limited to, pronuclear microinjection (Paterson et al., Appl. Microbiol. Biotechnol. 40:691-698 (1994); Carver et al., Biotechnology (NY) 11:1263-1270 (1993); Wright et al., Biotechnology (NY) 9:830-834 (1991); and Hoppe et al., U.S. Pat. No. 4,873,191 (1989)); retrovirus mediated gene transfer into germ lines (Van der Putten et al., Proc. Natl. Acad. Sci., USA 82:6148-6152 (1985)), blastocysts or embryos; gene targeting in embryonic stem cells (Thompson et al., Cell 56:313-321 (1989)); electroporation of cells or embryos (Lo, 1983, Mol Cell. Biol. 3:1803-1814 (1983)); introduction of the polynucleotides of the invention using a gene gun (see, *e.g.*, Ulmer et al., Science 259:1745 (1993)); introducing nucleic acid constructs into embryonic pluripotent stem cells and transferring the stem cells back into the blastocyst; and sperm-mediated gene transfer (Lavitrano et al., Cell 57:717-723 (1989); etc. For a review of such techniques, see Gordon, "Transgenic Animals," Intl. Rev. Cytol. 115:171-229 (1989), which is incorporated by reference herein in its entirety.

Any technique known in the art may be used to produce transgenic clones containing polynucleotides of the invention, for example, nuclear transfer into enucleated oocytes of nuclei from cultured embryonic, fetal, or adult cells induced to quiescence (Campell et al., Nature 380:64-66 (1996); Wilmut et al., Nature 385:810-813 (1997)).

The present invention provides for transgenic animals that carry the transgene in all their cells, as well as animals which carry the transgene in some, but not all their cells, *i.e.*, mosaic animals or chimeric. The transgene may be integrated as a single transgene or as multiple copies such as in concatamers, *e.g.*, head-to-head tandems or head-to-tail tandems. The transgene may also be selectively introduced into and activated in a particular cell type by following, for example, the teaching of Lasko et al. (Lasko et al., Proc. Natl. Acad. Sci. USA 89:6232-6236 (1992)). The regulatory sequences required for such a cell-type specific activation will depend upon the particular cell type of interest, and will be apparent to those of skill in the art. When it is desired that the polynucleotide transgene be integrated into the chromosomal site of the endogenous gene, gene targeting is preferred. Briefly, when such a technique is to be utilized, vectors containing some nucleotide sequences homologous to the endogenous gene are designed for the purpose of integrating, via homologous recombination with chromosomal sequences, into and disrupting the function of the nucleotide sequence of the endogenous gene. The transgene may also be selectively introduced into a particular cell type, thus inactivating the endogenous gene in only that cell type, by following, for example, the teaching of Gu et al. (Gu et al., Science 265:103-106 (1994)). The regulatory sequences required for such a cell-type specific inactivation will depend upon the particular cell type of interest, and will be apparent to those of skill in the art.

Once transgenic animals have been generated, the expression of the recombinant gene may be assayed utilizing standard techniques. Initial screening may be accomplished by Southern blot analysis or PCR techniques to analyze animal tissues to verify that integration of the transgene has taken place. The level of mRNA
-5- expression of the transgene in the tissues of the transgenic animals may also be assessed using techniques which include, but are not limited to, Northern blot analysis of tissue samples obtained from the animal, *in situ* hybridization analysis, and reverse transcriptase-PCR (rt-PCR). Samples of transgenic gene-expressing tissue may also be evaluated immunocytochemically or immunohistochemically using antibodies
10 specific for the transgene product.

Once the founder animals are produced, they may be bred, inbred, outbred, or crossbred to produce colonies of the particular animal. Examples of such breeding strategies include, but are not limited to: outbreeding of founder animals with more than one integration site in order to establish separate lines; inbreeding of separate
15 lines in order to produce compound transgenics that express the transgene at higher levels because of the effects of additive expression of each transgene; crossing of heterozygous transgenic animals to produce animals homozygous for a given integration site in order to both augment expression and eliminate the need for screening of animals by DNA analysis; crossing of separate homozygous lines to
20 produce compound heterozygous or homozygous lines; and breeding to place the transgene on a distinct background that is appropriate for an experimental model of interest.

Transgenic animals of the invention have uses which include, but are not limited to, animal model systems useful in elaborating the biological function of
25 polypeptides of the present invention, studying diseases, disorders, and/or conditions

associated with aberrant expression, and in screening for compounds effective in ameliorating such diseases, disorders, and/or conditions.

Example 30: Knock-Out Animals.

5 Endogenous gene expression can also be reduced by inactivating or "knocking out" the gene and/or its promoter using targeted homologous recombination. (*E.g.*, see Smithies et al., *Nature* 317:230-234 (1985); Thomas & Capecchi, *Cell* 51:503-512 (1987); Thompson et al., *Cell* 5:313-321 (1989); each of which is incorporated by reference herein in its entirety). For example, a mutant, non-functional
10 polynucleotide of the invention (or a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous polynucleotide sequence (either the coding regions or regulatory regions of the gene) can be used, with or without a selectable marker and/or a negative selectable marker, to transfect cells that express polypeptides of the invention *in vivo*. In another embodiment, techniques known in
15 the art are used to generate knockouts in cells that contain, but do not express the gene of interest. Insertion of the DNA construct, via targeted homologous recombination, results in inactivation of the targeted gene. Such approaches are particularly suited in research and agricultural fields where modifications to embryonic stem cells can be used to generate animal offspring with an inactive targeted gene (*e.g.*, see Thomas &
20 Capecchi 1987 and Thompson 1989, *supra*). However this approach can be routinely adapted for use in humans provided the recombinant DNA constructs are directly administered or targeted to the required site *in vivo* using appropriate viral vectors that will be apparent to those of skill in the art.

 In further embodiments of the invention, cells that are genetically engineered
25 to express the polypeptides of the invention, or alternatively, that are genetically engineered not to express the polypeptides of the invention (*e.g.*, knockouts) are

administered to a patient *in vivo*. Such cells may be obtained from the patient (i.e., animal, including human) or an MHC compatible donor and can include, but are not limited to fibroblasts, bone marrow cells, blood cells (e.g., lymphocytes), adipocytes, muscle cells, endothelial cells etc. The cells are genetically engineered *in vitro* using

5 recombinant DNA techniques to introduce the coding sequence of polypeptides of the invention into the cells, or alternatively, to disrupt the coding sequence and/or endogenous regulatory sequence associated with the polypeptides of the invention, e.g., by transduction (using viral vectors, and preferably vectors that integrate the transgene into the cell genome) or transfection procedures, including, but not limited

10 to, the use of plasmids, cosmids, YACs, naked DNA, electroporation, liposomes, etc. The coding sequence of the polypeptides of the invention can be placed under the control of a strong constitutive or inducible promoter or promoter/enhancer to achieve expression, and preferably secretion, of the polypeptides of the invention. The engineered cells which express and preferably secrete the polypeptides of the

15 invention can be introduced into the patient systemically, e.g., in the circulation, or intraperitoneally.

Alternatively, the cells can be incorporated into a matrix and implanted in the body, e.g., genetically engineered fibroblasts can be implanted as part of a skin graft; genetically engineered endothelial cells can be implanted as part of a lymphatic or

20 vascular graft. (See, for example, Anderson et al. U.S. Patent No. 5,399,349; and Mulligan & Wilson, U.S. Patent No. 5,460,959 each of which is incorporated by reference herein in its entirety).

When the cells to be administered are non-autologous or non-MHC compatible cells, they can be administered using well known techniques which

25 prevent the development of a host immune response against the introduced cells. For example, the cells may be introduced in an encapsulated form which, while allowing

for an exchange of components with the immediate extracellular environment, does not allow the introduced cells to be recognized by the host immune system.

Transgenic and "knock-out" animals of the invention have uses which include, but are not limited to, animal model systems useful in elaborating the biological function of polypeptides of the present invention, studying diseases, disorders, and/or conditions associated with aberrant expression, and in screening for compounds effective in ameliorating such diseases, disorders, and/or conditions.

Example 31: Production of an Antibody

10 a) Hybridoma Technology

The antibodies of the present invention can be prepared by a variety of methods. (See, Current Protocols, Chapter 2.) As one example of such methods, cells expressing polypeptide(s) of the invention are administered to an animal to induce the production of sera containing polyclonal antibodies. In a preferred method, a preparation of polypeptide(s) of the invention is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

Monoclonal antibodies specific for polypeptide(s) of the invention are prepared using hybridoma technology. (Kohler et al., Nature 256:495 (1975); Kohler et al., Eur. J. Immunol. 6:511 (1976); Kohler et al., Eur. J. Immunol. 6:292 (1976); Hammerling et al., in: Monoclonal Antibodies and T-Cell Hybridomas, Elsevier, N.Y., pp. 563-681 (1981)). In general, an animal (preferably a mouse) is immunized with polypeptide(s) of the invention or, more preferably, with a secreted polypeptide-expressing cell. Such polypeptide-expressing cells are cultured in any suitable tissue culture medium, preferably in Earle's modified Eagle's medium supplemented with 10% fetal bovine serum (inactivated at about 56°C), and supplemented with about 10

g/l of nonessential amino acids, about 1,000 U/ml of penicillin, and about 100 μ g/ml of streptomycin.

The splenocytes of such mice are extracted and fused with a suitable myeloma cell line. Any suitable myeloma cell line may be employed in accordance with the present invention; however, it is preferable to employ the parent myeloma cell line (SP2O), available from the ATCC. After fusion, the resulting hybridoma cells are selectively maintained in HAT medium, and then cloned by limiting dilution as described by Wands et al. (Gastroenterology 80:225-232 (1981)). The hybridoma cells obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding the polypeptide(s) of the invention.

Alternatively, additional antibodies capable of binding to polypeptide(s) of the invention can be produced in a two-step procedure using anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, protein specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody whose ability to bind to the protein-specific antibody can be blocked by polypeptide(s) of the invention. Such antibodies comprise anti-idiotypic antibodies to the protein-specific antibody and are used to immunize an animal to induce formation of further protein-specific antibodies.

For in vivo use of antibodies in humans, an antibody is "humanized". Such antibodies can be produced using genetic constructs derived from hybridoma cells producing the monoclonal antibodies described above. Methods for producing chimeric and humanized antibodies are known in the art and are discussed herein. (See, for review, Morrison, Science 229:1202 (1985); Oi et al., BioTechniques 4:214

(1986); Cabilly et al., U.S. Patent No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al., EP 173494; Neuberger et al., WO 8601533; Robinson et al., WO 8702671; Boulianne et al., Nature 312:643 (1984); Neuberger et al., Nature 314:268 (1985).)

5

b) Isolation Of Antibody Fragments Directed Against
Polypeptide(s) From A Library Of scFvs

Naturally occurring V-genes isolated from human PBLs are constructed into a library of antibody fragments which contain reactivities against polypeptide(s) of the invention to which the donor may or may not have been exposed (see e.g., U.S. Patent 5,885,793 incorporated herein by reference in its entirety).

Rescue of the Library.

A library of scFvs is constructed from the RNA of human PBLs as described in PCT publication WO 92/01047. To rescue phage displaying antibody fragments, approximately 10⁹ E. coli harboring the phagemid are used to inoculate 50 ml of 2xTY containing 1% glucose and 100 µg/ml of ampicillin (2xTY-AMP-GLU) and grown to an O.D. of 0.8 with shaking. Five ml of this culture is used to inoculate 50 ml of 2xTY-AMP-GLU, 2 x 10⁸ TU of delta gene 3 helper (M13 delta gene III, see PCT publication WO 92/01047) are added and the culture incubated at 37°C for 45 minutes without shaking and then at 37°C for 45 minutes with shaking. The culture is centrifuged at 4000 r.p.m. for 10 min. and the pellet resuspended in 2 liters of 2xTY containing 100 µg/ml ampicillin and 50 µg/ml kanamycin and grown overnight.

15

20

Phage are prepared as described in PCT publication WO 92/01047.

M13 delta gene III is prepared as follows: M13 delta gene III helper phage does not encode gene III protein, hence the phage(mid) displaying antibody fragments have a greater avidity of binding to antigen. Infectious M13 delta gene III

25

particles are made by growing the helper phage in cells harboring a pUC19 derivative supplying the wild type gene III protein during phage morphogenesis. The culture is incubated for 1 hour at 37° C without shaking and then for a further hour at 37°C with shaking. Cells are spun down (IEC-Centra 8,400 r.p.m. for 10 min), resuspended in
5 300 ml 2xTY broth containing 100 µg ampicillin/ml and 25 µg kanamycin/ml (2xTY-AMP-KAN) and grown overnight, shaking at 37°C. Phage particles are purified and concentrated from the culture medium by two PEG-precipitations (Sambrook et al., 1990), resuspended in 2 ml PBS and passed through a 0.45 µm filter (Minisart NML; Sartorius) to give a final concentration of approximately 10¹³ transducing units/ml
10 (ampicillin-resistant clones).

Panning of the Library.

Immunotubes (Nunc) are coated overnight in PBS with 4 ml of either 100 µg/ml or 10 µg/ml of a polypeptide of the present invention. Tubes are blocked with 2% Marvel-PBS for 2 hours at 37°C and then washed 3 times in PBS. Approximately
15 10¹³ TU of phage is applied to the tube and incubated for 30 minutes at room temperature tumbling on an over and under turntable and then left to stand for another 1.5 hours. Tubes are washed 10 times with PBS 0.1% Tween-20 and 10 times with PBS. Phage are eluted by adding 1 ml of 100 mM triethylamine and rotating 15 minutes on an under and over turntable after which the solution is immediately
20 neutralized with 0.5 ml of 1.0M Tris-HCl, pH 7.4. Phage are then used to infect 10 ml of mid-log E. coli TG1 by incubating eluted phage with bacteria for 30 minutes at 37°C. The E. coli are then plated on TYE plates containing 1% glucose and 100 µg/ml ampicillin. The resulting bacterial library is then rescued with delta gene 3 helper phage as described above to prepare phage for a subsequent round of selection.
25 This process is then repeated for a total of 4 rounds of affinity purification with tube-

washing increased to 20 times with PBS, 0.1% Tween-20 and 20 times with PBS for rounds 3 and 4.

Characterization of Binders.

Eluted phage from the 3rd and 4th rounds of selection are used to infect E. coli

- 5 HB 2151 and soluble scFv is produced (Marks, et al., 1991) from single colonies for assay. ELISAs are performed with microtitre plates coated with either 10 pg/ml of the polypeptide of the present invention in 50 mM bicarbonate pH 9.6. Clones positive in ELISA are further characterized by PCR fingerprinting (see, e.g., PCT publication WO 92/01047) and then by sequencing. These ELISA positive clones
- 10 may also be further characterized by techniques known in the art, such as, for example, epitope mapping, binding affinity, receptor signal transduction, ability to block or competitively inhibit antibody/antigen binding, and competitive agonistic or antagonistic activity.

15 **Example 32: Assays Detecting Stimulation or Inhibition of B cell Proliferation and Differentiation**

- Generation of functional humoral immune responses requires both soluble and cognate signaling between B-lineage cells and their microenvironment. Signals may impart a positive stimulus that allows a B-lineage cell to continue its programmed
- 20 development, or a negative stimulus that instructs the cell to arrest its current developmental pathway. To date, numerous stimulatory and inhibitory signals have been found to influence B cell responsiveness including IL-2, IL-4, IL-5, IL-6, IL-7, IL10, IL-13, IL-14 and IL-15. Interestingly, these signals are by themselves weak effectors but can, in combination with various co-stimulatory proteins, induce activation, proliferation,
- 25 differentiation, homing, tolerance and death among B cell populations.

One of the best studied classes of B-cell co-stimulatory proteins is the TNF-

superfamily. Within this family CD40, CD27, and CD30 along with their respective ligands CD154, CD70, and CD153 have been found to regulate a variety of immune responses. Assays which allow for the detection and/or observation of the proliferation and differentiation of these B-cell populations and their precursors are valuable tools in determining the effects various proteins may have on these B-cell populations in terms of proliferation and differentiation. Listed below are two assays designed to allow for the detection of the differentiation, proliferation, or inhibition of B-cell populations and their precursors.

In Vitro Assay- Purified polypeptides of the invention, or truncated forms thereof, is assessed for its ability to induce activation, proliferation, differentiation or inhibition and/or death in B-cell populations and their precursors. The activity of the polypeptides of the invention on purified human tonsillar B cells, measured qualitatively over the dose range from 0.1 to 10,000 ng/mL, is assessed in a standard B-lymphocyte co-stimulation assay in which purified tonsillar B cells are cultured in the presence of either formalin-fixed *Staphylococcus aureus* Cowan I (SAC) or immobilized anti-human IgM antibody as the priming agent. Second signals such as IL-2 and IL-15 synergize with SAC and IgM crosslinking to elicit B cell proliferation as measured by tritiated-thymidine incorporation. Novel synergizing agents can be readily identified using this assay. The assay involves isolating human tonsillar B cells by magnetic bead (MACS) depletion of CD3-positive cells. The resulting cell population is greater than 95% B cells as assessed by expression of CD45R(B220).

Various dilutions of each sample are placed into individual wells of a 96-well plate to which are added 10^5 B-cells suspended in culture medium (RPMI 1640 containing 10% FBS, 5×10^{-5} M 2ME, 100U/ml penicillin, 10ug/ml streptomycin, and 10^{-5} dilution of SAC) in a total volume of 150ul. Proliferation or inhibition is quantitated by a 20h pulse

(1uCi/well) with 3H-thymidine (6.7 Ci/mM) beginning 72h post factor addition. The positive and negative controls are IL2 and medium respectively.

In Vivo Assay- BALB/c mice are injected (i.p.) twice per day with buffer only, or 2 mg/Kg of a polypeptide of the invention, or truncated forms thereof. Mice receive this treatment for 4 consecutive days, at which time they are sacrificed and various tissues and serum collected for analyses. Comparison of H&E sections from normal spleens and spleens treated with polypeptides of the invention identify the results of the activity of the polypeptides on spleen cells, such as the diffusion of peri-arterial lymphatic sheaths, and/or significant increases in the nucleated cellularity of the red pulp regions, which may indicate the activation of the differentiation and proliferation of B-cell populations. Immunohistochemical studies using a B cell marker, anti-CD45R(B220), are used to determine whether any physiological changes to splenic cells, such as splenic disorganization, are due to increased B-cell representation within loosely defined B-cell zones that infiltrate established T-cell regions.

Flow cytometric analyses of the spleens from mice treated with polypeptide is used to indicate whether the polypeptide specifically increases the proportion of ThB+, CD45R(B220)dull B cells over that which is observed in control mice.

Likewise, a predicted consequence of increased mature B-cell representation in vivo is a relative increase in serum Ig titers. Accordingly, serum IgM and IgA levels are compared between buffer and polypeptide-treated mice.

The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides of the invention (e.g., gene therapy), agonists, and/or antagonists of polynucleotides or polypeptides of the invention.

Example 33: T Cell Proliferation Assay

A CD3-induced proliferation assay is performed on PBMCs and is measured by the uptake of ^3H -thymidine. The assay is performed as follows. Ninety-six well plates are coated with 100 μl /well of mAb-to-CD3-(HIT3a, Pharmingen) or isotype-matched control mAb (B33.1) overnight at 4 degrees C (1 $\mu\text{g}/\text{ml}$ in .05M bicarbonate buffer, pH 9.5), then washed three times with PBS. PBMC are isolated by F/H gradient centrifugation from human peripheral blood and added to quadruplicate wells ($5 \times 10^4/\text{well}$) of mAb coated plates in RPMI containing 10% FCS and P/S in the presence of varying concentrations of polypeptides of the invention (total volume 200 μl). Relevant protein buffer and medium alone are controls. After 48 hr. culture at 37 degrees C, plates are spun for 2 min. at 1000 rpm and 100 μl of supernatant is removed and stored -20 degrees C for measurement of IL-2 (or other cytokines) if effect on proliferation is observed. Wells are supplemented with 100 μl of medium containing 0.5 μCi of ^3H -thymidine and cultured at 37 degrees C for 18-24 hr. Wells are harvested and incorporation of ^3H -thymidine used as a measure of proliferation. Anti-CD3 alone is the positive control for proliferation. IL-2 (100 U/ml) is also used as a control which enhances proliferation. Control antibody which does not induce proliferation of T cells is used as the negative controls for the effects of polypeptides of the invention.

The studies described in this example tested activity of polypeptides of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides of the invention (e.g., gene therapy), agonists, and/or antagonists of polynucleotides or polypeptides of the invention.

Example 34: Effect of Polypeptides of the Invention on the Expression of MHC**Class II, Costimulatory and Adhesion Molecules and Cell Differentiation of****Monocytes and Monocyte-Derived Human Dendritic Cells**

Dendritic cells are generated by the expansion of proliferating precursors found in the peripheral blood: adherent PBMC or elutriated monocytic fractions are cultured for 7-10 days with GM-CSF (50 ng/ml) and IL-4 (20 ng/ml). These dendritic cells have the characteristic phenotype of immature cells (expression of CD1, CD80, CD86, CD40 and MHC class II antigens). Treatment with activating factors, such as TNF- α , causes a rapid change in surface phenotype (increased expression of MHC class I and II, costimulatory and adhesion molecules, downregulation of FC γ RII, upregulation of CD83). These changes correlate with increased antigen-presenting capacity and with functional maturation of the dendritic cells.

FACS analysis of surface antigens is performed as follows. Cells are treated 1-3 days with increasing concentrations of polypeptides of the invention or LPS (positive control), washed with PBS containing 1% BSA and 0.02 mM sodium azide, and then incubated with 1:20 dilution of appropriate FITC- or PE-labeled monoclonal antibodies for 30 minutes at 4 degrees C. After an additional wash, the labeled cells are analyzed by flow cytometry on a FACScan (Becton Dickinson).

Effect on the production of cytokines. Cytokines generated by dendritic cells, in particular IL-12, are important in the initiation of T-cell dependent immune responses. IL-12 strongly influences the development of Th1 helper T-cell immune response, and induces cytotoxic T and NK cell function. An ELISA is used to measure the IL-12 release as follows. Dendritic cells (10^6 /ml) are treated with increasing concentrations of polypeptides of the invention for 24 hours. LPS (100 ng/ml) is added to the cell culture as positive control. Supernatants from the cell cultures are then collected and analyzed for

IL-12 content using commercial ELISA kit (e.g, R & D Systems (Minneapolis, MN)).

The standard protocols provided with the kits are used.

Effect on the expression of MHC Class II, costimulatory and adhesion molecules.

- 5 — Three major families of cell surface antigens can be identified on monocytes: adhesion molecules, molecules involved in antigen presentation, and Fc receptor. Modulation of the expression of MHC class II antigens and other costimulatory molecules, such as B7 and ICAM-1, may result in changes in the antigen presenting capacity of monocytes and ability to induce T cell activation. Increase expression of Fc receptors may correlate with
- 10 improved monocyte cytotoxic activity, cytokine release and phagocytosis.

- FACS analysis is used to examine the surface antigens as follows. Monocytes are treated 1-5 days with increasing concentrations of polypeptides of the invention or LPS (positive control), washed with PBS containing 1% BSA and 0.02 mM sodium azide, and then incubated with 1:20 dilution of appropriate FITC- or PE-labeled monoclonal
- 15 antibodies for 30 minutes at 4 degreesC. After an additional wash, the labeled cells are analyzed by flow cytometry on a FACScan (Becton Dickinson).

- Monocyte activation and/or increased survival. Assays for molecules that activate (or alternatively, inactivate) monocytes and/or increase monocyte survival (or
- 20 alternatively, decrease monocyte survival) are known in the art and may routinely be applied to determine whether a molecule of the invention functions as an inhibitor or activator of monocytes. Polypeptides, agonists, or antagonists of the invention can be screened using the three assays described below. For each of these assays, Peripheral blood mononuclear cells (PBMC) are purified from single donor leukopacks (American
- 25 Red Cross, Baltimore, MD) by centrifugation through a Histopaque gradient (Sigma). Monocytes are isolated from PBMC by counterflow centrifugal elutriation.

Monocyte Survival Assay. Human peripheral blood monocytes progressively lose viability when cultured in absence of serum or other stimuli. Their death results from internally regulated process (apoptosis). Addition to the culture of activating factors, such as TNF-alpha dramatically improves cell survival and prevents DNA fragmentation.

Propidium iodide (PI) staining is used to measure apoptosis as follows. Monocytes are cultured for 48 hours in polypropylene tubes in serum-free medium (positive control), in the presence of 100 ng/ml TNF-alpha (negative control), and in the presence of varying concentrations of the compound to be tested. Cells are suspended at a concentration of 2×10^6 /ml in PBS containing PI at a final concentration of 5 μ g/ml, and then incubated at room temperature for 5 minutes before FACScan analysis. PI uptake has been demonstrated to correlate with DNA fragmentation in this experimental paradigm.

Effect on cytokine release. An important function of monocytes/macrophages is their regulatory activity on other cellular populations of the immune system through the release of cytokines after stimulation. An ELISA to measure cytokine release is performed as follows. Human monocytes are incubated at a density of 5×10^5 cells/ml with increasing concentrations of the a polypeptide of the invention and under the same conditions, but in the absence of the polypeptide. For IL-12 production, the cells are primed overnight with IFN (100 U/ml) in presence of a polypeptide of the invention. LPS (10 ng/ml) is then added. Conditioned media are collected after 24h and kept frozen until use. Measurement of TNF-alpha, IL-10, MCP-1 and IL-8 is then performed using a commercially available ELISA kit (e.g., R & D Systems (Minneapolis, MN)) and applying the standard protocols provided with the kit.

Oxidative burst. Purified monocytes are plated in 96-w plate at 2×10^5 cell/well. Increasing concentrations of polypeptides of the invention are added to the wells in a total volume of 0.2 ml culture medium (RPMI 1640 + 10% FCS, glutamine and antibiotics). After 3 days incubation, the plates are centrifuged and the medium is removed from the wells. To the macrophage monolayers, 0.2 ml per well of phenol red solution (140 mM NaCl, 10 mM potassium phosphate buffer pH 7.0, 5.5 mM dextrose, 0.56 mM phenol red and 19 U/ml of HRPO) is added, together with the stimulant (200 nM PMA). The plates are incubated at 37°C for 2 hours and the reaction is stopped by adding 20 μ l 1N NaOH per well. The absorbance is read at 610 nm. To calculate the amount of H₂O₂ produced by the macrophages, a standard curve of a H₂O₂ solution of known molarity is performed for each experiment.

The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polypeptides, polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

Example 35: Biological Effects of Polypeptides of the Invention

Astrocyte and Neuronal Assays

Recombinant polypeptides of the invention, expressed in *Escherichia coli* and purified as described above, can be tested for activity in promoting the survival, neurite outgrowth, or phenotypic differentiation of cortical neuronal cells and for inducing the proliferation of glial fibrillary acidic protein immunopositive cells, astrocytes. The selection of cortical cells for the bioassay is based on the prevalent expression of FGF-1 and FGF-2 in cortical structures and on the previously reported enhancement of cortical neuronal survival resulting from FGF-2 treatment. A thymidine incorporation assay, for example, can be used to elucidate a polypeptide of the invention's activity on these cells.

Moreover, previous reports describing the biological effects of FGF-2 (basic FGF) on cortical or hippocampal neurons *in vitro* have demonstrated increases in both neuron survival and neurite outgrowth (Walicke et al., "Fibroblast growth factor promotes survival of dissociated hippocampal neurons and enhances neurite extension." *Proc. Natl. Acad. Sci. USA* 83:3012-3016. (1986), assay herein incorporated by reference in its entirety). However, reports from experiments done on PC-12 cells suggest that these two responses are not necessarily synonymous and may depend on not only which FGF is being tested but also on which receptor(s) are expressed on the target cells. Using the primary cortical neuronal culture paradigm, the ability of a polypeptide of the invention to induce neurite outgrowth can be compared to the response achieved with FGF-2 using, for example, a thymidine incorporation assay.

Fibroblast and endothelial cell assays:

Human lung fibroblasts are obtained from Clonetics (San Diego, CA) and maintained in growth media from Clonetics. Dermal microvascular endothelial cells are obtained from Cell Applications (San Diego, CA). For proliferation assays, the human lung fibroblasts and dermal microvascular endothelial cells can be cultured at 5,000 cells/well in a 96-well plate for one day in growth medium. The cells are then incubated for one day in 0.1% BSA basal medium. After replacing the medium with fresh 0.1% BSA medium, the cells are incubated with the test proteins for 3 days. Alamar Blue (Alamar Biosciences, Sacramento, CA) is added to each well to a final concentration of 10%. The cells are incubated for 4 hr. Cell viability is measured by reading in a CytoFluor fluorescence reader. For the PGE₂ assays, the human lung fibroblasts are cultured at 5,000 cells/well in a 96-well plate for one day. After a medium change to 0.1% BSA basal medium, the cells are incubated with FGF-2 or polypeptides of the invention with or

without IL-1 α for 24 hours. The supernatants are collected and assayed for PGE₂ by EIA kit (Cayman, Ann Arbor, MI). For the IL-6 assays, the human lung fibroblasts are cultured at 5,000 cells/well in a 96-well plate for one day. After a medium change to 0.1% BSA basal medium, the cells are incubated with FGF-2 or with or without

5 polypeptides of the invention IL-1 α for 24 hours. The supernatants are collected and assayed for IL-6 by ELISA kit (Endogen, Cambridge, MA).

Human lung fibroblasts are cultured with FGF-2 or polypeptides of the invention for 3 days in basal medium before the addition of Alamar Blue to assess effects on growth of the fibroblasts. FGF-2 should show a stimulation at 10 - 2500 ng/ml which can be used

10 to compare stimulation with polypeptides of the invention.

Parkinson Models.

The loss of motor function in Parkinson's disease is attributed to a deficiency of striatal dopamine resulting from the degeneration of the nigrostriatal dopaminergic

15 projection neurons. An animal model for Parkinson's that has been extensively characterized involves the systemic administration of 1-methyl-4 phenyl 1,2,3,6-tetrahydropyridine (MPTP). In the CNS, MPTP is taken-up by astrocytes and catabolized by monoamine oxidase B to 1-methyl-4-phenyl pyridine (MPP⁺) and released. Subsequently, MPP⁺ is actively accumulated in dopaminergic neurons by the high-affinity

20 reuptake transporter for dopamine. MPP⁺ is then concentrated in mitochondria by the electrochemical gradient and selectively inhibits nicotinamide adenine disphosphate: ubiquinone oxidoreductionase (complex I), thereby interfering with electron transport and eventually generating oxygen radicals.

It has been demonstrated in tissue culture paradigms that FGF-2 (basic FGF) has

25 trophic activity towards nigral dopaminergic neurons (Ferrari et al., Dev. Biol. 1989).

Recently, Dr. Unsicker's group has demonstrated that administering FGF-2 in gel foam implants in the striatum results in the near complete protection of nigral dopaminergic neurons from the toxicity associated with MPTP exposure (Otto and Unsicker, J. Neuroscience, 1990).

5 Based on the data with FGF-2, polypeptides of the invention can be evaluated to determine whether it has an action similar to that of FGF-2 in enhancing dopaminergic neuronal survival *in vitro* and it can also be tested *in vivo* for protection of dopaminergic neurons in the striatum from the damage associated with MPTP treatment. The potential effect of a polypeptide of the invention is first examined *in vitro* in a dopaminergic
10 neuronal cell culture paradigm. The cultures are prepared by dissecting the midbrain floor plate from gestation day 14 Wistar rat embryos. The tissue is dissociated with trypsin and seeded at a density of 200,000 cells/cm² on polyorthinine-laminin coated glass coverslips. The cells are maintained in Dulbecco's Modified Eagle's medium and F12 medium containing hormonal supplements (N1). The cultures are fixed with paraformaldehyde
15 after 8 days *in vitro* and are processed for tyrosine hydroxylase, a specific marker for dopaminergic neurons, immunohistochemical staining. Dissociated cell cultures are prepared from embryonic rats. The culture medium is changed every third day and the factors are also added at that time.

 Since the dopaminergic neurons are isolated from animals at gestation day 14, a
20 developmental time which is past the stage when the dopaminergic precursor cells are proliferating, an increase in the number of tyrosine hydroxylase immunopositive neurons would represent an increase in the number of dopaminergic neurons surviving *in vitro*. Therefore, if a polypeptide of the invention acts to prolong the survival of dopaminergic neurons, it would suggest that the polypeptide may be involved in Parkinson's Disease.

25 The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to

test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

Example 36: The Effect of Polypeptides of the Invention on the Growth of

5 Vascular Endothelial Cells

On day 1, human umbilical vein endothelial cells (HUVEC) are seeded at 2.5×10^4 cells/35 mm dish density in M199 medium containing 4% fetal bovine serum (FBS), 16 units/ml heparin, and 50 units/ml endothelial cell growth supplements (ECGS, Biotechnology, Inc.). On day 2, the medium is replaced with M199 containing 10% FBS, 8
10 units/ml heparin. A polypeptide having the amino acid sequence of SEQ ID NO:Y, and positive controls, such as VEGF and basic FGF (bFGF) are added, at varying concentrations. On days 4 and 6, the medium is replaced. On day 8, cell number is determined with a Coulter Counter.

An increase in the number of HUVEC cells indicates that the polypeptide of the
15 invention may proliferate vascular endothelial cells.

The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

20

Example 37: Stimulatory Effect of Polypeptides of the Invention on the Proliferation of Vascular Endothelial Cells

For evaluation of mitogenic activity of growth factors, the colorimetric MTS (3-(4,5-dimethylthiazol-2-yl)-5-(3-carboxymethoxyphenyl)-2-(4-sulfophenyl)2H-tetrazolium) assay with the electron coupling reagent PMS (phenazine methosulfate) was
25 performed (CellTiter 96 AQ, Promega). Cells are seeded in a 96-well plate (5,000

cells/well) in 0.1 mL serum-supplemented medium and are allowed to attach overnight. After serum-starvation for 12 hours in 0.5% FBS, conditions (bFGF, VEGF₁₆₅ or a polypeptide of the invention in 0.5% FBS) with or without Heparin (8 U/ml) are added to wells for 48 hours. 20 mg of MTS/PMS mixture (1:0.05) are added per well and allowed to incubate for 1 hour at 37°C before measuring the absorbance at 490 nm in an ELISA plate reader. Background absorbance from control wells (some media, no cells) is subtracted, and seven wells are performed in parallel for each condition. See, Leak *et al. In Vitro Cell. Dev. Biol.* 30A:512-518 (1994).

The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

Example 38: Inhibition of PDGF-induced Vascular Smooth Muscle Cell

15 Proliferation Stimulatory Effect

HAoSMC proliferation can be measured, for example, by BrdUrd incorporation. Briefly, subconfluent, quiescent cells grown on the 4-chamber slides are transfected with CRP or FITC-labeled AT2-3LP. Then, the cells are pulsed with 10% calf serum and 6 mg/ml BrdUrd. After 24 h, immunocytochemistry is performed by using BrdUrd Staining Kit (Zymed Laboratories). In brief, the cells are incubated with the biotinylated mouse anti-BrdUrd antibody at 4 degrees C for 2 h after being exposed to denaturing solution and then incubated with the streptavidin-peroxidase and diaminobenzidine. After counterstaining with hematoxylin, the cells are mounted for microscopic examination, and the BrdUrd-positive cells are counted. The BrdUrd index is calculated as a percent of the BrdUrd-positive cells to the total cell number. In addition, the simultaneous detection of the BrdUrd staining (nucleus) and the FITC uptake (cytoplasm) is performed for

individual cells by the concomitant use of bright field illumination and dark field-UV fluorescent illumination. See, Hayashida et al., J. Biol. Chem. 6:271(36):21985-21992 (1996).

The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

Example 39: Stimulation of Endothelial Migration

10 This example will be used to explore the possibility that a polypeptide of the invention may stimulate lymphatic endothelial cell migration.

Endothelial cell migration assays are performed using a 48 well microchemotaxis chamber (Neuroprobe Inc., Cabin John, MD; Falk, W., et al., J. Immunological Methods 1980;33:239-247). Polyvinylpyrrolidone-free polycarbonate filters with a pore size of 8
15 um (Nucleopore Corp. Cambridge, MA) are coated with 0.1% gelatin for at least 6 hours at room temperature and dried under sterile air. Test substances are diluted to appropriate concentrations in M199 supplemented with 0.25% bovine serum albumin (BSA), and 25 ul of the final dilution is placed in the lower chamber of the modified Boyden apparatus. Subconfluent, early passage (2-6) HUVEC or BMEC cultures are washed and trypsinized
20 for the minimum time required to achieve cell detachment. After placing the filter between lower and upper chamber, 2.5×10^5 cells suspended in 50 ul M199 containing 1% FBS are seeded in the upper compartment. The apparatus is then incubated for 5 hours at 37°C in a humidified chamber with 5% CO₂ to allow cell migration. After the incubation period, the filter is removed and the upper side of the filter with the non-migrated cells is
25 scraped with a rubber policeman. The filters are fixed with methanol and stained with a Giemsa solution (Diff-Quick, Baxter, McGraw Park, IL). Migration is quantified by

counting cells of three random high-power fields (40x) in each well, and all groups are performed in quadruplicate.

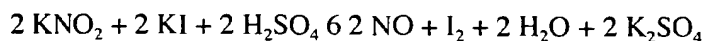
The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to
5 test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

Example 40: Stimulation of Nitric Oxide Production by Endothelial Cells

Nitric oxide released by the vascular endothelium is believed to be a mediator of
10 vascular endothelium relaxation. Thus, activity of a polypeptide of the invention can be assayed by determining nitric oxide production by endothelial cells in response to the polypeptide.

Nitric oxide is measured in 96-well plates of confluent microvascular endothelial cells after 24 hours starvation and a subsequent 4 hr exposure to various levels of a
15 positive control (such as VEGF-1) and the polypeptide of the invention. Nitric oxide in the medium is determined by use of the Griess reagent to measure total nitrite after reduction of nitric oxide-derived nitrate by nitrate reductase. The effect of the polypeptide of the invention on nitric oxide release is examined on HUVEC.

Briefly, NO release from cultured HUVEC monolayer is measured with a NO-
20 specific polarographic electrode connected to a NO meter (Iso-NO, World Precision Instruments Inc.) (1049). Calibration of the NO elements is performed according to the following equation:



The standard calibration curve is obtained by adding graded concentrations of
25 KNO_2 (0, 5, 10, 25, 50, 100, 250, and 500 nmol/L) into the calibration solution containing KI and H_2SO_4 . The specificity of the Iso-NO electrode to NO is previously determined by

measurement of NO from authentic NO gas (1050). The culture medium is removed and HUVECs are washed twice with Dulbecco's phosphate buffered saline. The cells are then bathed in 5 ml of filtered Krebs-Henseleit solution in 6-well plates, and the cell plates are kept on a slide warmer (Lab Line Instruments Inc.) To maintain the temperature at 37°C.

5 The NO sensor probe is inserted vertically into the wells, keeping the tip of the electrode 2 mm under the surface of the solution, before addition of the different conditions.

S-nitroso acetyl penicillamin (SNAP) is used as a positive control. The amount of released NO is expressed as picomoles per 1×10^6 endothelial cells. All values reported are means of four to six measurements in each group (number of cell culture wells). See,

10 Leak *et al. Biochem. and Biophys. Res. Comm.* 217:96-105 (1995).

The studies described in this example tested activity of polypeptides of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

15

Example 41: Effect of Polypeptides of the Invention on Cord Formation in Angiogenesis

Another step in angiogenesis is cord formation, marked by differentiation of endothelial cells. This bioassay measures the ability of microvascular endothelial cells to
20 form capillary-like structures (hollow structures) when cultured *in vitro*.

CADMEC (microvascular endothelial cells) are purchased from Cell Applications, Inc. as proliferating (passage 2) cells and are cultured in Cell Applications' CADMEC Growth Medium and used at passage 5. For the *in vitro* angiogenesis assay, the wells of a 48-well cell culture plate are coated with Cell Applications' Attachment Factor Medium
25 (200 ml/well) for 30 min. at 37°C. CADMEC are seeded onto the coated wells at 7,500 cells/well and cultured overnight in Growth Medium. The Growth Medium is then

replaced with 300 mg Cell Applications' Chord Formation Medium containing control buffer or a polypeptide of the invention (0.1 to 100 ng/ml) and the cells are cultured for an additional 48 hr. The numbers and lengths of the capillary-like chords are quantitated through use of the Boeckeler VIA-170 video image analyzer. All assays are done in triplicate.

Commercial (R&D) VEGF (50 ng/ml) is used as a positive control. b-esteradiol (1 ng/ml) is used as a negative control. The appropriate buffer (without protein) is also utilized as a control.

The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

Example 42: Angiogenic Effect on Chick Chorioallantoic Membrane

Chick chorioallantoic membrane (CAM) is a well-established system to examine angiogenesis. Blood vessel formation on CAM is easily visible and quantifiable. The ability of polypeptides of the invention to stimulate angiogenesis in CAM can be examined.

Fertilized eggs of the White Leghorn chick (*Gallus gallus*) and the Japanese qual (*Coturnix coturnix*) are incubated at 37.8°C and 80% humidity. Differentiated CAM of 16-day-old chick and 13-day-old qual embryos is studied with the following methods.

On Day 4 of development, a window is made into the egg shell of chick eggs. The embryos are checked for normal development and the eggs sealed with cellotape. They are further incubated until Day 13. Thermanox coverslips (Nunc, Naperville, IL) are cut into disks of about 5 mm in diameter. Sterile and salt-free growth factors are dissolved in distilled water and about 3.3 mg/ 5 ml are pipetted on the disks. After air-drying, the

inverted disks are applied on CAM. After 3 days, the specimens are fixed in 3% glutaraldehyde and 2% formaldehyde and rinsed in 0.12 M sodium cacodylate buffer. They are photographed with a stereo microscope [Wild M8] and embedded for semi- and ultrathin sectioning as described above. Controls are performed with carrier disks alone.

5 The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

10 **Example 43: Angiogenesis Assay Using a Matrigel Implant in Mouse**

In vivo angiogenesis assay of a polypeptide of the invention measures the ability of an existing capillary network to form new vessels in an implanted capsule of murine extracellular matrix material (Matrigel). The protein is mixed with the liquid Matrigel at 4 degree C and the mixture is then injected subcutaneously in mice where it solidifies. After
15 7 days, the solid "plug" of Matrigel is removed and examined for the presence of new blood vessels. Matrigel is purchased from Becton Dickinson Labware/Collaborative Biomedical Products.

When thawed at 4 degree C the Matrigel material is a liquid. The Matrigel is mixed with a polypeptide of the invention at 150 ng/ml at 4 degrees C and drawn into cold
20 3 ml syringes. Female C57Bl/6 mice approximately 8 weeks old are injected with the mixture of Matrigel and experimental protein at 2 sites at the midventral aspect of the abdomen (0.5 ml/site). After 7 days, the mice are sacrificed by cervical dislocation, the Matrigel plugs are removed and cleaned (i.e., all clinging membranes and fibrous tissue is removed). Replicate whole plugs are fixed in neutral buffered 10% formaldehyde,
25 embedded in paraffin and used to produce sections for histological examination after

staining with Masson's Trichrome. Cross sections from 3 different regions of each plug are processed. Selected sections are stained for the presence of vWF. The positive control for this assay is bovine basic FGF (150 ng/ml). Matrigel alone is used to determine basal levels of angiogenesis.

5 The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

10 **Example 44: Rescue of Ischemia in Rabbit Lower Limb Model**

 To study the in vivo effects of polynucleotides and polypeptides of the invention on ischemia, a rabbit hindlimb ischemia model is created by surgical removal of one femoral arteries as described previously (Takeshita *et al.*, *Am J. Pathol* 147:1649-1660 (1995)). The excision of the femoral artery results in retrograde propagation of thrombus and occlusion of the external iliac artery. Consequently, blood flow to the ischemic limb is dependent upon collateral vessels originating from the internal iliac artery (Takeshita *et al.* *Am J. Pathol* 147:1649-1660 (1995)). An interval of 10 days is allowed for post-operative recovery of rabbits and development of endogenous collateral vessels. At 10 day post-operatively (day 0), after performing a baseline angiogram, the internal iliac artery of the ischemic limb is transfected with 500 mg naked expression plasmid containing a polynucleotide of the invention by arterial gene transfer technology using a hydrogel-coated balloon catheter as described (Riessen *et al.* *Hum Gene Ther.* 4:749-758 (1993); Leclerc *et al.* *J. Clin. Invest.* 90: 936-944 (1992)). When a polypeptide of the invention is used in the treatment, a single bolus of 500 mg polypeptide of the invention or control is delivered into the internal iliac artery of the ischemic limb over a period of 1 min. through an infusion catheter. On day 30, various parameters are measured in these

rabbits: (a) BP ratio - The blood pressure ratio of systolic pressure of the ischemic limb to that of normal limb; (b) Blood Flow and Flow Reserve - Resting FL: the blood flow during undilated condition and Max FL: the blood flow during fully dilated condition (also an indirect measure of the blood vessel amount) and Flow Reserve is reflected by the ratio of max FL: resting FL; (c) Angiographic Score - This is measured by the angiogram of collateral vessels. A score is determined by the percentage of circles in an overlaying grid that with crossing opacified arteries divided by the total number in the rabbit thigh; (d) Capillary density - The number of collateral capillaries determined in light microscopic sections taken from hindlimbs.

- 10 The studies described in this example tested activity of polynucleotides and polypeptides of the invention. However, one skilled in the art could easily modify the exemplified studies to test the agonists, and/or antagonists of the invention.

Example 45: Effect of Polypeptides of the Invention on Vasodilation

- 15 Since dilation of vascular endothelium is important in reducing blood pressure, the ability of polypeptides of the invention to affect the blood pressure in spontaneously hypertensive rats (SHR) is examined. Increasing doses (0, 10, 30, 100, 300, and 900 mg/kg) of the polypeptides of the invention are administered to 13-14 week old spontaneously hypertensive rats (SHR). Data are expressed as the mean +/- SEM.
- 20 Statistical analysis are performed with a paired t-test and statistical significance is defined as $p < 0.05$ vs. the response to buffer alone.

 The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the

25 invention.

Example 46: Rat Ischemic Skin Flap Model

The evaluation parameters include skin blood flow, skin temperature, and factor VIII immunohistochemistry or endothelial alkaline phosphatase reaction. Expression of polypeptides of the invention, during the skin ischemia, is studied using in situ

5 hybridization.

The study in this model is divided into three parts as follows:

- a) Ischemic skin
- b) Ischemic skin wounds
- c) Normal wounds

10 The experimental protocol includes:

a) Raising a 3x4 cm, single pedicle full-thickness random skin flap (myocutaneous flap over the lower back of the animal).

b) An excisional wounding (4-6 mm in diameter) in the ischemic skin (skin-flap).

c) Topical treatment with a polypeptide of the invention of the excisional wounds
15 (day 0, 1, 2, 3, 4 post-wounding) at the following various dosage ranges: 1mg to 100 mg.

d) Harvesting the wound tissues at day 3, 5, 7, 10, 14 and 21 post-wounding for histological, immunohistochemical, and in situ studies.

The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to
20 test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

Example 47: Peripheral Arterial Disease Model

Angiogenic therapy using a polypeptide of the invention is a novel therapeutic strategy to obtain restoration of blood flow around the ischemia in case of peripheral arterial diseases. The experimental protocol includes:

- a) One side of the femoral artery is ligated to create ischemic muscle of the hindlimb, the other side of hindlimb serves as a control.
- b) a polypeptide of the invention, in a dosage range of 20 mg - 500 mg, is delivered intravenously and/or intramuscularly 3 times (perhaps more) per week for 2-3 weeks.
- c) The ischemic muscle tissue is collected after ligation of the femoral artery at 1, 2, and 3 weeks for the analysis of expression of a polypeptide of the invention and histology. Biopsy is also performed on the other side of normal muscle of the contralateral hindlimb.

The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

Example 48: Ischemic Myocardial Disease Model

A polypeptide of the invention is evaluated as a potent mitogen capable of stimulating the development of collateral vessels, and restructuring new vessels after coronary artery occlusion. Alteration of expression of the polypeptide is investigated in situ. The experimental protocol includes:

- a) The heart is exposed through a left-side thoracotomy in the rat. Immediately, the left coronary artery is occluded with a thin suture (6-0) and the thorax is closed.

b) a polypeptide of the invention, in a dosage range of 20 mg - 500 mg, is delivered intravenously and/or intramuscularly 3 times (perhaps more) per week for 2-4 weeks.

- c) Thirty days after the surgery, the heart is removed and cross-sectioned
5 for morphometric and in situ analyzes.

The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

10

Example 49: Rat Corneal Wound Healing Model

This animal model shows the effect of a polypeptide of the invention on neovascularization. The experimental protocol includes:

- 15 a) Making a 1-1.5 mm long incision from the center of cornea into the stromal layer.
- b) Inserting a spatula below the lip of the incision facing the outer corner of the eye.
- c) Making a pocket (its base is 1-1.5 mm from the edge of the eye).
- 20 d) Positioning a pellet, containing 50ng- 5ug of a polypeptide of the invention, within the pocket.
- e) Treatment with a polypeptide of the invention can also be applied topically to the corneal wounds in a dosage range of 20mg - 500mg (daily treatment for five days).

The studies described in this example tested activity of a polypeptide of the
25 invention. However, one skilled in the art could easily modify the exemplified studies to

test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

Example 50: Diabetic Mouse and Glucocorticoid-Impaired Wound Healing

5 **Models**

A. Diabetic db+/db+ Mouse Model.

To demonstrate that a polypeptide of the invention accelerates the healing process, the genetically diabetic mouse model of wound healing is used. The full thickness wound
10 healing model in the db+/db+ mouse is a well characterized, clinically relevant and reproducible model of impaired wound healing. Healing of the diabetic wound is dependent on formation of granulation tissue and re-epithelialization rather than contraction (Gartner, M.H. *et al.*, *J. Surg. Res.* 52:389 (1992); Greenhalgh, D.G. *et al.*, *Am. J. Pathol.* 136:1235 (1990)).

15 The diabetic animals have many of the characteristic features observed in Type II diabetes mellitus. Homozygous (db+/db+) mice are obese in comparison to their normal heterozygous (db+/+m) littermates. Mutant diabetic (db+/db+) mice have a single autosomal recessive mutation on chromosome 4 (db+) (Coleman *et al.* *Proc. Natl. Acad. Sci. USA* 77:283-293 (1982)). Animals show polyphagia, polydipsia and polyuria.
20 Mutant diabetic mice (db+/db+) have elevated blood glucose, increased or normal insulin levels, and suppressed cell-mediated immunity (Mandel *et al.*, *J. Immunol.* 120:1375 (1978); Debray-Sachs, M. *et al.*, *Clin. Exp. Immunol.* 51(1):1-7 (1983); Leiter *et al.*, *Am. J. of Pathol.* 114:46-55 (1985)). Peripheral neuropathy, myocardial complications, and microvascular lesions, basement membrane thickening and glomerular filtration
25 abnormalities have been described in these animals (Norido, F. *et al.*, *Exp. Neurol.* 83(2):221-232 (1984); Robertson *et al.*, *Diabetes* 29(1):60-67 (1980); Giacomelli *et al.*,

Lab Invest. 40(4):460-473 (1979); Coleman, D.L., *Diabetes* 31 (Suppl):1-6 (1982)). These homozygous diabetic mice develop hyperglycemia that is resistant to insulin analogous to human type II diabetes (Mandel *et al.*, *J. Immunol.* 120:1375-1377 (1978)).

The characteristics observed in these animals suggests that healing in this model
5 may be similar to the healing observed in human diabetes (Greenhalgh, *et al.*, *Am. J. of Pathol.* 136:1235-1246 (1990)).

Genetically diabetic female C57BL/KsJ (db+/db+) mice and their non-diabetic (db+/+m) heterozygous littermates are used in this study (Jackson Laboratories). The animals are purchased at 6 weeks of age and are 8 weeks old at the beginning of the study.
10 Animals are individually housed and received food and water ad libitum. All manipulations are performed using aseptic techniques. The experiments are conducted according to the rules and guidelines of Human Genome Sciences, Inc. Institutional Animal Care and Use Committee and the Guidelines for the Care and Use of Laboratory Animals.

15 Wounding protocol is performed according to previously reported methods (Tsuboi, R. and Rifkin, D.B., *J. Exp. Med.* 172:245-251 (1990)). Briefly, on the day of wounding, animals are anesthetized with an intraperitoneal injection of Avertin (0.01 mg/mL), 2,2,2-tribromoethanol and 2-methyl-2-butanol dissolved in deionized water. The dorsal region of the animal is shaved and the skin washed with 70% ethanol solution and
20 iodine. The surgical area is dried with sterile gauze prior to wounding. An 8 mm full-thickness wound is then created using a Keyes tissue punch. Immediately following wounding, the surrounding skin is gently stretched to eliminate wound expansion. The wounds are left open for the duration of the experiment. Application of the treatment is given topically for 5 consecutive days commencing on the day of wounding. Prior to
25 treatment, wounds are gently cleansed with sterile saline and gauze sponges.

Wounds are visually examined and photographed at a fixed distance at the day of surgery and at two day intervals thereafter. Wound closure is determined by daily measurement on days 1-5 and on day 8. Wounds are measured horizontally and vertically using a calibrated Jameson caliper. Wounds are considered healed if granulation tissue is no longer visible and the wound is covered by a continuous epithelium.

A polypeptide of the invention is administered using at a range different doses, from 4mg to 500mg per wound per day for 8 days in vehicle. Vehicle control groups received 50mL of vehicle solution.

Animals are euthanized on day 8 with an intraperitoneal injection of sodium pentobarbital (300mg/kg). The wounds and surrounding skin are then harvested for histology and immunohistochemistry. Tissue specimens are placed in 10% neutral buffered formalin in tissue cassettes between biopsy sponges for further processing.

Three groups of 10 animals each (5 diabetic and 5 non-diabetic controls) are evaluated: 1) Vehicle placebo control, 2) untreated group, and 3) treated group.

Wound closure is analyzed by measuring the area in the vertical and horizontal axis and obtaining the total square area of the wound. Contraction is then estimated by establishing the differences between the initial wound area (day 0) and that of post treatment (day 8). The wound area on day 1 is 64mm², the corresponding size of the dermal punch. Calculations are made using the following formula:

$$[\text{Open area on day 8}] - [\text{Open area on day 1}] / [\text{Open area on day 1}]$$

Specimens are fixed in 10% buffered formalin and paraffin embedded blocks are sectioned perpendicular to the wound surface (5mm) and cut using a Reichert-Jung microtome. Routine hematoxylin-eosin (H&E) staining is performed on cross-sections of bisected wounds. Histologic examination of the wounds are used to assess whether the

healing process and the morphologic appearance of the repaired skin is altered by treatment with a polypeptide of the invention. This assessment included verification of the presence of cell accumulation, inflammatory cells, capillaries, fibroblasts, re-epithelialization and epidermal maturity (Greenhalgh, D.G. *et al.*, *Am. J. Pathol.* 136:1235 (1990)). A calibrated lens micrometer is used by a blinded observer.

Tissue sections are also stained immunohistochemically with a polyclonal rabbit anti-human keratin antibody using ABC Elite detection system. Human skin is used as a positive tissue control while non-immune IgG is used as a negative control. Keratinocyte growth is determined by evaluating the extent of reepithelialization of the wound using a calibrated lens micrometer.

Proliferating cell nuclear antigen/cyclin (PCNA) in skin specimens is demonstrated by using anti-PCNA antibody (1:50) with an ABC Elite detection system. Human colon cancer can serve as a positive tissue control and human brain tissue can be used as a negative tissue control. Each specimen includes a section with omission of the primary antibody and substitution with non-immune mouse IgG. Ranking of these sections is based on the extent of proliferation on a scale of 0-8, the lower side of the scale reflecting slight proliferation to the higher side reflecting intense proliferation.

Experimental data are analyzed using an unpaired t test. A p value of < 0.05 is considered significant.

B. Steroid Impaired Rat Model

The inhibition of wound healing by steroids has been well documented in various *in vitro* and *in vivo* systems (Wahl, Glucocorticoids and Wound healing. In: Anti-Inflammatory Steroid Action: Basic and Clinical Aspects. 280-302 (1989); Wahlet *et al.*, *J. Immunol.* 115: 476-481 (1975); Werb *et al.*, *J. Exp. Med.* 147:1684-1694 (1978)).

Glucocorticoids retard wound healing by inhibiting angiogenesis, decreasing vascular

permeability (Ebert *et al.*, *An. Intern. Med.* 37:701-705 (1952)), fibroblast proliferation, and collagen synthesis (Beck *et al.*, *Growth Factors*. 5: 295-304 (1991); Haynes *et al.*, *J. Clin. Invest.* 61: 703-797 (1978)) and producing a transient reduction of circulating monocytes (Haynes *et al.*, *J. Clin. Invest.* 61: 703-797 (1978); Wahl, "Glucocorticoids and wound healing", *In: Antiinflammatory Steroid Action: Basic and Clinical Aspects*, Academic Press, New York, pp. 280-302 (1989)). The systemic administration of steroids to impaired wound healing is a well establish phenomenon in rats (Beck *et al.*, *Growth Factors*. 5: 295-304 (1991); Haynes *et al.*, *J. Clin. Invest.* 61: 703-797 (1978); Wahl, "Glucocorticoids and wound healing", *In: Antiinflammatory Steroid Action: Basic and Clinical Aspects*, Academic Press, New York, pp. 280-302 (1989); Pierce *et al.*, *Proc. Natl. Acad. Sci. USA* 86: 2229-2233 (1989)).

To demonstrate that a polypeptide of the invention can accelerate the healing process, the effects of multiple topical applications of the polypeptide on full thickness excisional skin wounds in rats in which healing has been impaired by the systemic administration of methylprednisolone is assessed.

Young adult male Sprague Dawley rats weighing 250-300 g (Charles River Laboratories) are used in this example. The animals are purchased at 8 weeks of age and are 9 weeks old at the beginning of the study. The healing response of rats is impaired by the systemic administration of methylprednisolone (17mg/kg/rat intramuscularly) at the time of wounding. Animals are individually housed and received food and water *ad libitum*. All manipulations are performed using aseptic techniques. This study is conducted according to the rules and guidelines of Human Genome Sciences, Inc. Institutional Animal Care and Use Committee and the Guidelines for the Care and Use of Laboratory Animals.

The wounding protocol is followed according to section A, above. On the day of wounding, animals are anesthetized with an intramuscular injection of ketamine (50

mg/kg) and xylazine (5 mg/kg). The dorsal region of the animal is shaved and the skin washed with 70% ethanol and iodine solutions. The surgical area is dried with sterile gauze prior to wounding. An 8 mm full-thickness wound is created using a Keyes tissue punch. The wounds are left open for the duration of the experiment. Applications of the testing materials are given topically once a day for 7 consecutive days commencing on the day of wounding and subsequent to methylprednisolone administration. Prior to treatment, wounds are gently cleansed with sterile saline and gauze sponges.

Wounds are visually examined and photographed at a fixed distance at the day of wounding and at the end of treatment. Wound closure is determined by daily measurement on days 1-5 and on day 8. Wounds are measured horizontally and vertically using a calibrated Jameson caliper. Wounds are considered healed if granulation tissue is no longer visible and the wound is covered by a continuous epithelium.

The polypeptide of the invention is administered using at a range different doses, from 4mg to 500mg per wound per day for 8 days in vehicle. Vehicle control groups received 50mL of vehicle solution.

Animals are euthanized on day 8 with an intraperitoneal injection of sodium pentobarbital (300mg/kg). The wounds and surrounding skin are then harvested for histology. Tissue specimens are placed in 10% neutral buffered formalin in tissue cassettes between biopsy sponges for further processing.

Four groups of 10 animals each (5 with methylprednisolone and 5 without glucocorticoid) are evaluated: 1) Untreated group 2) Vehicle placebo control 3) treated groups.

Wound closure is analyzed by measuring the area in the vertical and horizontal axis and obtaining the total area of the wound. Closure is then estimated by establishing the differences between the initial wound area (day 0) and that of post treatment (day 8).

The wound area on day 1 is 64mm², the corresponding size of the dermal punch.

Calculations are made using the following formula:

$$[\text{Open area on day 8}] - [\text{Open area on day 1}] / [\text{Open area on day 1}]$$

5

Specimens are fixed in 10% buffered formalin and paraffin embedded blocks are sectioned perpendicular to the wound surface (5mm) and cut using an Olympus microtome. Routine hematoxylin-eosin (H&E) staining is performed on cross-sections of bisected wounds. Histologic examination of the wounds allows assessment of whether the healing process and the morphologic appearance of the repaired skin is improved by treatment with a polypeptide of the invention. A calibrated lens micrometer is used by a blinded observer to determine the distance of the wound gap.

Experimental data are analyzed using an unpaired t test. A p value of < 0.05 is considered significant.

The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

20 **Example 51: Lymphadema Animal Model**

The purpose of this experimental approach is to create an appropriate and consistent lymphedema model for testing the therapeutic effects of a polypeptide of the invention in lymphangiogenesis and re-establishment of the lymphatic circulatory system in the rat hind limb. Effectiveness is measured by swelling volume of the affected limb, quantification of the amount of lymphatic vasculature, total blood plasma protein, and

25

histopathology. Acute lymphedema is observed for 7-10 days. Perhaps more importantly, the chronic progress of the edema is followed for up to 3-4 weeks.

Prior to beginning surgery, blood sample is drawn for protein concentration analysis. Male rats weighing approximately ~350g are dosed with Pentobarbital.

- 5 Subsequently, the right legs are shaved from knee to hip. The shaved area is swabbed with gauze soaked in 70% EtOH. Blood is drawn for serum total protein testing. Circumference and volumetric measurements are made prior to injecting dye into paws after marking 2 measurement levels (0.5 cm above heel, at mid-pt of dorsal paw). The intradermal dorsum of both right and left paws are injected with 0.05 ml of 1% Evan's
- 10 Blue. Circumference and volumetric measurements are then made following injection of dye into paws.

- Using the knee joint as a landmark, a mid-leg inguinal incision is made circumferentially allowing the femoral vessels to be located. Forceps and hemostats are used to dissect and separate the skin flaps. After locating the femoral vessels, the
- 15 lymphatic vessel that runs along side and underneath the vessel(s) is located. The main lymphatic vessels in this area are then electrically coagulated suture ligated.

- Using a microscope, muscles in back of the leg (near the semitendinosus and adductors) are bluntly dissected. The popliteal lymph node is then located. The 2 proximal and 2 distal lymphatic vessels and distal blood supply of the popliteal node are
- 20 then and ligated by suturing. The popliteal lymph node, and any accompanying adipose tissue, is then removed by cutting connective tissues.

- Care is taken to control any mild bleeding resulting from this procedure. After lymphatics are occluded, the skin flaps are sealed by using liquid skin (Vetbond) (AJ Buck). The separated skin edges are sealed to the underlying muscle tissue while leaving
- 25 a gap of ~0.5 cm around the leg. Skin also may be anchored by suturing to underlying muscle when necessary.

To avoid infection, animals are housed individually with mesh (no bedding). Recovering animals are checked daily through the optimal edematous peak, which typically occurred by day 5-7. The plateau edematous peak are then observed. To evaluate the intensity of the lymphedema, the circumference and volumes of 2 designated
5 places on each paw before operation and daily for 7 days are measured. The effect plasma proteins on lymphedema is determined and whether protein analysis is a useful testing perimeter is also investigated. The weights of both control and edematous limbs are evaluated at 2 places. Analysis is performed in a blind manner.

Circumference Measurements: Under brief gas anesthetic to prevent limb
10 movement, a cloth tape is used to measure limb circumference. Measurements are done at the ankle bone and dorsal paw by 2 different people then those 2 readings are averaged. Readings are taken from both control and edematous limbs.

Volumetric Measurements: On the day of surgery, animals are anesthetized with Pentobarbital and are tested prior to surgery. For daily volumetrics animals are under
15 brief halothane anesthetic (rapid immobilization and quick recovery), both legs are shaved and equally marked using waterproof marker on legs. Legs are first dipped in water, then dipped into instrument to each marked level then measured by Buxco edema software(Chen/Victor). Data is recorded by one person, while the other is dipping the limb to marked area.

20 Blood-plasma protein measurements: Blood is drawn, spun, and serum separated prior to surgery and then at conclusion for total protein and Ca^{2+} comparison.

Limb Weight Comparison: After drawing blood, the animal is prepared for tissue collection. The limbs are amputated using a quillitine, then both experimental and control legs are cut at the ligature and weighed. A second weighing is done as the tibio-cacaneal
25 joint is disarticulated and the foot is weighed.

Histological Preparations: The transverse muscle located behind the knee (popliteal) area is dissected and arranged in a metal mold, filled with freezeGel, dipped into cold methylbutane, placed into labeled sample bags at - 80EC until sectioning. Upon sectioning, the muscle is observed under fluorescent microscopy for lymphatics..

- 5 The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

10 **Example 52: Suppression of TNF alpha-induced adhesion molecule expression by a Polypeptide of the Invention**

- The recruitment of lymphocytes to areas of inflammation and angiogenesis involves specific receptor-ligand interactions between cell surface adhesion molecules (CAMs) on lymphocytes and the vascular endothelium. The adhesion process, in both
- 15 normal and pathological settings, follows a multi-step cascade that involves intercellular adhesion molecule-1 (ICAM-1), vascular cell adhesion molecule-1 (VCAM-1), and endothelial leukocyte adhesion molecule-1 (E-selectin) expression on endothelial cells (EC). The expression of these molecules and others on the vascular endothelium determines the efficiency with which leukocytes may adhere to the local vasculature and
- 20 extravasate into the local tissue during the development of an inflammatory response. The local concentration of cytokines and growth factor participate in the modulation of the expression of these CAMs.

- Tumor necrosis factor alpha (TNF-a), a potent proinflammatory cytokine, is a
- 25 stimulator of all three CAMs on endothelial cells and may be involved in a wide variety of inflammatory responses, often resulting in a pathological outcome.

The potential of a polypeptide of the invention to mediate a suppression of TNF- α induced CAM expression can be examined. A modified ELISA assay which uses ECs as a solid phase absorbent is employed to measure the amount of CAM expression on TNF- α treated ECs when co-stimulated with a member of the FGF family of proteins.

5 To perform the experiment, human umbilical vein endothelial cell (HUVEC) cultures are obtained from pooled cord harvests and maintained in growth medium (EGM-2; Clonetics, San Diego, CA) supplemented with 10% FCS and 1% penicillin/streptomycin in a 37 degree C humidified incubator containing 5% CO₂. HUVECs are seeded in 96-well plates at concentrations of 1×10^4 cells/well in EGM
10 medium at 37 degree C for 18-24 hrs or until confluent. The monolayers are subsequently washed 3 times with a serum-free solution of RPMI-1640 supplemented with 100 U/ml penicillin and 100 mg/ml streptomycin, and treated with a given cytokine and/or growth factor(s) for 24 h at 37 degree C. Following incubation, the cells are then evaluated for CAM expression.

15 Human Umbilical Vein Endothelial cells (HUVECs) are grown in a standard 96 well plate to confluence. Growth medium is removed from the cells and replaced with 90 μ l of 199 Medium (10% FBS). Samples for testing and positive or negative controls are added to the plate in triplicate (in 10 μ l volumes). Plates are incubated at 37 degree C for either 5 h (selectin and integrin expression) or 24 h (integrin expression only). Plates are
20 aspirated to remove medium and 100 μ l of 0.1% paraformaldehyde-PBS(with Ca⁺⁺ and Mg⁺⁺) is added to each well. Plates are held at 4°C for 30 min.

 Fixative is then removed from the wells and wells are washed 1X with PBS(+Ca,Mg)+0.5% BSA and drained. Do not allow the wells to dry. Add 10 μ l of diluted primary antibody to the test and control wells. Anti-ICAM-1-Biotin, Anti-VCAM-
25 1-Biotin and Anti-E-selectin-Biotin are used at a concentration of 10 μ g/ml (1:10 dilution

of 0.1 mg/ml stock antibody). Cells are incubated at 37°C for 30 min. in a humidified environment. Wells are washed X3 with PBS(+Ca,Mg)+0.5% BSA.

Then add 20 μ l of diluted ExtrAvidin-Alkaline Phosphatase (1:5,000 dilution) to each well and incubated at 37°C for 30 min. Wells are washed X3 with

5 PBS(+Ca,Mg)+0.5% BSA. 1 tablet of p-Nitrophenol Phosphate pNPP is dissolved in 5 ml of glycine buffer (pH 10.4). 100 μ l of pNPP substrate in glycine buffer is added to each test well. Standard wells in triplicate are prepared from the working dilution of the ExtrAvidin-Alkaline Phosphatase in glycine buffer: 1:5,000 (10^0) > $10^{-0.5}$ > 10^{-1} > $10^{-1.5}$. 5 μ l of each dilution is added to triplicate wells and the resulting AP content in each well is

10 5.50 ng, 1.74 ng, 0.55 ng, 0.18 ng. 100 μ l of pNPP reagent must then be added to each of the standard wells. The plate must be incubated at 37°C for 4h. A volume of 50 μ l of 3M NaOH is added to all wells. The results are quantified on a plate reader at 405 nm. The background subtraction option is used on blank wells filled with glycine buffer only. The template is set up to indicate the concentration of AP-conjugate in each standard well [

15 5.50 ng; 1.74 ng; 0.55 ng; 0.18 ng]. Results are indicated as amount of bound AP-conjugate in each sample.

The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the

20 invention.

It will be clear that the invention may be practiced otherwise than as particularly described in the foregoing description and examples. Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, are within the scope of the appended claims.

25 The entire disclosure of each document cited (including patents, patent applications, journal articles, abstracts, laboratory manuals, books, or other

disclosures) in the Background of the Invention, Detailed Description, and Examples is hereby incorporated herein by reference. Further, the hard copy of the sequence listing submitted herewith and the corresponding computer readable form are both incorporated herein by reference in their entireties.

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>87</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution <i>(including postal code and country)</i> 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit <div style="text-align: center;">26 April 1999</div>	Accession Number <div style="text-align: center;">203959</div>
C. ADDITIONAL INDICATIONS <i>(leave blank if not applicable)</i> This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE <i>(if the indications are not for all designated States)</i>	
Europe In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).	
E. SEPARATE FURNISHING OF INDICATIONS <i>(leave blank if not applicable)</i>	
The indications listed below will be submitted to the International Bureau later <i>(specify the general nature of the indications e.g., "Accession Number of Deposit")</i>	

<p style="text-align: center;">For receiving Office use only</p> <p><input checked="" type="checkbox"/> This sheet was received with the international application</p> <hr/> <p>Authorized officer Sonya D. Barnes PCT/Internat'l Appl Processing Div (703) 305-3665</p>	<p style="text-align: center;">For International Bureau use only</p> <p><input type="checkbox"/> This sheet was received by the International Bureau on:</p> <hr/> <p>Authorized officer</p>
---	--

ATCC Deposit No. 203959**CANADA**

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

ATCC Deposit No.: 203959

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

What Is Claimed Is:

1. An isolated nucleic acid molecule comprising a polynucleotide having
a nucleotide sequence at least 95% identical to a sequence selected from the group
- 5 consisting of:
- (a) a polynucleotide fragment of SEQ ID NO:X or a polynucleotide fragment
of the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to
SEQ ID NO:X;
 - (b) a polynucleotide encoding a polypeptide fragment of SEQ ID NO:Y or a
10 polypeptide fragment encoded by the cDNA sequence included in ATCC Deposit
No:Z, which is hybridizable to SEQ ID NO:X;
 - (c) a polynucleotide encoding a polypeptide domain of SEQ ID NO:Y or a
polypeptide domain encoded by the cDNA sequence included in ATCC Deposit
No:Z, which is hybridizable to SEQ ID NO:X;
 - 15 (d) a polynucleotide encoding a polypeptide epitope of SEQ ID NO:Y or a
polypeptide epitope encoded by the cDNA sequence included in ATCC Deposit
No:Z, which is hybridizable to SEQ ID NO:X;
 - (e) a polynucleotide encoding a polypeptide of SEQ ID NO:Y or the cDNA
sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X,
20 having biological activity;
 - (f) a polynucleotide which is a variant of SEQ ID NO:X;
 - (g) a polynucleotide which is an allelic variant of SEQ ID NO:X;
 - (h) a polynucleotide which encodes a species homologue of the SEQ ID
NO:Y;

(i) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(h), wherein said polynucleotide does not hybridize under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A residues or of only T residues.

5

2. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding a secreted protein.

10

3. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding the sequence identified as SEQ ID NO:Y or the polypeptide encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

15

4. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises the entire nucleotide sequence of SEQ ID NO:X or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

20

5. The isolated nucleic acid molecule of claim 2, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

25

6. The isolated nucleic acid molecule of claim 3, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

7. A recombinant vector comprising the isolated nucleic acid molecule of claim 1.

5 8. A method of making a recombinant host cell comprising the isolated nucleic acid molecule of claim 1.

9. A recombinant host cell produced by the method of claim 8.

10 10. The recombinant host cell of claim 9 comprising vector sequences.

11. An isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of:

(a) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence
15 included in ATCC Deposit No:Z;

(b) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z, having biological activity;

(c) a polypeptide domain of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

20 (d) a polypeptide epitope of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(e) a secreted form of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(f) a full length protein of SEQ ID NO:Y or the encoded sequence included in
25 ATCC Deposit No:Z;

(g) a variant of SEQ ID NO:Y;

- (h) an allelic variant of SEQ ID NO:Y; or
 - (i) a species homologue of the SEQ ID NO:Y.
12. The isolated polypeptide of claim 11, wherein the secreted form or the full length protein comprises sequential amino acid deletions from either the C-
- 5 terminus or the N-terminus.
13. An isolated antibody that binds specifically to the isolated polypeptide of claim 11.
- 10 14. A recombinant host cell that expresses the isolated polypeptide of claim 11.
- 15 15. A method of making an isolated polypeptide comprising:
- (a) culturing the recombinant host cell of claim 14 under conditions such that said polypeptide is expressed; and
 - (b) recovering said polypeptide.
16. The polypeptide produced by claim 15.
- 20 17. A method for preventing, treating, or ameliorating a medical condition, comprising administering to a mammalian subject a therapeutically effective amount of the polypeptide of claim 11 or the polynucleotide of claim 1.
- 25 18. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

(a) determining the presence or absence of a mutation in the polynucleotide of claim 1; and

(b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or absence of said mutation.

5

19. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

(a) determining the presence or amount of expression of the polypeptide of claim 11 in a biological sample; and

10 (b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide.

20. A method for identifying a binding partner to the polypeptide of claim 11 comprising:

15 (a) contacting the polypeptide of claim 11 with a binding partner; and

(b) determining whether the binding partner effects an activity of the polypeptide.

20 21. The gene corresponding to the cDNA sequence of SEQ ID NO:Y.

22. A method of identifying an activity in a biological assay, wherein the method comprises:

(a) expressing SEQ ID NO:X in a cell;

(b) isolating the supernatant;

25 (c) detecting an activity in a biological assay; and

(d) identifying the protein in the supernatant having the activity.

23. The product produced by the method of claim 20.

<110> Human Genome Sciences, Inc.

<120> 49 Human Secreted Proteins

<130> PS549PCT

<140> Unassigned

<141> 2000-04-06

<150> 60/128,694

<151> 1999-04-09

<150> 60/176,931

<151> 2000-01-20

<160> 156

<170> PatentIn Ver. 2.0

<210> 1

<211> 733

<212> DNA

<213> Homo sapiens

<400> 1

gggatccgga gccc aaatct tctgacaaaa ctcacacatg cccaccgtgc ccagcacctg.	60
aattcgaggg tgcaccgtca gtcttcctct tcccccaaa acccaaggac accctcatga	120
tctcccgga ccttgaggtc acatgcgtgg tgggtggacgt aagccacgaa gaccctgagg	180
tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg	240
aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact	300
ggctgaatgg caaggagtag aagtgcaagg tctccaacaa agccctcca acccccatcg	360
agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc	420
catcccgga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc aaaggcttct	480
atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagAAC aactacaaga	540
ccacgcctcc cgtgctggac tccgacggct ccttcttct ctacagcaag ctcaccgtgg	600
acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggctctgc	660
acaaccacta cagcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc	720
gactctagag gat	733

<210> 2

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> Site

<222> (3)

<223> Xaa equals any of the twenty naturally occurring L-amino acids

<400> 2

Trp Ser Xaa Trp Ser
1 5

<210> 3

<211> 86

<212> DNA

<213> Homo sapiens

<400> 3

gcgcctcgag atttccccga aatctagatt tccccgaaat gatttccccg aaatgatttc 60
cccgaaatat ctgccatctc aattag 86

<210> 4

<211> 27

<212> DNA

<213> Homo sapiens

<400> 4

gcggcaagct ttttgcaaag cctaggc 27

<210> 5

<211> 271

<212> DNA

<213> Homo sapiens

<400> 5

ctcgagattt ccccgaaatc tagatttccc cgaaatgatt tccccgaaat gatttccccg 60
aaatatctgc catctcaatt agtcagcaac catagtcccc cccctaactc cgcccatccc 120
gccctaact ccgcccagtt ccgcccattc tccgccccat ggctgactaa ttttttttat 180
ttatgcagag gccgaggccg cctcggcctc tgagctattc cagaagtagt gaggaggctt 240
ttttggaggc ctaggctttt gcaaaaagct t 271

<210> 6

<211> 32

<212> DNA

<213> Homo sapiens

<400> 6

gcgctcgagg gatgacagcg atagaacccc gg 32

<210> 7

<211> 31

<212> DNA

<213> Homo sapiens

<400> 7
gcgaagcttc gcgactcccc ggatccgcct c 31

<210> 8
<211> 12
<212> DNA
-----<213> Homo sapiens

<400> 8
ggggactttc cc 12

<210> 9
<211> 73
<212> DNA
<213> Homo sapiens

<400> 9
gcggcctcga ggggactttc ccggggactt tccggggact ttccgggact ttccatcctg 60
ccatctcaat tag 73

<210> 10
<211> 256
<212> DNA
<213> Homo sapiens

<400> 10
ctcgagggga ctttcccgga gactttccgg ggactttccg ggactttcca tctgccatct 60
caattagtc gcaaccatag tcccgcacct aactccgccc atcccgcccc taactccgcc 120
cagttccgcc cattctccgc cccatggctg actaattttt tttatttatg cagaggccga 180
ggccgcctcg gcctctgagc tattccagaa gtagtgagga ggcttttttg gaggcctagg 240
cttttgcaaa aagctt 256

<210> 11
<211> 840
<212> DNA
<213> Homo sapiens

<400> 11
aattcggcac gaggtagctg cggtgggtca tcttccacc tccacagtgg gccgagctgc 60
caaacaagg gtagacatgt gcccctgac ataggccagg tggctctctgc cctctgtagc 120
tcccatgaga gagggtcct cggaccgaaa caggaggcca ctgcccttgc gcacacaccg 180
tggccgggtc ctctgggctg gagcgctttc cgtgtgtggg aaagtcaagg gcagccccga 240
gcctcgaagc ccaggctccc agccccgcgc catgttgcat tcccgctct actccttggg 300
aggctgggtg ctttgagtgg ttctttttaa ttctttctgt tggtttctcc ttttctttg 360
cctgggtttt gctttaacct ctctgttgca gagatgcaga gcactcagag agcctatttc 420
tatcatcgct ttctattct ccacctagaa ccagggtgact ggccgcccga gtggtgtctc 480
ttgtgtgtgt ggtgcgtcca aagctgtgca agaaatgctt ctgcctagggt tttctcgcgc 540

cccccccttg	ccttggtttt	tcctgcctgc	ttacaccccc	gtttccctga	tctgccccctg	600
ggcttctg	caggttcccc	gcactgtgcc	tatcgccggg	cctgtaagta	agcaaaactgg	660
gcaaatgagg	ggctgtgtct	ggaatttgga	gacgtcacat	ttaaatctta	aaacactgta	720
atcccagcaa	tctgggaggg	tgaggcgagg	ggattgcttg	agtccaggag	tttgagacca	780
ttctgggcaa	catagggaga	ccctcatctc	tacaaaaaaa	ttaaaaaaa	aaaaaaaaaac	840

<210> 12

<211> 2387

<212> DNA

<213> Homo sapiens

<400> 12

agatggcggc	gctgaggggt	cttgggggct	ctaggccggc	cacctactgg	tttgacagcg	60
agacgacgca	tggggcctgc	gcaataggag	tacgtgcct	gggaggcgtg	actagaagcg	120
gaagtagttg	tgggcgcctt	tgcaaccgcc	tgggacgcgc	ccgagtggtc	tktgacaggtt	180
cgcggggtcg	tggcgggggg	cgtgagggag	tgcgcgggga	gcggagatat	ggagggagat	240
ggttcagacc	cagagcctcc	agatgccggg	gaggacagca	agtccgagaa	tgggggagaat	300
gcgcccattc	actgcattct	ccgcaaaccg	gacatcaact	gcttcatgat	cgggtgtgac	360
aactgcaatg	agtggttcca	tggggactgc	atccggatca	ctgagaagat	ggccaaggcc	420
atccgggagt	ggtactgtcg	ggagtgcaga	gagaaagacc	ccaagctaga	gattcgctat	480
cggcacaca	agtcacggga	gcgggatggc	aatgagcggg	acagcagtga	gccccgggat	540
gaggggtggg	ggcgcaagag	gcctgtccct	gatccagacc	tgcagcgcgc	ggcagggtca	600
gggacagggg	ttggggccat	gcttgctcgg	ggctctgctt	cgccccacaa	atcctctccg	660
cagccccttg	tggccacacc	cagccagcat	caccagcagc	agcagcagca	gatcaaaccg	720
tcagcccgcg	tgtgtggtga	gtgtgaggca	tgtcggcgca	ctgaggactg	tggtcactgt	780
gatttctgtc	gggacatgaa	gaagtccggg	ggccccaaca	agatccggca	gaagtgccgg	840
ctgcgccagt	gccagctcg	ggcccgggaa	tcgtacaagt	acttcccttc	ctcgtctca	900
ccagtgcagc	cctcagagtc	cctgccaaag	ccccgcgggc	caactgccac	ccaacagcag	960
ccacagccat	cacagaagtt	agggcgcatc	cgtgaagatg	agggggcagt	ggcgtcatca	1020
acagtcaagg	agcctcctga	ggctacagcc	acacctgagc	cactctcaga	tgaggaccta	1080
cctctggatc	ctgacctgta	tcaggacttc	tgtgcagggg	cctttgatga	ccatggcctg	1140
ccctggatga	gcgacacaga	agagtcacca	ttcctggacc	ccgcgctgcg	gaagagggca	1200
gtgaaagtga	agcatgtgaa	gcgtcgggag	aagaagtctg	agaagaagaa	ggaggagcga	1260
tacaagcggc	atcggcagaa	gcagaaacac	aaggataaat	ggaaacaccc	agagagggct	1320
gatgccaagg	accctgcgtc	actgccccag	tgccctgggg	ccggctgtgt	gcgccccgcc	1380
cagcccagct	ccaagtattg	ctcagatgac	tgtggcatga	agctggcagc	caaccgcac	1440
tacgagatcc	tccccagcg	catccagcag	tggcagcaga	gcccttgcac	tgctgaagag	1500
cacggcaaga	agctgctcga	acgcattcgc	cgagagcagc	agartgccc	cactcgcctt	1560
caggaaatgg	aacgccgatt	ccatgagctt	gaggccatca	ttctacgtgc	caagcarcag	1620
gctgtgcscs	aggwtragg	gtatgagaag	ccagacgtcc	tttgggtcca	tgtaccccc	1680
acgcattgaa	ggggccacac	gactcttctg	tgtgtgtgat	aatcctcaga	gcaaaacata	1740
ctgtaagcgg	ctccaggtgc	tgtgccccga	gcactcacgg	gaccccaaa	tgccagctga	1800
cgaggatg	gggtgcccc	ttgtacgtga	tgtctttgag	ctcacgggtg	acttctgccg	1860
cctgcccagg	cgccagtgc	atcgccatta	ctgctgggag	aagctgcggc	gtgcggaagt	1920
ggacttgagg	cgctgcgtg	tgtggtacaa	gctggacgag	ctgtttgagc	aggagcgcaa	1980
tgtgcgcaca	gccatgacaa	accgcgcggg	attgctggcc	ctgatgctgc	accagacgat	2040
ccagcacgat	cccctcacta	ccgacctgcg	ctccagtgcc	gaccgctgag	cctcctggcc	2100
cggacccttt	acaccctgca	ttccagatgg	gggagccgcc	cgggtgccgt	gtgtccgttc	2160
ctccactcat	ctgtttctcc	ggttctccct	gtgcccaccc	accggttgac	cgcccatctg	2220
cctttatcag	agggactgtc	cccgtcgaca	tgttcagtgc	ctgggtgggg	tgccggagtcc	2280

actcatcctt gcctcctctc cctgggtttt gttaataaaa ttttgaagaa accaaaaaaa 2340
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 2387

<210> 13
 <211> 2064
 <212> DNA
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (1596)
 <223> n equals a,t,g, or c

<220>
 <221> SITE
 <222> (2005)
 <223> n equals a,t,g, or c

<220>
 <221> SITE
 <222> (2047)
 <223> n equals a,t,g, or c

<220>
 <221> SITE
 <222> (2057)
 <223> n equals a,t,g, or c

<400> 13
 ccggagggcc gctggtgtct gtgtacaggg cgtgctgtct gtggaaacgc gagggcacac 60
 tagcactttc ctactgcstc tgtcaccggg tccctccacc cttgtctcct gtgcggccag 120
 cgtcagagcc atggcgacgg aggagaagaa gcctgagacc gagggccgca gagcacagcc 180
 aaccccttcg tcatccgcca ctacagagaa gcctacacct gtgaagccaa actatgctct 240
 aaagtgcacc cttgctggcc acaccaaacg agtgtcctcc gtgaaattca gcccgaatgg 300
 agagtggctg gcaagtcat ctgctgataa acttattaaa atttggggcg cgtatgatgg 360
 gaaatttgag aaaaccatat ctggtcacaa gctgggaata tccgatgtag cctggtcgtc 420
 agattctaac cttcttgttt ctgcctcaga tgacaaaacc ttgaagatat gggacgtgag 480
 ctcgggcaag tgtctgaaaa ccctgaaggg acacagtaat tatgtctttt gctgcaactt 540
 caatccccag tccaacctta ttgtctcagg atcctttgac gaaagcgtga ggatattgga 600
 tgtgaaaaca gggagtgcc tcaagacttt gccagctcac tcggatccag tctcgccgt 660
 tcattttaat cgtgatggat ccttgatagt ttcaagtagc tatgatggtc tctgtcgcac 720
 ctgggacacc gcctcaggcc agtgctgaa gacgctcatc gatgacgaca accccccgt 780
 gtcttttgtg aagtctctcc cgaacggcaa atacatcctg gccgccacgc tggacaacac 840
 tctgaagctc tgggactaca gcaaggggaa gtgcctgaag acgtacactg gccacaagaa 900
 tgagaaatac tgcatatttg ccaatttctc tgttactggg gggagtgga ttgtgtctgg 960
 ctacagagat aaccttgttt acatctggaa ccttcagacg aaagagattg tacagaaact 1020
 acaaggccac acagatgtcg tgatctcaac agcttgctac ccaacagaaa acatcatcgc 1080
 ctctgctgcg ctagaaaatg acaaaacaat taaactgtgg aagagtgact gctaagtccc 1140
 tttgctcctg cccgcgagag actgtcggga agtygacctg gattggcaag aaacaggggtg 1200
 tcttgagggt ggtccccag atctgcgcct gggggtcagg acagggcctg atttgagcct 1260

cctctctgaa	gatgatttgg	ccgagcggaa	ggtgtggacc	accggaaagt	tcttaaaagt	1320
tgctggtgac	atttcttgcc	aattctaaca	ctgtctaggg	aagagttcct	agtctattgt	1380
gttcaaacag	agtcaacaaa	agtttttaat	tttttattac	agaaggggtga	agttcaattt	1440
aacatgcggt	gtgttttttc	agtaaacggt	ctgtatcttt	ttgatattcc	atgaccaggt	1500
gcacgctgtg	gcctgtcacc	gccaccgtgg	ccccgccagc	tggcctcccc	tttggtccac	1560
gccggccgcc	cccattctct	gctgcgtaga	tgcccnngcc	cagggccctg	actcctccat	1620
tcccgccagt	agctgttcct	agtgtatttt	cgtctttctg	gaaaacagca	ttgagtgggt	1680
gttttctgtg	taaagagccg	tttgtgtctt	gggagtttgt	ggcccacatg	ccgatagcac	1740
ggtcatcgca	catgactctc	ccgtttgtct	cagtgtccct	gcaacaagca	gcaccgcaga	1800
ctgtaataaa	aggtgggggt	ttgtgaatgg	ttgtggcaag	tcgctccttg	tgaagctcgt	1860
ctccatgtgg	ctttcttgga	gaaaggctcc	cctggggcaa	gaggggtggaa	ggtttctttg	1920
gacaggaggt	gctgargctg	gctgcamctg	ctctctgaag	acgccttcct	ytctaggttc	1980
attgttaatg	ttgctggrgc	cgggnaacgg	ggttgggaag	ttcttaattt	cccaaggagc	2040
cagcccngat	ggacttncct	tgga				2064

<210> 14

<211> 1898

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (265)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (1854)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (1859)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (1888)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (1897)

<223> n equals a,t,g, or c

<400> 14

gggtggagag	agttcggcgc	tcagagaggt	accagaccat	gaagctcttc	accagatct	60
tcggggtcgg	tgtaagact	gctgaccggt	ggtaccggga	aggactgcga	accttagatg	120
acctccgaga	gcagccccag	aaactaaccc	aacagcagaa	agcggggctc	cagcaccacc	180
aggacctgag	caccccagtc	ctgcggtccg	atgtagatgc	cctgcagcag	gtggtggagg	240

aagctgtggg	gcaggccctg	ctggngccac	cgtcacgctg	accggcggtg	tccgcagggc	300
ctcatcctgt	accaccagca	ccagcacagc	trctgtragt	cccctacccg	cctggcccaa	360
caragccaca	tggacgcttt	tragagaagt	ttctgcattt	tccgcctacc	acaacctcca	420
ggggctgctg	tggggggatc	cacgaggccc	tgcccacctt	ggaagccgtg	agagtggact	480
tggtagtgc	acccgtcagc	cagttccctt	tcgccctgct	cggttggact	ggctccaagc	540
ttttccagcg	ggagctgcgc	cgcttcagcc	ggaaggagaa	gggcctgtgg	ctgaacagcc	600
atgggctgtt	tgaccgcgag	cagggaaagca	gcagtggcaa	gactcctagg	tcacggaagt	660
cctgcttctg	ttgcagaaga	cattttttcca	mgmggcttca	gaggaagaca	tcttcagaca	720
cctgggcctt	gagtaccttc	ctccagagca	gagaaacgcc	tgagcctgcc	tgktkccccc	780
acttccactc	aggaaaattg	gctgccccca	acctggccac	tgaatgtctc	caggcagata	840
tgctgcccc	tgacccccac	cttcaccctt	ccccgccaag	gcctggctct	tccggaggtc	900
aattgtgcct	gcaggatcag	ttgagccctt	gctggtgtgc	tgagggtgt	gatgaggtgg	960
gagccctcag	tgccagcctc	atcactgtgt	gaccctgggt	ctgctcttag	cctccccatg	1020
gctcacgttc	ctgccctgga	tgggatgtga	gtggggccca	catcgtggag	ctgtggtggg	1080
gcctgcagtc	atgaatggca	agtgttcctt	gatgtgcagt	gtctcattag	ttgcactgca	1140
gttaactgtg	gctcctgcag	ggcaccctgc	ccagaatgcc	cagaagagaa	ccatgcatac	1200
ctgcactgca	tttgagagcc	atgagctgga	ggctgtggtt	cgtgccagca	aggagcctac	1260
tgtctggtgt	gctgtaggca	tctggagagg	gagagggcct	gggtaggagc	tgggaggaag	1320
ataattttca	actatggggc	ttcagtactg	cagcgccccg	agccaggctc	tgtgcttctg	1380
cctttaaggc	ctgtttctcag	cacaatgtct	caaaaaatagg	tcatatcctg	ccactcccgt	1440
cgcagagccc	tttaatgggt	ccaaacccta	agtccacaca	tagcccctgg	ctctggcatc	1500
tctccagccc	cactggcccc	gagctgcttg	actcacgggc	ttcctatttg	atgcaccag	1560
gcccccttgt	ggccaactcc	ctccccctt	cactgaggca	gaagcactga	ggtgggctgg	1620
acatgggtgc	cctccacgtc	cctcatatcc	ccaggcacac	tctggcctca	ggttttgccc	1680
tggccatgtc	atctacctgg	agtggggcct	cccccttctc	aggccttgaa	tcaaaagcca	1740
ctttgttagg	cgaggatttc	ccagaccact	catcacatta	aaaaatattt	tgaaaacatg	1800
cagtaaaaaa	aaaaaaaaaa	aaaaagggcg	gccgctttaa	aaggatcctt	cganggggnc	1860
ccaagcttac	gccgggcatt	gccaacgnca	taacttnt			1898

<210> 15

<211> 1701

<212> DNA

<213> Homo sapiens

<400> 15

gggcagacgg	aagccgaacg	agttcctcgg	cggtgcagg	atgggggact	ccaaagtga	60
agtggcggtg	cggatacgac	ccatgaaccg	gcgagagact	gacttgcata	ccaaatgtgt	120
ggtggatgtg	gatgcaaaca	aggttattct	taatcctgta	aatacgaatc	tttccaaagg	180
agatgcccg	ggccagccga	agtgtttgct	tatgatcatt	gtttctggtc	tatggatgaa	240
tctgtcaaag	aaaagtatgc	aggtcaagat	attgttttca	agtgccttgg	agagaatatc	300
ctgcagaatg	ctttttratg	ctacaatgca	tgtatctttg	cctatggaca	gactggctct	360
ggaaaatctt	ataccatgat	gggcacagct	gaccaacctg	gattaatccc	aagactttgc	420
agtggactct	ttgaacgaac	tcagaaagag	ggaaatgaag	aacagagttt	taaagtagaa	480
gtgtcctaca	tggaaattta	taatgaaaaa	gttcgagacc	ttcttgatcc	caaaggaagc	540
cgtcagacgt	tgaagtgcag	agagcatagt	gtgttgggac	cttatgtcga	cggactttct	600
aaactggctg	tcacaagcta	caaggatatt	gagtcgttga	tgtctgaggg	taacaaatct	660
cgcacagttg	ctgcaaccaa	catgaacgag	gagagttagc	gatcccatgc	agttttcaaa	720
atcacctcoa	cacatactct	ctacgatgtg	aagtctggga	catctggaga	gaaagtgggc	780
aaastcagcc	tgggtgattt	agmtggcagy	gaacgagcaa	cgaagacagg	cgctgcaggg	840
gacaggctga	aggaagggag	caacattaac	aagtccctca	caacctcgg	tctggttatc	900

tcagctcttg	cagatcagag	tgctggcaaa	agcargaata	aatttggtcc	atatcgtgac	960
tcagtttcca	cttggtgct	caaagacagc	ctcgggggta	acagcaagmc	cgccatggtg	1020
gctactgtga	gtcctgcagc	tgataactat	gatgaaaccc	tctcaactct	gcggtatgca	1080
gacgcagcca	agcacattgt	aaaccacgct	gtggtgaatg	aggaccctaa	tgcccgaatt	1140
atccgggatc	tccgggaaga	agttgagaaa	ctccggggagc	agctgaccaa	agcagaggca	1200
atgaaatctc	cagagctaaa	ggaccggctg	gaagaatctg	agaagctaat	ccaggaaatg	1260
actgtgacct	gggaggagaa	attaaggaaa	acggaggaga	ttgcacagga	acgacagaaa	1320
cagcttgaga	gtcttggaat	atctcttcag	tcttcgggaa	tcaaagttgg	ggatgataaa	1380
tgcttccttg	tgaatctgaa	tgctgaccca	gctctgaatg	agcttctggt	gtactattta	1440
aaggaacata	cattgatagg	gtcagcaaat	tccaagata	tccaactgtg	cgccatggga	1500
attcttcctg	aacactgtat	tatagacatc	acgtcagaag	gccaggttat	gctgactcct	1560
cagaagaaca	ccagaacatt	tgtaaatggg	tcatctgtct	ccagtccaat	acagctacac	1620
catggggaca	ggatattatg	gggaaacaat	catttcttca	gactcaattt	gcctaaaaaa	1680
aaaaaaaaaa	aggcgggccg	c				1701

<210> 16

<211> 1175

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (740)

<223> n equals a,t,g, or c

<400> 16

tcgaccacg	cgctccgcca	cgcgctccggc	ctccacagtt	tcctgcggt	gtctgcacac	60
ccagaccaga	gcagttcctg	cctttgctg	ttgcaccatt	ttccttggtg	aacttctatt	120
catccttcaa	agcccagcag	taatcatcct	ttagaaagtc	ttctttcaga	gggaacccaaa	180
aaggtaatcg	ctggagacag	acagatgctg	cctgaatgcc	tggtgtgttg	tggtgtgttg	240
ggaatgttac	ttcacctctc	cgctgcctcag	tttctcagc	tgtaatgggg	atggtaacag	300
tgtctagggg	tactgcttgg	aatgcacata	gggagatgag	tgaaggccca	gcactagaag	360
agtgcaggca	ctagcagagt	gcaggcgcaa	ttgctgctgg	gaccagcagg	taactcgcac	420
ccaagttaca	gtgcccagcc	ccagcagcag	cctcagcacc	aggcagagt	tgctcagcam	480
tggtgggggg	caagaggact	tgaggggccgc	tggtctgtga	ttctctcatc	tcttttgagg	540
ttmarsamtt	ggcgtctctc	ctagaagctc	tggggaamct	gacaaatcct	ccaggaggga	600
cacagaacgc	caggaagggc	tggtctgggg	tgaccaaga	tggtgcccc	gagamaccgt	660
atctgagggc	ttgggtggaa	ctgaggagag	gccggctggg	aagsgcatcc	gggaggaaar	720
ggcagacggc	tamggcagcn	tcaggtggta	cagtttgccc	cggaagtga	gtagagaaga	780
gagcgggagg	agagagggcc	acatgcctct	cagccatggc	cctgaatgct	ggcttggtg	840
agcctcatct	ttgctgtttg	cagaatgggg	agaattgtgc	ctgcccagcc	tcctccttgg	900
ggactccagg	ggcccaaaga	accaagagct	gcaaattgtc	tggtggcctt	ggaagtttat	960
ggatggtaca	gatctggggg	ggaggggcatg	gccaggacag	ggagggctgt	cagagagagg	1020
gtctgtgggt	ttgtggagtg	tggggatcag	tcgctgactc	attagatgaa	ccaggagcct	1080
gcatgctaca	gccacctgc	caaactcttg	ccccacctgc	tttttaaaat	aaagttttat	1140
tggaacatga	aaaaaaaaaa	aaaaagggcg	gccgc			1175

<210> 17

<211> 1827

<212> DNA

<213> Homo sapiens

<400> 17

ggcaccgagca	rgaggaagat	ggcggcgctcc	gcagctgccg	ctgagctcca	ggcttctggg	60
gggtccgcggc	acccagtgtg	tctgttgggtg	ttgggaatgg	cgggatccgg	gaaaaccact	120
tttgtacaga	ggctcacagg	acacctgcat	gcccaaggca	ctccaccgta	tgtgatcaac	180
ctggatccag	cagtacatga	agttcccttt	cctgccaaata	ttgatattcg	tgatactgta	240
aagtataaag	aagtaatgaa	acaatatgga	cttggaccca	atggcggcat	agtgacctca	300
ctcaatctct	ttgctaccag	at ttgatcag	gtgatgaaat	ttattgagaa	ggcccagAAC	360
atgtccaaat	atgtgttgat	tgacacacct	ggacagattg	aggtattcac	ctggtcagct	420
tctgggacaa	ttatcactga	agcccttgca	tcctcatttc	caacagttgt	catctatgta	480
atggacacat	cgagaagtac	caacccagtg	accttcatgt	ccaacatgct	ctatgcctgc	540
agcatcttat	acaaaaccaa	gctgcctttc	attgtgggtca	tgaataaaac	tgacatcatt	600
gaccacagct	ttgcagtgga	atggatgcag	gattttgagg	ctttccaaga	tgcttgaat	660
caagagacta	catacgtcag	taacctgact	cgttcaatga	gcctgggtgt	agatgagttt	720
tacagctcac	tcaggggtgt	gggtgtctct	gctgttcttg	gtactggatt	agatgaactc	780
tttgtgcaag	ttaccagtgc	tgccgaagaa	tatgaaaggg	agtatcgtcc	tgaatatgaa	840
cgtctgaaaa	aatcactggc	caacgcagag	agccaacagc	agagagaaca	actggaacgc	900
cttcgaaaag	atatgggttc	tgtagccttg	gatgcaggga	ctgccaaaga	cagcttatct	960
cctgtgctgc	acccttctga	tttgatcctg	actcgaggaa	ccttggatga	agaggatgag	1020
gaagcagaca	gcgatactga	tgacattgac	cacagagtta	cagaggaaag	ccatgaagag	1080
ccagcattcc	agaattttat	gcaagaatcg	atggcacaaat	actggaagag	aaacaataaa	1140
taggagactt	tagcacactt	cacttgtttc	tagaagtcca	gaattttgga	cctccacgtg	1200
aaagaactgt	tcttacctct	gaactggggg	ctcccataag	ggataatttt	cctcagagta	1260
gcaaagtttc	tcttattaga	gaaatcttgt	gactcagatg	aagtcaggga	tagaagaccc	1320
ttggacctgg	cagggttaatg	ctgattattc	cttggccttt	cccttgattt	tatgcaagga	1380
aggatatact	gagctgatac	tsttccaagc	ctacaacttc	aagttttatc	atttgaactc	1440
aagtactttt	gctgctgagg	aatggaatca	aaagaacgta	gtctcctggg	raccacctca	1500
gatctctatt	attaggctag	atgtatagcc	tctactcccc	cagcttcttg	ctcttgaccc	1560
tgcaactgta	gttgcccttc	tattagcagc	caaggaaaag	ggaaacatga	gcttatccag	1620
aacggtggca	gagtcctcct	ggcaatcaac	caacgttgct	atgaaatatg	cctcactg	1680
tatagctcat	tataggacgt	caggtttggt	gaaaaaagtg	ggcaagacat	gattaatgaa	1740
tcagaatcct	gtttcattgg	tgacttggat	aaagactttt	taatttttaa	aaaaaaaaaa	1800
aaaaaaaaaa	aaaaaaaaaa	aaaaatt				1827

<210> 18

<211> 2345

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (1088)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (1909)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (1913)

<223> n equals a,t,g, or c

<400> 18

```

ggaactcctc gatgaggacc atctacagtg cttttttttt tctatctctc tgtctctcag      60
ttctgctttc ttctacagta tttgatgact ggcatcccat ttctataagc tgggtccaga      120
actttgggct cacaccttcc tttgacgtgc aagtgccaca gaccttgaga tgtttcttca      180
gatcaggggtg ccgctggcat ccactgaact tgcttcagtt taagctgagc accttcctga      240
gaatcatttc attttatctt tcattctgta gtgagaagag gcttcagcat gaatagtcta      300
gggacatgca agatgtataa aatagaatgg agttgtgaat taggktatat gagggrgaaa      360
tttataaaaa atataaagca ttgtaaagac aaatgcatgt tacacaaaac caggrgacca      420
cttcatttta agaggtacct gctggctctc gaagctttaa gtgatttata atctagtcaa      480
caataagtgg cagatgaact gaaaatata ttgcatgaag ttcttagttc agaggtaaag      540
ctagggatgc tatgcatggc aacactggaa gggaaagagc ttttgawac caggctctggg      600
catttgcyct aatcagaggt caacatcttc tctgccctca taaccamtc cccgccaggg      660
gtcctgtctc ctgaccaca cattagcaga tataatayck gkcawtctgg kttctcattc      720
tctttccaga aaaatccaga catgatttta ttgcaagatg gagagaaaag gagacagcat      780
cacatgtctt atattagtca caaaaactgg atgggtttta tttcaggcgc taattccttt      840
gagaacacaa gggaaacttt gatcttaatc tatttgatgt ggttttaagt aaaggagcat      900
cttgtgctta ctttgaaagt gtttttttac ttggggcttg gtcaaattt acattttgtt      960
ccagagaaaa actcatttgg aaggcagcat ggagtataga attagacatc cctgggcttg      1020
aagcccatct cagccatgaa ctacctttat gactttcagc tagttacttt tcctcactca      1080
gcttcagntt ctccatttat aaagyaagt cctcaacatc gctttttgac tttcttaatc      1140
ttgtctacgc atctacaagt agccctttta ttactgattt ttaactactc ctggccattg      1200
gaatgaccga gaagcccatg tctcattctc agacggggga ttttgattct aatgacagtc      1260
atgggtgaga gtccactgtg ttaaagtctc ttcatgtgaa gcatctgatg tgaattctat      1320
tttctgctta aacccagac atagatgtta agtttcaaaa ttatgtcgta cattcactcc      1380
cactacatac tcattgaatg cttaccatgt acagactctg tgatagacta tggaaataca      1440
tagaaagaaa ttccctgttt ttaagaactt tacctagtgt ttagaaattg catttaaaac      1500
tgataattaa aatactatag accttggtct aaaggatgca ccttgtaatc tgtaatcata      1560
tttgtagtta tatattgctt tgaaaataca ctgtagacag taagacaaaa aaggaaataa      1620
aaagtacatg aattgcgaag gagaaaataa aattggcttt ggtcacagat gacatgattg      1680
gctatgtaga aaatcccag gaactgacaa aacaaacaaa caaacaaatc tagaactaat      1740
tagttctaga ttatagcaag gktgcaggat caagcttaat acctgaaagw aaattccttt      1800
cctatatacc agccmtgaac cattggaatt tgaaatcaaa atacmacacc attaatawta      1860
ttaccaaag agagagagg agamaatatg tattatgcta acaaaagang taaaaagggt      1920
atgtgagaaa aactacaaat ctctgatgaa ataaatcaaa ggagatctaa attaatggaa      1980
agacaaacta tgctaatgga taagaaaact caatcttggt atgtgtcagt tcattccaat      2040
ttgatccata gattcaatgc aatcctagaa agctactttg tggacatctg caaactgatt      2100
ctaaggttta cacgaaaagg caaaaagatg caatagtoga aacaatattg aagaagaaca      2160
aagaagtcgg actcttcttg acttcaagtc tttctataaa gctacaataa tcaaaatagt      2220
gtggcattgg tgaagaata gatagatcaa aaccaattca atggagaaa ggaaaagaca      2280
gtctttttta caaatggtgc tggaactgga gttccttatg aaaaaaaaaa aaaaagggcg      2340
gccgc                                           2345

```

<210> 19

<211> 854

<212> DNA

<213> Homo sapiens

<400> 19

ccacgcgtcc gccaccccag tcccgcagcc ggcaccccca tcccacagcc ggcactcacc	60
ccagtcctcat agccagcacc tcgatcccat agatgacacc ccgatcccgcc cccagtccta	120
tagcccgcac cccgatccca cccgagtcct gcagccggca ccccatccca cccatgtccc	180
acagtcggca cccgatccc actcggatcc ggcagccagc ttggatcctg tggccctcct	240
ccagcccca gggctcattt atatgtttta ttggcagagg ctggggctgg ctctgttggc	300
ctctgtgctg ggtttcttcc tctgcaccgc agactggctc tcctgacctc tccaggtgtc	360
atcgaacacc cttgtgcttg ctgtcaccgc ctgcctgtct gcaggatccc ggattccgta	420
tcaggggacc gaaattagtc ggaataagg aagcaggtgc tcgcttgat ggaaccctga	480
ccctgtgctc acactttagt gagggggct ctgcaggccg cctcccgga cgggaggttc	540
ccaagccact gcacttcgga gggctgttaa tttagagttgc acattcattc agttcccagt	600
aaagtagaac gtgtccagc cagttaggaa aagggtgttt taaaaattag attggccgag	660
tgcggtggct catgcctttt acctcaacac tttgggagac aaaggtggga ggatcacctg	720
tggccaggag ttcaagacca gcctgggcaa cagagcctgt ctctggggaa gaataaaaaa	780
aaaaattgag ccttaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	840
aaaaaaaaa aaaa	854

<210> 20

<211> 1450

<212> DNA

<213> Homo sapiens

<400> 20

ggcacgagat tttcttaagt acatctggct aaacatattt cctgtatgct ttggatgatg	60
gcacaataca aatacaggac tatcccttac atctggaagc acaaagtata gctttcacia	120
caaaagacaa atgcccatac atggcatttc ataacaatgt tgctcatgtt ttttactttt	180
tggacaaggg agaggctctg acagtgttga ctcatatcgt ctatccagaa aacactggct	240
tgatgttat tgtggaatct tatggcccaa aaatattaca agagagtcac gagatttcct	300
ttgaagctgc ctttggatac tgcacaaaaa ctctgacact aacattttat cagaatgtag	360
attatgagag aatatctgat tactttgaga cacagtgttc caaatagctg ttggctgtga	420
tgataaaaaa ttcattgcaa ttaaaggatt tagtaaaaaa ggatgtcatc accatgattt	480
ttcatatctg attgaaaagt catatctgag gcatcagcca tcgaaaaact tgagagtaag	540
gtatatttgg ggagaatatg gctgccctct gaggcttgac ttcacagaaa agtttcaacc	600
tgtggttcaa ctatttgatg ataattggct tgttaaagac gttgaagcaa atttcatagt	660
gtgggaaata cacggcaggg atgactatag ctttaataat actatggcac agagtgggtg	720
tttcatgaa gcacagacat ggaagtcaat gattgaactt aacaagcacc tcccactaga	780
agaagtctgg ggacctgaga actataaaca ctgtttttct tatgctattg gaaaaccagg	840
agacttaaat caaccatacg agattatcaa cagtctcaat ggtaaccata tattttggcc	900
catgggccat tctggaatgt atgtatttcg tgtgaagac ctggatccaa actatagttt	960
ctgtaacctc acagctatgt ttgcaataga gacatttgga ctgattccca gtccaagtgt	1020
ctacctggtg gcttctttcc tcttcgtcct gatgctgctc ttcttacta ttcttgtttt	1080
gagctacttt cggtagatga ggatttatag acgatataat tatgaaccac ttcacaaacc	1140
tcaaagaaaa cgtaagaaga attaggaaaa ctgaaagttt gtttattaca gatatatgca	1200
tatagagaaa cagtgtatta catagtata ttgagagggtg tgtttgccct aacatactat	1260
atataagctc gtagtaggca tcaccaaatt caagatctgg atatattctg aactatctcc	1320
taaatagaat gttttcatat atattgttat taaattaatc ctttgtttgc attcattttt	1380
aagatatata tgtacttcac atggcatgaa aaataaacta aatttgacta ttaaaaaaaa	1440

aaaagaagta

1450

<210> 21

<211> 1248

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (607)

<223> n equals a,t,g, or c

<400> 21

ggtttgtcag	acactgtttt	aggtatgagg	aaatgacagt	gagcaataca	aaggccacat	60
tctcatggag	taaaattcca	gaggtggaga	catgtaatta	atacttaa	ataaaacagt	120
agattttcta	aacgcagaaa	acggaagagt	aacaagaaac	taaatcaagg	agcattatat	180
agcctagact	gcagagactc	aatataataa	agttggcgat	tcttccta	tatcaaattt	240
actgcaattc	cagccaaaat	gtttcagtgg	ttttttttgt	ttggtgtttt	tgtttttgtt	300
ttgcccttta	gcttcacagg	tttgttctga	aatttatgag	gtataaattc	ttaagagcag	360
caagaaaaat	ttcgaatcta	tttgtagaaa	ctgcatatga	tgatggttca	taccagtaga	420
gagaaagatt	ggatttgggg	gtattactag	tagtaagggg	attcactagt	agtaagggaa	480
atgcaaaaata	aaatcacatt	gaactagtgc	aaaatcatca	cattggcaaa	agcatttagag	540
tgccaattac	tggaaagatg	tggagcaata	ggaacactca	tacggtgcta	taggaagtag	600
ttgtgtntag	cataatttgg	caatgtctag	taaagttgaa	gatgtgaata	atctttgacc	660
cagcaattcc	atgtttaaac	ctctacatak	tctctcctcg	tgtttcaagg	aratacatat	720
gatggtccat	tcgagaactg	tgagaatgag	aagttgaaag	caatctaacc	attagggttaa	780
atacaagata	gaatgcaaac	taaaatgaat	aactagagat	atttctgtca	acatgggtaa	840
acctcaaaaa	tagtattaat	gaaattgaac	tacagactat	tttatataat	acagtataac	900
gtacaatttc	aaaacatgca	aattagtgtt	atgtattttt	gtcatggcta	aatactatat	960
aaaaaggatc	taaaagaatt	aataaaataa	tcatcagatt	cagaacagtg	gtgacctgca	1020
gggagaaaga	caactgagat	tggggaaagg	atgcaaatga	aaataccttt	aattattcat	1080
ttctttttaa	aataagcaaa	tactgtatag	ccaattctta	aaatttgata	aagctggctg	1140
tgagtatatg	agtcagttct	tactctctgt	atctttctgt	ataaactatt	tcataatgca	1200
aaaaaataaa	gaatatttaa	atgaaaaaaa	aaaaaaaaaa	aaactcga		1248

<210> 22

<211> 3268

<212> DNA

<213> Homo sapiens

<400> 22

cccggtcgca	cccacgcgtc	cggctctgcgg	ccagcaacac	tggcaccccc	gatgggcctg	60
aggccccccc	aggcccagat	gcctcccccg	atgccagctt	tgggaagcag	tggtcctcat	120
cctcccgctt	ctcctactca	tcccaacatg	gaggggctgt	gtctccccag	agcttgtctg	180
agtggcgcat	gcagaacatt	gcccagagact	ctgagaacag	ctccgaggaa	gagttccttg	240
atgccacga	aggcttctcg	gacagtgagg	aggtcttccc	caaggagatg	accaagtgga	300
actccaatga	cttcattgat	gcctttgcct	ccccagtgga	ggcagaggga	acgccagagc	360
ctggagccga	ggcagctaaa	ggcattgagg	atggggccca	agcaccagag	gactcagagg	420
gcctggatgg	agccggggag	ctgggggctg	aggcatgcgc	agtccacgcc	ctcttcctta	480

tcctgcacag	cggaacatc	ctggactcag	gccctggaga	cgccaactcc	aagcaggcgg	540
atgtgcagac	gctgagctcc	gccttcgagg	ccgtcaccgc	catccacttc	cctgaagcct	600
tggggccacgt	ggcgtgcga	ctggtgcct	gtccacccat	ctgcgcgcgc	gcctatgccc	660
ttgtctccaa	cctgagccct	tacagccacg	atggggacag	cctgtctcgc	tcccaagacc	720
acattccact	ggctgccctg	ccactgctgg	ccacctcatc	ctcccgtac	cagggcgcgc	780
tggccaccgt	cattgcccgc	accaaccagg	cctactagc	cttcctgcgc	tcacctgagg	840
gtgccggcct	ctgtgggcag	gtcgcactga	ttggagatgg	tgttggtggc	atcctgggct	900
ttgatgcact	ctgccacagt	gctaacgcgg	gcaccgggag	tcggggcagc	agccgcctg	960
ggagcatgaa	caatgagctg	ctctctccgg	agtttgccc	agtgcgggac	ccctggcag	1020
atggtgtgga	aggcctgggt	cggggcagcc	cagaaccctc	ggccttgcc	ccccagcgca	1080
tccccagcga	catggccagt	cctgagcccg	agggtctca	gaacagcctt	caggcagccc	1140
ccgcaaccac	ctcctcctgg	gagccccggc	gggcaagcac	ggccttctgc	ccaccgcctg	1200
ccagttccga	ggcacctgac	ggccccagca	gcactgcccg	ccttgacttc	aaggctctctg	1260
gcttcttct	cttcggctcc	ccactgggcc	tgggtgctggc	tctgcgcaa	actgtgatgc	1320
ccgcctggag	ggcctggcta	cagaagggga	acctgaggcc	cagaaagaag	ggactcgcca	1380
aggcagccca	gatgcgcccc	gcctgtgaac	agatctacaa	cctcttcac	gcggccgacc	1440
cctgcgcctc	acgcctcgag	cccctgctgg	ccccgaagtt	ccaggccatc	gccccactga	1500
ccgtgccccg	ctaccagaag	ttccccctgg	gagatggctc	atccctgctg	ctggccgaca	1560
ctctgcagac	gcactccagc	ctctttctgg	aggagctgga	gatgctgggt	ccctcaacac	1620
ccacctctac	tagcgggtgc	ttctggaagg	gcagtgaagt	ggccactgac	ccccggccc	1680
agccagccgc	cccagacca	ccagtgaagt	ggttaagatc	ctggagcgct	ggtgggggac	1740
caagcggatc	gactactcgc	tgtactgcc	cgaggcgctc	accgcttcc	caccgtcacg	1800
ctgcccacct	cttccacgcc	agctactggg	agtcgcgccg	cgtggtggcg	ttcatcctgc	1860
gccaggtgat	cgagaaggag	cgccacagc	tggcggaatg	cgaggagccg	tccatctaca	1920
gcccggcctt	ccccaggag	aagtggcagc	gaaaacgcac	gcaggtaag	atccggaacg	1980
tcacttccaa	ccaccggcg	agcgacacgg	tgggtgtcga	gggcccgc	cagggtgtaa	2040
gcgggcgctt	catgtacggg	cccctggacg	tcgtcacgct	cactggagag	aagggtgatg	2100
tctacatcat	gacgcagccg	ctgtcgggca	agtggatcca	ctttggcacc	gaagtcacca	2160
atagctcggg	ccgtcacct	tcccagttcc	cccagaacgc	gcgctgggca	ttggtgtcta	2220
ccccgtgcgc	atggtggtca	ggggcgacca	cacctatgcc	gaatgctgcc	tgactgtggt	2280
ggcccgcggc	acggaggtg	tggctctcag	catcgacggc	tccttcaccg	ccagcgtctc	2340
catcatgggc	agcgacccca	aggtgcgagc	tggcgccgtg	gacgtggtea	ggccggccgg	2400
atatgcagaa	gcaccgcgtg	gtggcatggc	tgtcgcagca	caacttcccc	cacggcgctc	2460
tctcctctctg	cgacggcctc	accacgacc	cactacgcca	gaaggcaatg	tttctgcaga	2520
gcctggtgca	ggaggtagaa	ctgaacatcg	tggccgggta	tgggtctccc	aaagatgtgg	2580
ctgtatacgc	ggcgtgggg	ctgtccccga	gccagacctc	catcgtgggc	cgtgccgtgc	2640
ggaagctaca	ggcgcaagtgc	cagttcctgt	cagacggcta	tgtggcccac	ctgggccagc	2700
tggaaagcggg	ctcgcactcg	catgcctcct	cgggaccccc	gagagctgcc	ttgggcaaga	2760
gcagctatgg	tgtggctgcc	cccgtggact	tcctgcgcaa	acagagccag	ctgcttcgct	2820
cgagggggccc	cagccaggcg	gagcgtgagg	gcccgggaac	accacccacc	accctggcac	2880
ggggcaaaagc	acggagcatc	agcctgaagc	tggacagcga	ggagtgaagg	ccacaccagc	2940
ctggacctgg	gttattttatt	gacacacca	aggggcccga	ggggctgcgt	ttgggaggct	3000
ggggacccag	acttttgccc	ccagcgtg	ccccccagc	cccacacct	atatctccgt	3060
gtgctcctcg	gtgttacttc	cctttcatat	gaggggaccc	agcgcggggg	ggagggagga	3120
gggcgtgggc	atgggcgcag	aggcttttcc	agtgtgtata	aatccatgaa	aataaacgcc	3180
acctgcaccc	aaaaaaaaa	aaaaaaaaa	aaaaaaaaa	aaaaaaaaa	aaaaaaaaa	3240
aaaaaaaaaag	ggcggccgct	ctagagga				3268

<210> 23

<211> 1673

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (515)

<223> n equals a,t,g, or c

<400> 23

tctccggata	actgtgctcc	tgacatcctt	ccttatgggt	ttgggaactg	gtctaagatg	60
catacctata	tcagacttaa	tccttaaaaag	aagattaatt	catggaggac	agatgttaaa	120
tggattggca	ggtccaactg	taatgaatgc	agcaccattt	ctctctacga	cgtgggtttc	180
tgcagatgaa	agggccacag	ccacagctat	tgcatcaatg	ctcagttatc	ttgggggagc	240
atgtgcattt	ttagttggac	cacttggtgt	tccagctccc	aatggacatc	acctcttctt	300
gctgcagaga	gcagcagggc	gcatattaaa	gatcgcatag	aggctgtgtt	atatgcagaa	360
tttggagttg	tctgcttaat	atcttctgca	acactagctt	atttcccacc	cgcacctcct	420
cttctcctcc	gtgttgctgc	agctagccag	cgtgagttat	cggagaagcg	tttgtagatt	480
attaagcaat	tttcgatttt	tgatgattgc	tttanatatg	ccataccact	tgggtatttg	540
ctggctggtc	tggagttctg	gacttaattt	taacaccagc	gcatgtcagc	caagtagatg	600
ctggctggat	tggatttttg	tccatagtgt	gaggctgtgt	tggttggaata	gctatggcaa	660
ggtttgcaga	ttttatcagg	ggtatgctga	aactaattct	tctcctcctg	ttttcgggag	720
ctacactgtc	atccacgtgg	ttcacctga	actgtttgaa	cagcatcaca	cacctacctt	780
taaccacagt	gacattgtat	gcctcctgta	ttctcctggg	agtgttcttg	aatagcagcg	840
tgcctatat	ttttgagctt	tttgtggaaa	ctgtctaccc	agttccagaa	ggaattactt	900
gtggagttgt	cactttttta	agtaatatgt	ttatgggagt	acttttattt	tttctcacat	960
tttatcatac	agagttgtct	tggttcaact	ggtgccttcc	cgggtcgtgt	ttgtcagtc	1020
tctcctcat	tctgtgcttc	agggaatcct	atgacagact	ctatcttgat	gtggttgtct	1080
ccgtttaata	gcacagactt	gaaggagttt	aaaaggaggc	tggaaatcaa	tactgcacac	1140
tgcacatttg	ctcagaattg	cacatctaac	aggaaaagag	ggagaagaaa	gaaacttcat	1200
tcagaggttt	tgtaggtta	cagattatca	cattaattta	attactacta	ggtaataata	1260
atgggagact	tgagtataa	taggggattt	taaaactcta	cagatggcat	acctgtgcct	1320
gcttctgggg	ttggaagtgt	gacttcttac	acataaagca	ctacctaaagt	aattctctct	1380
ctgttttggt	ccagtgttaa	actactgatt	acttgtaatt	atgaaaagaa	ataaagggtg	1440
tctatcatat	gaagataacg	ccttccttaa	gtcacataat	agaataggaa	gatatgccac	1500
taacttctaa	agaagttcaa	accctgtatc	caattttta	gataaaatag	ccaagaggta	1560
tatcgatgat	ggaaattagc	cacatgtaca	ctacattttt	tctaataaa	ccatttctta	1620
tatgaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaa	1673

<210> 24

<211> 946

<212> DNA

<213> Homo sapiens

<400> 24

ggcacgagt	cagacgtgg	tctggttcct	gctcaccctg	ctgctggcgc	tcttcatccc	60
tgacatcggc	aagggtgat	cagtcattgg	aggcctggcc	gcctgcttca	tcttcgtctt	120
cccagggctg	tgctcattca	agccaaactc	tctgagatgg	aagaggtcaa	accagccagc	180
tggtgggtgc	tggtcagcta	cggagtcttc	ttggtcacc	tgggagcctt	catcttcggc	240
cagaccacag	ccaacgccat	ctttgtggat	ctcttggcat	aaccactgcc	tcccagggaa	300
cacaaggcct	ttgccattgg	tcgcaggaac	ccatctctta	gagctatggg	gccattctta	360

gtccacgac	attccaactg	gtgggatgac	atccggacat	cctcttccag	ggactggggc	420
aaactcaggc	cccacacctc	tggacagctc	aatccagtc	ccctctcctg	ctccccagtc	480
ctggcagtg	cgtggatggc	ggcaggaagt	ctcacatcaa	ggaggacccc	tcctcctctc	540
ccagttctca	actttctcat	gcctggaatc	cacgggtgaa	gagagtcggg	agatctcata	600
agaaagaatc	cagtctgact	tccctctgga	gaatgactat	ggacagaagg	ccaccatcct	660
ccacagagca	ccctgtcctg	agtaggggtt	gtgctcatta	ccccaggcca	gtggtagctt	720
cctcaggagc	ctggccactt	ccaacggtag	cactgaagtc	atgcaaagtc	atagtcaggt	780
agattcagac	cttgtccaca	ccttcctggg	caacccccac	catgaacctg	tcagcctctt	840
tcccatagct	aatagacatt	tcccaggcct	taaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	900
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaa		946

<210> 25

<211> 621

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (616)

<223> n equals a,t,g, or c

<400> 25

attcggcacg	agggaggaaa	gaggggtggaa	tctggacagt	atgaaggatt	tgtattgtac	60
ctgtaatgtt	tgatgtctga	agctgggtgg	tgggcatggc	tgtttggtat	tctccatcct	120
tttggtatgc	ctgatacatt	tcataataat	tttaaaaagg	acaagactac	tgcagagaaa	180
tgcataagag	gagctctgtt	tgggttttta	aaatgattcc	tacatctatg	cttgcatag	240
taagcaccag	ccctggaaaa	cattgcaagg	gattccttag	aggcccaagc	tttgggaaa	300
ggccaagggg	gctggggagt	tgattaggag	gggatacatg	ctttttcctg	ctgccttttg	360
aattttgtac	cacacgtagt	attacttatt	aattaaaaaa	taatctgaac	tagccaggcg	420
tggtggcaca	tacctagtct	cagttacttg	gaaggctgag	gcaggaggat	cacttgagcc	480
caggtgggtg	cggccagcct	gggcaacata	gtgagaccct	gtctcttttag	aaaaaacagg	540
ccaggcatgg	tggctcacac	ctgtaatccc	agcacttttg	gaggctgagg	tgggtggatc	600
acctgaggtc	gggagntcga	g				621

<210> 26

<211> 1736

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (369)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (605)

<223> n equals a,t,g, or c

<400> 26

gaattcggca	cgaggaggcc	ccacaatgtc	ccccaaactgc	cacttgctgg	agaccagacc	60
ctcagcctcc	ctgtctctgc	tgggcatccc	tctgctcagg	ggagcatctt	gaggctatac	120
aggtctcagg	tgcagctggc	agcaaagaga	cataggagga	ggtggttgaa	cccaccctgc	180
aatgtccaag	gtccagggtta	aaccctgaga	gtgggtgagt	gtgtctggtc	ctgtgactca	240
gtttccctac	ctgtaaaaca	gagcttcaac	gagatgaacg	atagtcctga	gcataacagt	300
ccacaggggc	ccacgagccg	cttctgcgtc	ccaagccctc	gtttctgcat	ccwgtctyca	360
tctgctcanc	tctgaatgaa	cccatgggtc	cctggaggac	takgtgaaga	aataccctaa	420
acacctcccc	aggcatcgag	ctcatgcctc	cagcacaagg	cctggggctg	taacgcaggg	480
agctgggctc	cagcttgaat	gctgctctty	ctttctttct	ttttttttaa	aaggggtgaa	540
atccacataa	cacaaagtga	accactttaa	agtgaacact	ttcatggcgt	gtggtacatt	600
cacanattca	tggatgctcg	tctcctatac	ctgagctata	tctgcctgt	cacaattcca	660
taggaagtaa	aaccagccac	tttctgtaaa	tgggatctta	agcagaactc	taacactgtg	720
cacaraaagt	gtgactgtgc	tgggttcgag	gaaracaggg	tctggtctgt	gtccccagcc	780
gaatctcatg	acaaattgta	attcccacg	tgaaggarg	gamctgggtg	gaartgatgg	840
gatcatgggg	aargattttc	ccctcgctgt	tctcatgata	gggagtgcgt	tctcgtgaga	900
tctggtggtt	taaaattgtg	tagtgcttcc	cctcctttct	ctgtctctct	cccgtctgac	960
cgtgtgaggg	ccttgcccac	tcccccttca	cctgcgtcat	gattgtaagt	ttcctgaggg	1020
ctccccagcc	acgytcctg	caaagcctgt	gaactttgag	ccaattaaac	ctcttttctt	1080
tataaactac	gcagtcctaa	ctaaagaaag	gcagttcttt	atagcaatgt	gagaarggac	1140
taatacggag	aagggccacc	tgtcctttca	aaggccccgc	ccaggaccct	ttgaaaccag	1200
agcgtccagg	tgccctctcg	gatgttttct	catctcggga	gtcctgtggt	tttaacgttc	1260
ttttacgatc	acacctctag	agagtgtgta	ttccctggat	accacaggac	ctccctgagg	1320
tgtccaggac	agagcaagct	tagatattag	gcagaggttc	taggagctgt	gcacccttgc	1380
acccctggac	cagagagtct	gggtgaggaa	gtgggggcgg	gatgtggggc	ctgatctctg	1440
ggctgctgac	cacagaaaag	gtcacaccg	ggaagtggac	ttgggcctgt	ccagggcagt	1500
tccggggcag	aaatgggagc	tggagatgtt	tgtggctgtt	cccgtgagga	tgctccagcc	1560
ccaggaggcc	gtcggggaga	ggccggtgct	gtgtggaacc	acacatgtgt	gagccagtca	1620
ggagactgct	gtgtcagtca	ggaaaggcca	acacagtgca	ctgtcctcac	actgggagga	1680
ccggcttccc	acccactcc	agggctttgt	ggtaagcctg	acgcacccca	ctcgta	1736

<210> 27

<211> 1803

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (18)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (24)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (46)

<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (106)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (1788)
<223> n equals a,t,g, or c

<400> 27
caccctgggc gcccaatnec caancegctt ttccccggcg cgttgncgga ttcattaatg 60
cagttggcac gacaggtttc ccgactgaaa gcggcagtga gcgcancgca attaatgtga 120
gttagctcac tcattaggca cccaggtt tacactttat gcttccgggc tcgtatgttg 180
tgtgaattgt gagcggtac caatttcaca caggaaccag ctatgaccat gattacgcca 240
agctctaata cgactcacta tagggaaagc tggtagcct gcaggtaccg gtccggaatt 300
cccgggtcga ccacgcgtc cgcttcata catggaaagt gtctttgaag aagtatttaa 360
actgctggag tgccctcacc tgaatgtgcg gaaggcagcc catgaggctc tgggtcagtt 420
ttgctgtgca ctgcacaagg cctgtcaaa cgtccccctc gaacccaaca ctgctgcttt 480
gcaggctgcc ctggcccagc tcgtgccatc ctacatgcag gcagtgaaca gggagcggga 540
acgccaggtg gtgatggccg tgcgtggagg cctgacaggg gtgctccgca gctgtgggac 600
cctcacactg aagccccctg ggcgcctcgc tgagctctgt ggcgtgctca aggtgtgct 660
gcagaggaag acagcctgtc aggatactga cgaggaggag gaagaggaag atgatgatca 720
ggctgaatac gacgccatgt tgcgtggagc cgctggagag gccatccctg ccttggcagc 780
cgcggtctgg ggagactcct ttgccccatt ctttgccggt ttcttgccat tattggtgtg 840
caagacaaaa cagggctgca cagtggcaga gaagtccttt gcagtgggga ccttggcaga 900
gactattcag ggcctgggtg ctgcctcagc ccagtttgtg tctcggtgc tccctgtgct 960
gttagcacc gcccaagagg cagaccccgga ggtgcgaagc aatgccatct tcgggatggg 1020
cgtgctggca gagcatgggg gccaccctgc ccaggaacac ttccccaagc tgcgtggggt 1080
cctttttccc ctctggcgc gggagcgaca tgatcgtgtc cgtgacaaca tctgtggggc 1140
acttggccgc ctgttgatg ccagtccac caggaaacca gagccccagg tgcgtggctgc 1200
cctactgcat gccctgccac tgaaggagga cttggaggag tgggtcacca ttgggcgcct 1260
cttcagcttc ctgtaccaga gcagccctga ccaggttata gatgtggctc ccgagcttct 1320
gcgtatctgc agcctcattc tggctgacaa caagatccca ccagacacca aggcgcact 1380
gttgcgtgc ctgacgttcc tggccaaaaca gcacaccgac agctttcaag cagctctggg 1440
ctcactgect gttgacaagg ctcaggagct ccaggctgta ctgggcctct cctagactgc 1500
aggctgcagc cagtccagag agaataagagc ctgcccaggc cttaagacca cctctcagcc 1560
cagttcagtt ctgccttacc aaagattctg agactcatat ccatttgag ccagccccac 1620
ttgctgcctt acagggctgt ccctgaggct ggatctgtta caaatgagtc atgacatcat 1680
actgtaataa aagcagcttg ttttctgctt gaacaataaa aaaaaaaaaa aagcggccgg 1740
tctagaggat ccaagcttac gtacgcgtgc atgcacgcac agctcttnta taggggacct 1800
aaa 1803

<210> 28
<211> 2287
<212> DNA
<213> Homo sapiens

<400> 28

tggaacgaggt ggaattgctg gatctggaga gcgtagcgcc tggcgggacg aggacgacta	60
cacctgggta tacattggct cttcaaagac gttcacctca tcagagaaat ccctgactcc	120
tttgacagtgg tgtagacatg tcctagataa cccaactcct gagatggaag cagcgagacg	180
ttccctgtgc tttagactgg agcaagggtta cacttccagg ggctccccac tcagtcccca	240
gtcatctatc gacagtgagc tgagtacttc agaattggag gatgattcta tctccatggg	300
atataaatta caggacctca ctgatgttca gatcatggct cgtctgcaag aagaaagtct	360
caggcaagat tatgcttcta cttcagcatc tgtatcaaga catagttcca gtgtgtcatt	420
gagttcagga aaaaaaggga catgtagtga tcaagaatat gaccaatata gtctggagga	480
tgaagaggaa tttgatcatt tgccaccacc tcagcctcgt cttccaagat gttccccctt	540
ccaaagagga attccccatt cacagacttt ctccagcatt cgggagtgtg ggaggagccc	600
cagttcccag tattttcctt caaataatta ccagcagcaa cagtattatt cacctcaagc	660
ccaaactcca gatcagcaac caaataggac caatggagat aagctccgaa gaagtatgcc	720
taacctagcc cggatgccaa gtacaactgc cattagtagc aacattagtt ctccggtcac	780
cgtgcgaaat agtcagagtt ttgactcaag cttgcatgga gctggaaatg gaatttcaag	840
aatacaatct tgtattccat caccgggaca gcttcaacac aggggtccaca gcgtggggca	900
tttcccagtg tctatccgac agcctcttaa agccacagcc tatgtgagtc caaccgttca	960
aggcagcagt aacatgcctt tatcaaacgg ctacagctg tattccaaca caggaatccc	1020
cacaccgaac aaagctgcag cttctgggat aatgggtcgc agtgactcc caagaccttc	1080
gttggcaata aatgggagta acctgcctcg aagcaaaatt gcacaacctg ttagaagttt	1140
tcttcagcct ccaaagcctc tgtcttcaact cagcactctg agggatggaa attggagaga	1200
tggttgctac taatgcagtt ttatgtaccc ttgaaaaatg ggaaagaagt aaaaatgagg	1260
gttgtgttac ctagctggct gggtagcagt ggatgttggg atattctttc ccttttgtgt	1320
tttaatatat ttactgcatt gtttctcaat ggaccagtca ccagagacta attattgcac	1380
ttaaatatat gcctgagata ctgcaacatt ctcaaaccca tgggtgcagt attgtgacac	1440
ttagatctag gaagtttttg tagaactgct ctgtacctga atactttttg agagaattaa	1500
gatgtatcaa taatgccttg ccatatgagt tttttaagt aactgttca atttactcac	1560
gtgttctaaa catctttcca ttacatgttc tgtattttaa tacattgcat attgacaact	1620
aggttctata atgtatgctt tgaaatttac tttttatag ttacaggaa ttttattttt	1680
tgtgcctatt tctttttaca cctatgtgaa ccactatgga acaacttaaa ttttgtgcca	1740
taaaaatatt tttgtggtaa ggtactatth ttttagctct agggatata cagcaaaaac	1800
acatcatgca atttgagaca cataattttg tgttgaaatg gcacaacata atttgaagca	1860
ttgcaaggag atarccagac agcagaatta aatggctcctg tctttttcat ttttaattta	1920
ttgtcataca tgggtttcat atttataacg gcacatgag ctcattgcac ttaatacctg	1980
caatgtttgc tactgtacca caattgattt tcaatacttt attacgaagg atgaaactgt	2040
aatgttttat taacaatgct tctggaaatg aatgcatttt aaagcaaata aatctttttg	2100
atagaccttt tacaaaatcc atttgacta atgaatgctt tcttatggca tataacttaa	2160
tatttgttac tgtgtacact gctgttttgg aatgttcaga aataaagact ctatttcagc	2220
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaggg	2280
cggccgc	2287

<210> 29

<211> 927

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (883)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (912)

<223> n equals a,t,g, or c

<400> 29

gcttcacg	ggaacaagg	tggttactga	atgtggagaa	gtcagtga	tctccacagt	60
gacagatgca	ctctggagat	ggggctgagg	ctaggtgtgc	acctcccctg	ccagccatca	120
gcagcctgcc	cacgtctgtc	gcgttatgag	ttgttgatct	taaatttctg	caaagtgttc	180
ttgttacaga	gtatggtgtt	tgcrataaact	tgcggaagct	ggagatcaca	ggcgtgtctt	240
gtcgggacgt	ctatgcgaag	cgtattaaac	cctcgcgtga	agtcgggacg	ttttgtgaaa	300
attctcccctg	attatgagca	catggcgtac	agagacgttt	acacctgcct	gcttcaccga	360
tatagacaca	ttttgggatt	gtggcagcca	gatatacggtc	catacggagg	actgctgaac	420
gtggtggtgg	acggcctgtt	catcatcgta	atgaggcgtg	cgccgccaat	atgcactgta	480
cattccacaa	gcattgcctt	cttattttac	ttcttttagc	tgtttaactt	tgtaagatgc	540
aaagaggttg	gatcaagttt	aaatgactgt	gctgccccctt	tcacatcaaa	gaactactga	600
caacgaaggc	cgcgcctgcc	tttcccatct	atctatctgg	ctggcaggga	aggaaagaac	660
ttgcatgttg	gtgaagggaag	aagtgggtg	gaagaagtgg	ggtgggacga	cagtgaatc	720
tagagtaaaa	ccaagctggc	ccaaggtgtc	ctgcaggctg	taatgcagtt	taatcagagt	780
gccatttttt	ttttgttca	aatgatttta	attattggaa	tgacaaattt	ttttaatatg	840
caaataaaaa	gtttaaaaaac	ttataaaaaa	aaaaaaaaaa	aanccccggg	gggggccccg	900
gwaccaattt	cnccccaaaa	gggagcc				927

<210> 30

<211> 3287

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (1412)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (3169)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (3246)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (3273)

<223> n equals a,t,g, or c

<400> 30

atagtccttt	ctatttttca	tctgtcatca	gtgggagggt	gtaagccatt	gctttcagaa	60
------------	------------	------------	------------	------------	------------	----

cagaatcggc	agtgtcgctc	acagtctttc	tactaaacca	gttgcattct	acagagcagc	120
gtggatgagt	gctaagaacc	ggctgtgtga	ccttcagcaa	ggactttctc	accacaaaaa	180
tagagttgcc	caaagtcagg	cagaggtgat	aatgtgtaaa	agtgactggc	tccaggcaga	240
cttgtagtga	acattgtttt	tcttccttcc	tgctagaaat	gagtataatt	ttagacttat	300
gttttaggtta	tgaagagcaa	attgaaaaga	gcacaggggt	tccagaccag	gagtctggag	360
tggcatttat	gagagcctgc	cctgaaatgg	cactcagtgt	tgtcctaagg	tcgcatggcc	420
tctgtggggc	atgggtgggc	tcagtggggc	tcagggctct	cagtcataaa	atgggaatgt	480
ctaccctaac	cacctctcaa	ggccattttg	agaacagatg	gccaatttac	ataaaagcat	540
actatagatg	taaagtaacg	tcatacggct	tcattcatcaa	cccctacatc	tatatgcttt	600
aactgtttta	gagtacattg	atctcataga	atgttattgc	ctcaaaaata	tccgtttatt	660
ttcccagaaa	ttaagaaaag	ccatgaaata	gaaaagaaat	cgcttgaaga	tttactttct	720
gagaagcagg	aatcgctaga	gaagcaaatc	aatgatctga	agagtgaaaa	tgatgcttta	780
aatgaaaaat	tgaatcaga	agaacaaaaa	araaragcaa	gagaaaaagc	aaatttgaaa	840
aatcctcaga	tcattgtatc	agaacaggag	ttagaaaagc	tgaagctgt	gttagagatc	900
agaatgaga	aactgcatca	acaggacatc	aagttaatga	aaatggagaa	actggtggac	960
aacaacacag	cattggttga	camattgaag	cgtttccagc	aggagaatga	agaattgama	1020
gctcggatgg	acaagcacat	ggcaatctca	aggcagcttt	ccacggagca	ggctgttctg	1080
caagagtcgc	tggagaagga	gtcgaaagtc	aacaagcgac	tctctatgga	aaacgaggag	1140
cttctgtgga	aactgcacaa	tggggacctg	tgtagcccca	agagatcccc	cacatccctc	1200
gccatccctt	tgcagtcacc	aaggaattcg	ggctccttcc	ctagccccag	catttcaccc	1260
agatgacacg	tccccaaagt	ccacagactc	tctgaaagca	ttttgatgca	ggctctgcagg	1320
actgacccca	aggaggaacg	tgggcacaa	aggtatatca	gcacacgtgt	gatcaccgta	1380
ggtaactgga	gcgtcaccac	cggcggaatc	gnagcttctg	agactggaag	tctggaggaa	1440
gacttttgcc	tccgtccaaa	agattcctcc	aaaaaaagat	ttaaaaaaag	atttcggcat	1500
cgacacggac	gttgttgac	aaagcactta	aagaacgaga	gcattctgtt	cattgccttt	1560
ttcacctaag	cataagggga	aaaactctca	gggccctatt	aagatttata	acctttgtaa	1620
gtttcttcac	cacagacacc	ttcttgtgag	tttctagtct	gactgtgggg	gtgggggggtg	1680
tgaatgaaat	ggatgtcaca	gagtgtcatg	tgtctgatgc	agcctcctct	gctgtgtatt	1740
aaatgtcaaa	atctgaatat	atctggatat	gtactaatca	aataataatc	aatcaatcag	1800
catatacatt	tcagccaaag	ccatagaaga	aaaagcaata	gttgcttgaa	ttatgatcat	1860
ctaccaccaa	cctgtctcag	ccctgtaaca	gggtagggag	aggtataaac	aggaagagct	1920
ttgacttgtc	cctgtctata	cattctctgt	atcttttggg	ggtaacttct	tggcagtttt	1980
tcagtgttca	gccatgtcag	ttgaaactag	atttttctgt	agatttttta	cttaccctatg	2040
tgagcctaac	actatcctgt	aattcatttt	ctcaggctat	gtgtaaagt	agaaccctaa	2100
ttttcttata	aaaaaacaaa	ctaactaact	gtgtaaagaa	agaaaaagg	aagtaccaat	2160
gggtttttcc	accttatatt	tacctttgat	ctacccttgc	agatttaacc	tgtcttcttc	2220
cctcccatia	ttctcatttt	ccttttacct	ttctccacca	tccagagcca	caaaagcaaa	2280
ccttctacct	cctacctact	ttctctggg	acaaggataa	aggaatatga	ttttccagag	2340
ccccagagcc	agctcatctt	ccaggtgctg	aaaccacttt	ccaaataaac	taaagcctgg	2400
atttgatatt	acaaattttg	ggaaatctta	gaataaagaa	cgagaacaag	gaagtcattg	2460
gctagtataa	ttaagaaagg	taggattcag	tgtttaccga	tgatgcagta	cttgatagaa	2520
gaaaacagtc	tgggaggata	gcgtcatttt	ttcagttacc	ctttaaggag	tccctttgtc	2580
tttgggaaa	tagcagaatg	gtccgcttct	ttcccatgag	tggaaaatgt	ggcttgtcca	2640
actctcctcc	aggttgcat	tcagtttctt	tccaaaactt	attacctccc	ctaactctga	2700
gactttggaa	aaggtggaag	gaagaactgt	tgttttatct	ccccctccct	gcattgtgtca	2760
acattgtgat	gtcagtatct	actaatctac	attcagtggt	tgtacaaata	acagctgtag	2820
taagaagaga	ttcaggatgc	tagaggtgaa	tatttggtgc	atttacctgt	acactacata	2880
gcaagttgat	actcatgttg	catgttcttt	taaattagtg	attttgtgtc	ttaagtcttt	2940
aacttccaat	acttcatcat	gtatgtaacc	ttccatgttt	gcttctgata	aatggaaatg	3000
taggttcact	gccacttcat	gagatatctc	tgtcacgct	tccaagttgt	tctcaatgac	3060
attagccaaa	gttgggtttg	ccattcatcc	cctagggcat	gggtaaatct	tgtgttgttc	3120

cctgctgtcc	tccgtattac	gtgaccggca	aataaatctc	ataggcagnt	taattataaa	3180
acmtcttttg	gaggggtggg	aggaggacag	gaggggaagk	tggggggaam	caaattaggg	3240
gattcnttaa	gggatttttg	ttttaaaccc	aangttttcc	tgtaggg		3287

<210> 31

<211> 5083

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (5079)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (5080)

<223> n equals a,t,g, or c

<400> 31

ctcgagtttt	tttttttttt	tttttatgga	attactgatt	ttaatttttg	ctttattaaa	60
tgttctcatt	tttctatcat	gagaatagat	tactatatcc	aacaaaaggg	agggacagaa	120
agaaaagaat	taacaaataa	tctcattgca	atcgctactg	catacctaga	agctaactgg	180
taatacacac	ttgcctaaga	actaacaat	caattcaaca	gacacttcaa	aagaacccat	240
gttacaaggc	atcctatgca	tgggacgaat	gcaaagtccc	acctacaatg	tcacttatcc	300
ccagattccc	catctaataa	aaattttcta	tcttcccaca	gcacatgcct	tgcttctaac	360
agacaattat	tgratgraaa	aawtwaaagc	aagtacctta	gtamcatgaa	tcacaaaagc	420
aatgtattct	gaacctgaaa	ytgacaatta	caaaacaaat	gctatcctgg	gaaaagcatt	480
tcctagacaa	tacctggagg	ccaactggca	ttgctggatt	tacttccgat	tttatttggt	540
ggtggagatt	tggcaggtaa	ccagctatca	ccagcaggac	ccgtatggcc	accagtggtg	600
tcaccaggga	tgatatcaaa	ctggttgtag	ggtgaccctc	cccgggtttt	accaggggce	660
actatagcgc	catttttgtg	catattggct	tctgtgtggt	ctacagaggg	cagcccctcc	720
atcatggagg	tccactgttt	aaagcgagac	tcggttccag	cctccttccc	accaaccatg	780
ccatagtcca	tgccgccaga	gctgaagcca	gaaccatata	caggtattgg	ccctttgggt	840
tgaagggtctg	ggagccccac	attcaatgcg	ttgggtacca	tgtgtgccag	atgcggcttg	900
ggcccaacag	gatgagaggg	cgagtgcctc	atgcctgggt	gcctctgctg	ctgctgctgc	960
tgctgctgca	gtgcactcac	cattcgagcc	agctgctgct	cttgcctgtt	gcgtacagct	1020
tgagaaatct	ttctctgggt	ctgtaacaac	tgctgctggt	gctgctgctg	caagagaagc	1080
tgacatgcc	actgaaactg	gggaatttgt	ggaagctggc	tcagcatggc	aatttggtga	1140
ggagataact	ggggccccac	attgaaaaga	cctggactca	ggccactggt	gggaaactgc	1200
ttgagcattg	aggcagaaac	ctggggggaa	ataaactggg	gaggcacttg	cgcccgagga	1260
ctgggagaag	aatttagtggt	ctgcacgggt	gtgtgcagac	ctctcgattg	tgctgtgctg	1320
tttccaaaca	aaccatgact	accgcccttc	tyaaaataag	gccactatc	tgtgggtccc	1380
atgtcttttg	aattaggtgg	acggaaccca	gatcgatcct	tcctcatgat	atcattaaaa	1440
tccccgagat	tcatogetcg	cttgtccaca	tcaaatTTTT	tatctgaaag	gcttccctaca	1500
gacaaatcca	ttttgctgct	tggattatct	tcagtctgac	tcagcaatcc	catatttgaa	1560
aactgttttg	caagaggatt	catccatgaa	tcattgtttc	ctcctttgag	tgagcacttc	1620
atttgtttct	ttcctccttg	tccccagctt	gctgagttgt	gggaggaagc	actgccctga	1680
gagccagtgg	tgttccagac	tcctccatcc	tcctcctctt	cccagctggg	atggcgagct	1740
cctgtgactg	gcccgteact	ctccccccag	ccgtcttgca	tagatttgga	attaggtctc	1800

atggcattgg	gagcgttggc	gggcgtgttc	ccccagcctg	tggtcgatgc	tcctgtatca	1860
tccatctcgc	cccacccagg	actgctttca	tttggtctac	cccaagcgga	agtaccatta	1920
tctggagcag	gtggtgtgct	tttgctccag	actgatgccg	atttactggg	cattgggggtg	1980
ggcaggtttg	gttctcgagg	tgctgggccc	ccttggggaat	tcttatccca	cagattcaca	2040
ttctttagt	tataactggt	agggctctcc	catgctgaag	tgccatcatc	aatgtccatt	2100
ttccgactaa	ttgactgtgg	ggatggctct	tcccaaccac	tggtgtcctc	atccttargt	2160
gttgacaggt	gtggcccgcg	gctycagctg	gaattggaag	gtcgaacggt	gcctggagggt	2220
ggtggkgtg	ggcctcccca	cgaaccagaa	gcctctgggt	gtggtggcgg	cggtgtctgt	2280
gggggctgct	gctgttgggt	ttgtttatyc	caggaawtgg	gctgtcggcc	cgtctcattc	2340
catgctgggg	atcttttgca	atcctcccac	ccaccttttg	aagctagggt	tgcatcgcca	2400
ccattacccc	aagtcccgat	ttcattctgc	cctccttcac	cccacccaga	cacaggttta	2460
cttgacagaac	tttcccaatt	gctgtttttt	gtctgatcga	cttcctcccc	ccaaccattc	2520
ttccacagaag	ccatccttga	ttgggtgggc	gtccacctcc	ccacccctga	tccttgctgg	2580
gattctcatt	ccaagaggaa	ggtgtctttt	catcaggctg	tcctcctccc	cagttggaag	2640
agttgttgtt	cttgtagtca	ttccagcctc	ctgtgttctt	gggtcttttc	cactctgtag	2700
aggtctgagag	ctccccccat	ccagacttca	tttgattgct	ttggctgggt	gcattctccc	2760
agccccctga	gttcttgggc	tgtgtggcag	cgctctccca	ccccctcagt	cctttgtcag	2820
atttccccct	aggccttggc	acctcttcaa	tgtcccacac	tgtgtcctgc	ttaatttgag	2880
tttgggcccca	gccagtgttt	gagagcacc	tggtgtccaa	atcagttcgg	ctcaaaagag	2940
tctgcaagac	agcctgacaa	tcaggatgtg	tggtgctgta	cgaccgacgg	ccagagttat	3000
gactgtcact	acttctgtct	wtgtggttgc	ttccagtgtc	ttgacctcca	acttcacttc	3060
ctgtgragct	ggaagatctt	ccccaacagg	gagcctgggc	attgccttgg	ttttcagggg	3120
gggggtggcc	cttttgattg	tcccatgtct	cagtgtctaga	atttggttgg	tttgaccac	3180
tccattctcc	aattttcaac	tcattcagacc	cagtctggctg	tttccattct	ccctgagaga	3240
ccccagatgt	cattttgttc	ccttcacccc	atttgttgtc	attagagtcc	tggtggccaa	3300
agttccaggga	cccaccgcta	gacctgttat	tgtgttccca	agagtcattt	tttgaccacg	3360
ttgatttctg	aacagaagct	cctttccagg	agtcctctct	ctcttttcca	ttgttcccat	3420
tgtttccaga	attgctttgt	ccagagactg	wgycagttcc	agaaggcccc	ctagctgcac	3480
cccaagatcc	aacactccca	gtctttcgat	ctccagtgtc	ttgtgaaggg	gcattcagtc	3540
tcctggagggt	gttccccaag	cccattccaa	agggcattcc	cttattctcc	atgggggttg	3600
gtgaacttaa	gttcaaggag	ttagtgttcc	catttttttg	tcctcagtg	ttatgaattt	3660
gagcctgttc	tctgccagag	acaacaaaat	taacaccgcg	attttccatc	tttgactgct	3720
gttccctgga	tgtctgacct	actgtgtctaa	cctgtgcact	ggaattacta	ttatctgttt	3780
ccaatgcccc	tttcttagaa	gttccttctt	ggaccagtgc	tggtcaggca	gatgggttgc	3840
tatttgggtt	aaagtgtctg	aagccagagc	caggtccaat	tctatcctga	ccactcacat	3900
tcctccaatt	tcctagtcca	ttgttgttct	ctgtagttaga	gttggaagat	tgaacagatt	3960
tagccttagg	gtcagatttc	cagaccccaa	gattacattc	gttcccagaa	cttgacagct	4020
ggcactggct	cccttttctt	ttgttactag	tggtgcttcc	tggtcagagt	ctcttctcag	4080
agccagggtt	cgaggcactg	ttgttatcgg	tggtgtttts	ggaagaarat	tcartgtytt	4140
tgytggaaw	acaargccay	tyttcmatkt	cagaccctgy	tacaatcacc	ttktcccaga	4200
tgtgaattgg	gttgggggag	gtgccgttgt	tggaggaggy	tcccagagccc	caagtggaaat	4260
ttgcataatt	tgaagcagca	gcacctccaa	gggttgagtc	tggtgcagtc	ccactctcay	4320
tctgcagcag	cgtctctgtc	acttgtgcgt	tggttgggtt	tgctccaggt	gctgtgcagg	4380
gaggaggccc	tgccccaccc	ccaaggagca	tgaggagcgg	tggtgggggc	tgccacggtt	4440
ttagtaacac	tttgtgttcc	tgctggcaac	ggaattgcgg	cggcacctcc	cgaggcatgt	4500
agcgggcggc	gcttggcggg	tgtccgttcc	gcaactgccac	ccttttggca	ttgttgccac	4560
cattgactgg	tggtgatgga	gagctgccaa	ttgggtgggc	ggcgttgggt	tggtttaaac	4620
ttgttttctg	cacttggggc	actttgggtt	ttgttctcgt	gaccttctga	gtggcttctt	4680
ttttcttttt	atcctctttc	ttccttttct	tgtcttccat	taactgttct	tccttttctt	4740
gctccttctc	tctcataaag	tgacagcgtg	cttaaatcca	gcaaattgag	gcatacaagg	4800
tagaaatgga	aatgaaaaaa	ggtccaaaaa	atgaattctt	tttgtctatc	tggttttttg	4860

tattttaaat attcagaaac cagcagagac tctgtcgcc attttggtt gaactaactc	4920
tctctcacac actctccctc ttgtctctc gtcgacgcg cgcgaattc ccgggtcgac	4980
gagctcacta gtcggcgcc gctctagagg atccctcgag gggcccaagc ttacgcgtgc	5040
atgcgacgtc atagctctct accctatagt gggtcgtann aaa	5083

<210> 32

<211> 2108

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (5)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (34)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (41)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (2045)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (2075)

<223> n equals a,t,g, or c

<400> 32

atccntaatc cggcacttgt agaagtcctc catngagttg nccaagttcc tagattagat	60
ttggtttagca cctttgcaga cttcaggcct gatgtgtgtt tttcttagta caccatatca	120
ggaggcacag atatggatca gttctattac tggttatgtt aacttcagct tggttaagat	180
ggtgtctgcc aggtgtctcc attgtaagtt attcattttc cctttacaat taataagatc	240
ttgtrgggwa gaaagtaatc tttctttaaa taaagcagca atagaatgag agatttttaa	300
acatatataaa agcagaaaaa tataaatgaa tcaggagtaa agtaacatta aaaattggaa	360
tacatttataa gaaccatcta ctaatttcta accatatatt atttttaata atggtcttaa	420
aattttctttt tctatagaca ccaaactctg ctgaatgaaa taaattggtg ataagtggaa	480
aaaagagaaa aaccaatgat tcataacaat gtatgtgaaa gtgtaaaata gaatgttact	540
ttggaatgac tataaacatt aaaagaagac tgggaagcata caactttgta catttgtggg	600
ggaaaactat taattttttg caaatggaaa gatcaacaga ctatataatg atacatgact	660
gacacttgta cactaggtaa taaaactgat tcatacagtc taatgatatc accgctgtta	720
gggttttata aaactgcatt taaaaaaga tctatgacca gatattctcc tgggtgctcc	780
tcaaaggaac actattaagg ttcatgaaa tgttttcaat cattgccttc ccattgatcc	840

ttctaacatg	ctgttgacat	cacaccta	attcagaggg	aatgggcaag	gtatgaggg	900
aggaaataaa	aaataaaa	aataaaatag	aatgacacaa	atttgagttt	tgtgaacccc	960
tgaacagatg	gtcttaagga	yggtatctgg	aactggagaa	aagcagagtt	gagagacaat	1020
tctatagatt	aaatcctggt	aaggacaaac	attgccatta	gaagaaaagc	ttcaaaatag	1080
acctgtggca	gatgtcacat	gagtagaatt	tctgcccagc	cttaactgca	ttcagaggat	1140
aatatcaatg	aactaaactt	gaactaaaaa	ttttttaaac	aaaaagttat	aatgaagac	1200
acatggttgt	gaatacaatg	atgtatttct	ttattttcac	atacactcta	gctaaaagag	1260
caagagtaca	catcaacaaa	aatggaaaaca	aggctttggc	tgaaaaaaac	atgcatttga	1320
caaatcatgt	taatagctag	acaagaagaa	agtttagctt	gtaaaacttct	acttcatttg	1380
attcagagaa	acagagcatg	agttttctta	aaagtaacaa	gaaaaggaac	aaaaaaaatg	1440
aggtttgaaa	tctttttacca	tggcaaaaaca	ttaacatctt	tctcaaaaac	atagagaaat	1500
ctggaaaaat	caagaagata	aaattcttga	ccagtttagt	acattctttc	aagcatactt	1560
gtaaaatggt	tccttaaagt	gttcttggga	tgaaaatgat	tgatcatgtct	ccaacaacag	1620
tgaactgatg	ttgttccttg	gaataaaagt	caatccccac	cttaaaaaat	gtatggcttc	1680
tttgaggaat	tcttatgtct	taaagacttt	ttacattcta	gacaattaaa	ttgattgagg	1740
tcataaatta	agaagtgaat	agttaccact	acacggtaag	gtaagcagcc	tgaaagcatt	1800
tgtatcatat	atgtgtgtgt	gtgtgtgtgt	gtgtgtgtgt	gtgtgtgtga	tatatataat	1860
aaaaaamtyc	ttctacttgt	actttggcat	tcaattttta	gaaattcagt	ctcaaagtc	1920
attatggtat	ttttcaaagt	atacctttta	gtcaatgggt	tctttcgact	gcaatagaga	1980
agatatggca	agaaaaatgt	tgcagtacca	tcttctggga	gaacattcat	gaaatccttc	2040
agttntagtt	ccacagcaac	aattgacaat	gtttntttta	atgatgacag	gtagagttga	2100
tactttctc						2108

<210> 33

<211> 1248

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (8)

<223> n equals a,t,g, or c

<400> 33

aacctttntt	agttgagcaa	aagamcaagc	aatttgcttt	tgcaamcaat	aaaaaactca	60
ctttttttwat	atgkgcttat	cttatcatga	ttccattttt	acccttaa	ttttataggg	120
tgcaatagga	tctgtggcct	tggacacagc	aaggctcacat	ggagagaaac	aattagaaga	180
ctatggaatg	gatgtgttga	cagtggcatt	tttgtccatc	ctcatcacag	ccccattgg	240
aagtctgctt	attggtttac	tgggccccag	gcttctgcag	aaagttgaac	atcaaaaataa	300
agatgaagaa	gttcaaggag	agacttctgt	gcaagtttag	aggtgaaaag	agagagtgt	360
gaacataatg	tttagaaagc	tgctactttt	ttcaagatgc	atattgaaat	atgtaatgtt	420
taagcttaaa	atgtaataga	accaaaagt	tagctgtttc	tttaa	atcttttagcc	480
cttgctcttt	ccatgtgggt	ggtaatgatc	tatatcacca	accttaattct	ctctgccttt	540
tttttcaa	accccttcat	catccatctt	aatttgcata	aggacatata	tactttaatg	600
tactaccaca	gtttacagtt	aatgtgggaa	agaccagctt	cagtatcctc	ttcagctagg	660
attgccctaa	cttttaactt	tcacagtttc	ctgattcata	tttggccagg	ctctgatgcc	720
ttgaattgggt	tttggctctc	ttttttggat	ctgtttttgt	tgttaaacat	cataatgcag	780
tctctcatta	atttttacca	tcattttacc	tgataatctg	cctcttctcc	atctctcctt	840
cccttactac	ctttctttga	attactgtaa	ctgattgggt	ccacccaaa	tttaaagtac	900
atgaagtatc	ttcattgggt	catcctcttg	ccccctccag	atgtcaaaaa	actttatcct	960

gccccctagc	tgaccaccca	ggttccttta	tttcagtggc	ccatgtgagt	ctaccttccc	1020
ctaaggagtg	ccctaatacca	gccctttttt	tgtttcttat	gacccatatac	tttaggctct	1080
tcccatttct	agggtgggaga	taggtaagtt	tcaaatactat	gccagtctta	tgaatattac	1140
attagggtaa	tgtgtctataa	tgaagaaata	aaaaatacag	tgcttaaaaag	aaaataaaat	1200
tctatttctg	tctaaaaaaa	aaaacggcac	gtaggggggg	gccccggt		1248

<210> 34

<211> 1911

<212> DNA

<213> Homo sapiens

<400> 34

ggcacgagcg	gcacgagcgg	atcctcacac	gactgtgatc	cgattctttc	cagcggettcc	60
tgcaaccaag	cggttcttac	ccccggctct	ccgcgtctcc	agtcctcgca	cctggaaccc	120
caacgtcccc	gagagtcccc	gaatccccgc	tcccaggcta	cctaagagga	tgagcgggtgc	180
tccgacggcc	ggggcagccc	tgatgtcttg	cgccgccacc	gccgtgctac	tgagcgtctca	240
gggaggaccc	gtgcagtcca	agtcgccgcg	ctttgcgtcc	tgggacgaga	tgaatgtcct	300
ggcgcacgga	ctcctgcagc	tcggccaggg	gctgcgcgaa	cacgcggagg	cacccgcagt	360
cagctgagcg	cgctggagcg	gcgcctgagc	gcgtgcgggt	ccgctgtcag	gaaccgaggg	420
gtccaccgac	ctcccgttag	cccctgagag	ccgggtggac	cctgaggtcc	ttcacagcct	480
gcagacacaa	ctcaaggctc	agaacagcag	gatccatcaa	ctcttccaca	aggtggccca	540
gcagcagcgg	cacctggaga	agcagcacct	gcgaattcag	catctgcaaa	gccagtttgg	600
cctcctggac	cacaagcacc	tagaccatga	ggtggccaag	cctgcccga	gaaagagget	660
gcccagagatg	gcccagccag	ttgacccggc	tcacaatgtc	agccgcctgc	accggctgcc	720
cagggattgc	caggagctgt	tccaggttgg	ggagaggcag	agtggactat	ttgaaatcca	780
gcctcagggg	tctccgccat	ttttggtgaa	ctgcaagatg	acctcagatg	gaggctggac	840
agtaattcag	aggcgccacg	atggctcagt	ggacttcaac	cgccctggg	aagcctacaa	900
ggcggggttt	ggggatcccc	acggcgagtt	ctggctgggt	ctggagaagg	tgcatagcat	960
catgggggac	cgcaacagcc	gcctggccgt	gcagctgcgg	gactgggatg	gcaacgccga	1020
gttgctgcag	ttctccgtgc	acctgggtgg	cgaggacacg	gcctatagcc	tgacagctcac	1080
tgcacccgtg	gccggccagc	tgggcgccac	caccgtccca	cccagcggcc	tctccgtacc	1140
cttctccact	tgggaccagg	atcacgacct	ccgcagggac	aagaactgcg	ccaagagcct	1200
ctctggaggc	tggtggtttg	gcacctgcag	ccattccaac	ctcaacggcc	agtacttccg	1260
ctccatccca	cagcagcggc	agaagcttaa	gaagggaaac	ttctggaaga	cctggcgggg	1320
ccgtacttac	ccgtgcagag	ccaccaccat	gttgatccag	cccatggcag	cagaggcagc	1380
ctcctagcgt	cctggctggg	cctggctcca	ggcccacgaa	agacggtgac	tcttggtctt	1440
gcccagaggat	gtggccgttc	cctgcctggg	caggggctcc	aaggaggggc	catctggaaa	1500
cttgtggaca	gagaagaaga	ccacgactgg	agaagccccc	tttctgagtg	caggggggct	1560
gcatgcgttg	cctcctgaga	tcgaggctgc	aggatatgct	cagactctag	aggcgtggac	1620
caaggggcat	ggagcttcac	tccttgctgg	ccaggaggtt	ggggactcag	agggaccact	1680
tggggccagc	cagactggcc	tcaatggcgg	actcagtcac	attgactgac	ggggaccagg	1740
gcttgtgtgg	gtcgagagcg	ccctcatggt	gctggtgctg	ttgtgtgtag	gtccctggg	1800
gacacaagca	ggcgccaatg	gtatctgggc	ggagctcaca	gagttcttgg	aataaaaagca	1860
acctcagaac	acttaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	a	1911

<210> 35

<211> 996

<212> DNA

<213> Homo sapiens

<220>
 <221> SITE
 <222> (514)
 <223> n equals a,t,g, or c

<220>
 <221> SITE
 <222> (574)
 <223> n equals a,t,g, or c

<400> 35
 gcggcacgag cacatctcat cttccactgg aacgtttaga taaaggagtg tgggggtgtaa 60
 taaagaacta agctaaagcg agagaaacac tgaaaaacta cgaaatgtca cacaagtacc 120
 ataaagagag tgattacttg attaattaat gataggaacc ctacatttaa gtctttcagt 180
 tatacttgca tcagtcctct ttgcctatca gaatgcggtt tgtttctgcc aacgaataac 240
 tatcaaacca ctgaggccta actgatgtgt gattaatgtg ggctccatta attgtgtggc 300
 tgagttttat gcatgaagct gtatccttga tttttcacct ttaatttcct cctgtttaac 360
 tgctggtcat aaaattgttt caaatgtatc tgctgagtct gagagcaagt tttgcaactt 420
 gaaaagtgcc tgagtcagtt tgggcacctt gtttggtaaa accgacttgg gggaactctt 480
 aacgctgtaa gatgaattgc tacttggtt ccantcccag ccctgctggc tcccttcctg 540
 ccactgctca ctggcactgc atctcatcta ttancattaa gcacatgcat agcattgata 600
 atggcaaaag gcttaataac tttctttctg atagcccatc atatgtggct ctattcaacc 660
 ttatttttaga cagctagaga tgatgacatc tgtctttctg gtctttttca cattcattta 720
 ccactctctgt taatatcacc tgattttctt ttggggcagc accccttccc atctctgctt 780
 ttattttctg tgtttcaagt agggctggtc tcatttccct ggctccggag ctaggcctgg 840
 acaattagaa ttccagtgat tggttcgggg ataggcatgt gacccaagct cgggtcaactc 900
 tcggtcaact agagagacaa cctaggtcaa ctagacaggc aaccctagga ctttagcagg 960
 aactattagg agaaaaaaaa aaaaaaaaaa ctcgag 996

<210> 36
 <211> 1320
 <212> DNA
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (1024)
 <223> n equals a,t,g, or c

<220>
 <221> SITE
 <222> (1309)
 <223> n equals a,t,g, or c

<400> 36
 gcagggtttc accatttttg gcaggctggt cttgaactcc tgacctcagg tgatctgcct 60
 gccttggcct cccaaagtgc tgggattaga ggcgtaagca ccgcgccag cccctatcct 120
 ttttgttttt tattataaaa gtaatatctg aatacatgat tgtttaaata aatgctgtgt 180
 aagtgtataa aatgaaaagt aaaaggcccc catgaatgga cattaagata cttccgatgt 240

<213> Homo sapiens

cgcacgggcg	cgcgcatggt	gacgcgttc	ttagctggtg	cgcgccggag	cccaaatcc	60
aagtggaaac	tgcaggcgca	cgagggagga	acgcgtggag	catgaaaagg	cagggggcct	120
cctctgagcg	aaaacgagcg	cggataccgt	ccgggaaggc	cggagcagca	aatggatttc	180
tcatggaagt	ttgtgttgat	tcagtggaat	cagctgtgaa	tgcagaaaaga	ggagggtgtg	240
atcggattga	attatgttct	ggtttatcag	aggggggaac	tacaccagc	atgggtgtcc	300
ttcaagtagt	gaagcagagt	gttcagatcc	cagtttttgt	gatgattcgg	ccacggggag	360
gtgatttttt	gtattcagat	cgtgaaattg	aggtgatgaa	ggctgacatt	cgtcttgcca	420
agctttatgg	tgctgatggt	ttggtttttg	gggcattgac	tgaagatgga	cacattgaca	480
aagagctgtg	tatgtccctt	atggctattt	gccgccctct	gccagtcact	ttccaccgag	540
cctttgacat	ggttcatgat	ccaatggcag	ctctggagac	cctcttaacc	ttgggatttg	600
aacgcgtgtt	gaccagtgga	tgtgacagtt	cagcattaga	agggctaccc	ctaataaagc	660
gactcattga	gcaggcaaaa	ggcaggattg	tggtaatgcc	aggagtggtg	ataacagaca	720
gaaatctaca	aaggatcctt	gagggttcag	gtgctacaga	attccactgt	tctgctcggt	780
ctactagaga	ctcgggaatg	aagtttcgaa	attcatctgt	tgccatggga	gcctcacttt	840
cttgctcaga	atattcccta	aaggtaacag	atgtgaccaa	agtaaggact	ttgaatgcta	900
tcgcaaagaa	catcctggtg	tagccagacc	tctctgagag	acatggatat	cacaggatga	960
aggtagaact	ataatctgca	attctctatg	acacagcttt	aaccttcttc	tctggccagg	1020
acagtcgcaa	tctttgtttt	aagtttcaca	tggccatgga	gaatgtgccc	aagaagaaaa	1080
agaatttgaa	acagagatac	agtcacttcc	tttgcttagt	cttaccagtg	attgtcatca	1140
tggttaaagc	tggtctgtgc	ttcttccata	gacagaagct	tagtctgttt	tcagtggaat	1200
taattgatga	actgggaaaa	ttttaactgc	atgggatgaa	ttcagagtgt	gacttaaggg	1260
tcaattcaaa	gcagtatttt	gacttttcat	ttgtaaaata	aaaatttcca	ctattacaaa	1320
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	ctcgaq	1376

<210> 38
 <211> 1953
 <212> DNA
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (1362)
 <223> n equals a,t,g, or c

<400> 38
 tttttttttt tttttttttt tttttttcac caatgaaaac atttttttta aattaacaga 60
 catcaactgg tataaataca ctgtctaaag catttaatgg tctttcttta acacagccaa 120
 ctccccggg tttgaaacag tgttaaattc tctcttgctt gtggcaaaag aagctgtcaa 180
 gtccaacact gaaaaattgg taccatttcc tggccagtaa gcacagaaca gaggggctaa 240
 atattttatg gttttattya ttactgtgt ttcacatgtg tgtttttctt ttctctgtct 300
 ctccctcctg ctctgtgtctg cccagggtg attgttgtga cattggccgt atgctggatg 360
 cccaaccaga ttcggaggat catggctgctg gccaaaccca agcacgactg gacgaggtcc 420
 tacttccggg cgtacatgat cctcctcccc ttctcggaaga cgtttttcta cctcagctcg 480
 gtcacaaacc cgtcctgtga cacgggtgtcc tcgcagcagt ttcggcgggt gttcgtgcag 540
 gtgtgtgtgt gccgcctgtc gctgcagcac gccaaaccag agaagcgcct gcgcgtacat 600
 gcgcactcca ccaccgacag cgcgcgtttt gtgcagcgcc cgttgctctt cgcgtcccg 660
 cgccagtcct ctgcaaggag aactgagaag attttcttaa gcacttttca gagcgaggcc 720
 gagccccagt ctaagtccca gtcattgagt ctgcagtcac tagagcccaa ctcaggcgcg 780
 aaaccagcca attctgtctg agagaatggt ttccaggagc atgaagtgtg aatgtcaagc 840
 gagggagcct tgagtgggaa ctggccctcc agccctaaga aaacgtcact ctcactctgc 900
 agtctcaaac tatgccccca tcagggatgg aatggacact ggaggcttta caaaaggcag 960
 atgccacact cagtgaactt taaggactga ctctgccagc ctggccttga ctccggttac 1020
 acagacatgg ggggtgaactt tcaactccacc tccttccttc aagtacatac tgaaaattca 1080
 gtcargctga atttattcag aatgctttac cgagctcttt cattatttgc acaggaacaa 1140
 aagagaacac ggaactccgc tcctaccca gaataaaagg acaccagaa gaaactcact 1200
 cagggagggtg ggggggttggg ggcgaggggt ggaagaacaa tgcaggaggg ggtggcatct 1260
 ccttcagctt cagcagtgtg ccgagaagag ggctaatttg aggaacagga tgggtgtgcg 1320
 gagccctgcc tgagggccga ggcagaactt ccccttttct tnggccttg cccgttacia 1380
 agaggggtgt tgcagcagct gatgcaaaact gagttcagtt tccctgggga gcagaaggac 1440
 tggtagcccg cagaggcgat gagacaggcc gctgatgatg cacaggactt gcggtacatg 1500
 atcccggcac tttgtcccat cacttcttct tgacacatgt cttgaacgtt caccgtgcaa 1560
 ttcacaatga actcggggga ggagcagtcg ttgttcagct ggaattcttc aactggtag 1620
 cactggattt gcagcgcaaa gcctggaagc aagaacaatc cgcaaaaagt tgccgcgatg 1680
 cctaggaccc acattctccc ggagtcccgg ggccgggaga gggcaagcgc atcagaggag 1740
 gcgacagcag cggaggctgc cccggctgca gcggctgtgg ctgccgagge tgcgtgggccc 1800
 cgcgtgtctg ccgcggagac gacggctgta gcttagagga gccgcagggt ccgctcgcgg 1860
 agcctgcata gccgcgcgtc gggctcccgg ctgcgggtct ctgctcctcc cgcctcgcgt 1920
 cccggggccga gcaccgcgcc tccggagttg gcg 1953

<210> 39
 <211> 2793
 <212> DNA
 <213> Homo sapiens

<220>

<221> SITE

<222> (2762)

<223> n equals a,t,g, or c

<400> 39

aatttgtagg	caggagtaaa	cggttaactga	cggtgggtta	gtgccctgca	tcttgcatat	60
ttgaactgtc	tagagttcct	gccattgctg	ggtataaaac	gaggagctct	ctgttgacct	120
gtaaatcatt	aatacttctt	gacttagagt	gtcacttcac	tttatagatg	acattttcct	180
ctttcccctt	gatattttct	atgttggtgt	agataattgg	tagataatrt	gttggtggtt	240
agtacattta	gggcttctat	ttatttagat	tttgtttgtt	ggagtctgtt	tccaaaaggg	300
aatgtgccat	ttagtctgca	tctgtatctt	tgtggacttg	atgatcactg	gtttgatttt	360
gaaaaatgtc	ttttccagct	tttagttact	ctcatcaaat	gtcacatatt	tctaatacaca	420
tgcactcctt	taccacagag	gcacataatc	atltggcctc	atagcagtta	tccatggccg	480
tactgtagta	aagttcctta	gaactttgcc	aggagtgaac	tagaaaaaag	tgtttactag	540
ggcctaagag	ttgctttgtg	ccgtgtagtc	cggtctttgc	actagtagat	cattgctgac	600
ataggtcagt	ttagagacct	ttctgtgtta	atgcctcctg	gtactgtctt	aagatacgt	660
cagtgtctgt	tttttagatct	atgcataatg	catgaagctc	cttgtgggct	ctgcatgaag	720
ctgctgcttt	gtttttgggt	taacagatgt	gcctgtcaac	tagcatgtgt	attgtccaaa	780
ttccataaac	ttaaggtttt	taagggtctg	gtggtttctg	agctctatgt	gtctttccta	840
tccttgtacc	ttcaaagggt	gagaaatgag	atltatacat	ccaaagttag	tctgataaat	900
atggcttttt	gtttctccat	gtaacctaga	ctgtcaaaaa	taagtgatgg	tgataagtag	960
gcctggagcc	tcagcttctg	taaatctcat	tcctaaaatt	ttgctagact	cgtgttgcca	1020
aaaacaaata	cctgtggatt	gtccttaagg	cttttaataca	gataacctgt	ttgctgttag	1080
ctgaactgta	gtgaagcatc	gatccaaatc	ggctcttctga	agtatcagtt	atgcttttga	1140
gttttagaaa	tacttaggtg	ttagtctagt	cttcccattc	atgaatcagt	gtatgtccat	1200
atcagagagc	ctcaacttct	tttttcttcc	tttttaaaaa	tgattttagt	gttttgattt	1260
agtgtatact	acatagttca	gtattattgg	ctttaccagt	gttgacagaa	aaattttaaa	1320
tctccagttg	caaacagcaa	tggattagga	tatggaaaata	aaatcatggt	gacatcactg	1380
ctgagttatc	ttaaacctct	gctacttaat	tctccatatt	gaaatgcata	ctcctccaca	1440
tacatggcct	ccaagtaaag	gcaattgtag	aggggccctg	tctatcccag	tatggttgga	1500
ttttaaacat	atctgtgttt	ccgttatttt	gggaactgat	taatatttac	aatttttttt	1560
gtttatgagt	tattttgata	ctaagaaaag	agagaatcta	gaacatcttg	magttgaaat	1620
acaaatttta	ttcttttggt	cttggggagaa	tttaagcagt	ctatgcaact	catcaaatgg	1680
tgagaaatag	ccctccgagg	ttccagtaag	ctttcagtga	ctttgatacc	tccccaagtt	1740
tcttgagttg	ctgcttggtt	acaccagctt	tttaactgag	tgtttgctcc	tgatggttta	1800
ggagattttc	atgttgatc	acactgtcaa	gttttatttt	gtctttttat	ccctccgtgg	1860
atgtgagttt	gaaacaagca	cggtacagta	atcctgcctg	atagagtagt	ctggaatgag	1920
aattactttt	tgggtgagag	agttctccat	tttaatgttt	ctaaagtttt	tcatatgaac	1980
ttggcattgg	aaaaggagg	taaagaaaaa	ggacgtttac	taaaagcagt	gtctactctt	2040
cccctttgtg	agtgtttatt	catggctaatt	gaaaaaaaaga	gaaggactct	tgggttttgt	2100
gttgccatgt	taagcatgga	gagggatgct	tgacagcatg	ctaattgaag	ccagagcaag	2160
tatgtccttc	atcaggtaat	caggaaactct	tcagttgaag	ctgaggaact	aactgattag	2220
ttgtgatca	taatataatt	ggttaciaaag	tggaagtgcc	agctggctta	agtacccaaa	2280
gaaaagaatg	cagcagccta	acttagtggt	accatatgtt	actgaatttg	aaactgacct	2340
tttttcccac	cctacttcac	acacctaaaa	ctcttttctt	gtcagaccaa	agagcgaaaa	2400
gaaaaaaaaa	aagtaaaaca	ctttaccaat	ctgtcactca	ggtacaattt	tgtggtgaga	2460
tttttgtctg	ttctctttgt	attgctctta	agagtccttt	ctcagcataat	tattctgccca	2520
ttgcctctgt	cttccttggg	gcacctcagc	tctggatgct	acccctggga	tatctactgc	2580
tgttatgtga	atgataggag	gtaagtgaac	attatagtaa	gggtcttttg	taaaaaaatt	2640
caaaaaattt	aaaaaggatg	tatacatttt	atagtctggc	tatcagtttg	atatcttgct	2700

gtcaagtatg tttctcaatc tgtatttatc catcccatca ataaatgtta atggtaaaac 2760
ancaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 2793

<210> 40

<211> 1367

<212> DNA

<213> Homo sapiens

<400> 40

gcattgacct acatgggttca gagaacaccc cacgggctgt ttgtccacga cccaggctgg 60
acgaatgcct ggtcagaggg tgacctgaac cagagctgga gtgaggatca aacaggccca 120
ggagcctgag gaaataccca gtcagtcctc ccagccgcga tggagagggg cctttgcagg 180
cgttcggaat ctcggtgaa ttcaggacct gggaatacag ggttcagaga ggagaggagg 240
aagatggtga catgatttgg ttagaagcac aagcaaactg atcagcctcc cagacctgcc 300
agcagatgct gtgtgagggg gatggagcac ggggtcacac ccctgcccc aaggccactg 360
gtctccctgg gcttgacgtg cagaggcctc aggggtgtctg ggattgctgg ggaggcctgt 420
gctgccccct ggtggcgctt cctggcgctg cgccctgtcc acagtcacct taggtccctt 480
tggaaacatt ccatttgact ttccctggt gtttgaaatc ccatgtttcc ctaaacctct 540
agcctgattg ttctttccct aattcattgc acaagctcct ttgcttttag tgttaccgct 600
cattgcctct ctaatcctgc ctgatttgtt ttacagaagc ttctgatttg cattgaacat 660
gctctaactg gcctgtgcta cttattaccg ggcttgtaat agcggttctt gtctccatag 720
cctgttgagt gttcccagat gtgactcacc tttctgctgc cctcttcatg caggcctact 780
gactcataat tcacttgtcc caaaagccac cccacaagcc tgagccaacc tgcctgctga 840
cgccacagtc attggcagag gtctgggcat tattaattta taaaaatcca tgctttacac 900
ctggacagta gacagggact tcagagattg cacgtttgaa tacattctcc caagactgag 960
gttggttygg ttaatttcc ttagtccaat cacacaattt cttatggaaa accttttgtg 1020
tttctggtat ttaataactt gaagggatag caaaatatac tgtgtattca gagggcctct 1080
ctgcagctgc tagctcagac accaaagggg taaggcccag gacattcata tctttaaaag 1140
ctgcaaacct ggtaaccttt aaacttttaa aacaaatgtc atatggggta aactgacct 1200
tttataattt gatgtctcaa atgtagagat tatctaaaaa tcgtaacttg aataccttgt 1260
aatTTTTctc ttaaaaaaga agacttgtgt aagtctctgc atcaacgcca ataaacatgt 1320
tgcttaataa taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1367

<210> 41

<211> 1906

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (9)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (20)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (35)

<223> n equals a,t,g, or c

<400> 41

cgggctcgna	tgttgtgtgn	aattgtgagc	gatancaattt	tcacacagga	accagctatg	60
mccatgatta	cgccaagctc	gaaattaacc	ctcactaaag	ggaccaaaag	ctggagctcc	120
accgcggtgc	ggccgctcta	gaactagtgg	atcccccg	ctgcaggaat	tcggcacgag	180
gtcttaacca	tgtgtgtgga	tttgcaagtc	gaaccagtaa	agctttcagc	aacaaacaga	240
ctgtgaaaca	atgtggctgt	tccgaagttt	atctggactg	tttacagaca	ttcttgccag	300
ccctcagttg	tcccttacia	aaggatattc	tcagaagtgg	agtcctgact	ttccttcac	360
gaatgattat	ttgcttgag	gaagaagttc	ttccgttcac	tccatctgct	tcagaacata	420
tgtctaaaga	ttgtgaagca	aaagatctcc	aggagtccat	tcctcttacc	aaccagatta	480
cggccaaatt	caagatacag	gtatccccgt	ttttacaaca	gatgttcacg	cccctgcttc	540
atgcaatttt	tgaagtgtcg	ctccggccag	cagaagaaaa	tgaccagtct	gctgctttag	600
agaagcagat	gttgcggagg	agttactttg	ctttctgca	aacagtcaca	ggcagtgga	660
tgagcgaagt	tatagcaaat	caaggtgcag	agaatgtaga	aagagtgttg	gttactgtta	720
tccaaggagc	agttgaatat	ccagatccaa	ttgcacagaa	aacatgtttt	atcatctct	780
caaagtgtgt	agaactctgg	ggaggtaaag	atggaccagt	gggatttgct	gattttgttt	840
ataagcacat	tgtccccgca	tgtttcctag	cacctttaa	acaaaccttt	gacctggcag	900
atgcacaaac	agtattggct	ttatctgagt	gtgcagtgac	actgaaaaca	attcatctca	960
aacggggccc	agaatgtgtt	cagtatcttc	aacaagaata	cctgccctcc	ttgcaagtag	1020
ctccagaaat	aattcaggag	ttttgtcaag	cgcttcagca	gcctgatgct	aaagttttta	1080
aaaattactt	aaaggtgttc	ttccagagag	caaagccctg	aggactggat	ttccctgtgc	1140
ctacttcacg	atcatgaatt	ccagttaatt	tataaagagg	cgatttttgt	gtgccattca	1200
cactggctct	tttcacattg	ttttgagctt	attgcagtat	atgttttggg	atttttctgt	1260
aaaatgggtg	taattttcct	aatacaggta	tgtacaaca	aaagaagtgg	cctgcatgcc	1320
ggtccaaatt	gttctgtata	aagatgctct	taaaagacac	aagagtattc	ctagaacctt	1380
aattcttttt	tatttgaaat	tttaagtcaa	gtcctttata	aagaccatag	cagtggaaaa	1440
cagtgtactt	tttaaaaaat	tgtgaatat	aaaatctttg	aaaattttct	ttatgtgtga	1500
agacacaaag	tatgggggaa	gacagcaatc	aaaactaact	ttttgtagat	agccatttca	1560
tttctttaa	ctgtttcaac	gccaatatgt	attctacaaa	agagaatggg	tttaggctcc	1620
agtggtatac	ttttttttat	atatatatat	aaaaataaac	tttacgtagt	gaaatcttcc	1680
aagtcttttc	tgggaattatt	ataaataact	tagttttatt	ttctcatctt	aatctctcca	1740
taatttccca	tttaagggtt	tacaaatatg	agtggtgtga	tgctttaatt	catttaacct	1800
cactcctcaa	aggtaacatg	caacttagtt	ctgttatatg	agagtctttt	tctttaatgt	1860
actggaaaaa	gcctatgtga	atctgttgat	agaattttaa	attcca		1906

<210> 42

<211> 1723

<212> DNA

<213> Homo sapiens

<400> 42

gcttaagctt	ccaaggctaa	agttggaggt	aatgcttgaa	gataatgttt	gcttgcccag	60
caatggcaaa	ttatatacaa	aggtaatcaa	ctgggtgcag	cgtagcatct	gggagaatgg	120
agacagtctg	gwwgwgctga	tgggaagaggt	tcaaaccttg	tactactcag	ctgatcacia	180
gctgcttgat	gggaacctac	tagatggaca	ggctgaggtg	tttggcagtg	atgatgacca	240
cattcagttt	gtgcagaaaa	agccaccacg	tgagaatggc	cataagcaga	taagtagcag	300
ttcaactgga	tgtctctctt	ctccaaatgc	tacagtacaa	agccctaagc	atgagtggaa	360

aatcgttgct	tcagaaaaga	cttcaaataa	cacttacttg	tgcttggtg	tgctggatgg	420
tatatctgt	gtcatttttc	ttcatgggag	aaacagccca	cagagctcac	caacaagtac	480
tccaaaacta	agtaagagtt	taagctttga	gatgcaacaa	gatgagctaa	tcgaaaagcc	540
catgtctcct	atgcagtacg	cacgatctgg	tctgggaaca	gcagagatga	atggcaaac	600
catagctgca	ggtggctata	acagagagga	atgtcttcga	acagtcgaat	gctataatcc	660
acatacagat	cactggtcct	ttcttgctcc	catgagaaca	ccaagagccc	gatttcaa	720
ggctgtactc	atgggccagc	tctatgtggt	aggtggatca	aatggccact	cagatgacct	780
gagttgtgga	gagatgtatg	attcaa	acat	agatgactgg	attcctgttc	840
aactaaccgt	tgtaatgcag	gagtgtgtgc	tctgaatgga	aagttatata	tcgttggtgg	900
ctctgatcca	tatgggtcaaa	aaggactgaa	aaattgtgat	gtatttgatc	ctgtaacaaa	960
gttgtggaca	agctgtgccc	ctcttaacat	tcggagacac	cagtctgcag	tctgtgagct	1020
tggtgggttat	ttgtacataa	tcggaggtgc	agaatcttgg	aattgtctga	acacagtaga	1080
acgatacaat	cctgaaaata	atacctggac	tttaattgca	cccatgaatg	tggttaggcg	1140
aggagctgga	gtggctgttc	ttaatggaaa	actgtttgta	tggtgggtg	ttgatgggtc	1200
tcatgccatc	agttgtgtgg	aaatgtatga	tccaactaga	aatgaatgga	agatgatggg	1260
aaatatgact	tcaccaagga	gcaatgctgg	gattgcaact	gtagggaaca	ccatttatgc	1320
agtgggagga	ttcgaatggca	atgaatttct	gaatacgggtg	gaagtctata	accttgagtc	1380
aaatgaatgg	agccccata	caaagatttt	ccagttttta	caaattttaag	accctctcaa	1440
actaacaggc	ttagtgatgt	aattatggtt	agyagaggta	cacttgatga	ttaaaggagg	1500
gggtgggtat	agatgttgct	aacagcaaca	caaagctttt	gcatattgca	tactattaaa	1560
catgctgtac	atactttttg	ggttttattg	gaaaggaatg	caaagatgaa	ggtctgtttt	1620
gtgtactttt	aagacttttg	ttattttact	ttttggaaaa	gaataaacca	agaattgatt	1680
gggcacatca	aaaaaaaaa	aaaaaaaaa	aaaaaaaaa	aaa		1723

<210> 43

<211> 2074

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (2019)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (2043)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (2048)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (2061)

<223> n equals a,t,g, or c

<400> 43


```

cttccgacat gcctccagcc tccattttct cccttcccag ttattcctta gccagccat      60
ctctgtcttt agctcctaca attttcttag gatattctgg gaaagatgag cggagactgc     120
ccgccttgtc aaatctagtg tcttttttct agtccctaca ctgcttgacc tatgtataac     180
ctcctatact tccctctttg catactcctc tgggttttct gtggtagtc aagattcctcc     240
ctgagattta tttcccatga gtcttgaccc ctccctcag ttggtgctat ttccctctac     300
ccgcccctcg atgatcttat cagagcccac aggttcagtt ttctttcatg ctacctgaat     360
gtcctgataa actggctcgc tctcttcttt accttccata atggcattac catttaccac     420
----- gccaccaag atacttacta ggaacctcaa agtattgtat tctttttctc catecacctc ----- 480
atacttaatc atcaagycct tttgagcttg tctcctcttg aatatgtccc ttcttaattc     540
ctgctgcctt cttagtaaag gcyttcattc ttttttccct agtaataatc ttttccatat     600
gttccagtta aaataccatg ttctccctat tccttattac atagctagca ttcttgaaa     660
aaaaacaatt ctctcaggcc tccatacctt tagcatgtta cccactctgc ctctgctctt     720
ctggaactag aacactcatc cttgaaggct gggcttctgt atgaagggtg gtctgcctc     780
cttacttgag gtgaagcttt gtacatgcct gtattacgga catcctctta ttttaagtgtt     840
tgtctcttct gtcatggga ctccagcacc cagcatagtc cctagtatac tagttgggtgc     900
cgaataaata gtagctatta ttagaaaagg aagggtgaaa ttgacatggg agttagtaaa     960
atgtatatgg aaatgatatt taaagggaaa ggtaatgatt ttctggcagg aaaagcagca    1020
atgacaagat tacttaagtc ttgtgaaata acacttctct tccttgacct gctgcttccc    1080
ttttttacca cacacacacg cacacatacc acagcccttt gagactgaaa gcagctctat    1140
tgagaatagt agtgtaact gtattatgta gaaattctaa agtttttggg attatttcat    1200
agccctgacc ttgctacttc tctccacttt atgtggcagg tttaatctca ggtctccctc    1260
atacacttct cagcctcagc acctaacctt cacacaacac tccagtattg atgcagtcaa    1320
tcttgataaa cattttttga atgtccaatg tgcaaagcac gatgttgga attatacaga    1380
gggtgaataa acaaaaactc ttgctctcaa agatgtcagt ctttttcttt gcaaggataa    1440
cacatgtaga gtaaaatgca taaaggggac taatttttaa tgtacagctt aattaatttt    1500
tatgtatggt aacacccatg tcaccacatg gtttaggaca tttccagcac ccctgaaatt    1560
tccttcatgc cccttcccag tctgtacctc cacctctaaa tctattttca atcttaatgg    1620
ccttttaaat aactgggctt ctcaacaaca tagtgaacag aaacagctgg gttgtcaacg    1680
tctaacctaa tacttcagga aaactcatga tggtttccat gtttaagagag acatggagca    1740
gggcactggc atggyggatg gatcacgcct gtaatcccag cactttggga ggccgaggta    1800
gggggattgc ttgagcccag gagttcaaga ctagcctggg taatataagg aaaacctgtc    1860
tctgcaaaaa aaaaaaaaaa aagaggatac aaccaaatgg aagaacattc catgctcatg    1920
ggtaggaaga atcaatatcg tgaatatggc catactgcc aaggtaattt acagattcag    1980
tgccatcccc atcaagctac catgccttct ttcacagant gggaaaaact actttaaagt    2040
tcnatgggnac caaaagagcc ntatcgccag tcat                                2074

```

<210> 44

<211> 822

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (47)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (799)

<223> n equals a,t,g, or c

<220>
 <221> SITE
 <222> (809)
 <223> n equals a,t,g, or c

<220>
 <221> SITE
 <222> (815)
 <223> n equals a,t,g, or c

<220>
 <221> SITE
 <222> (819)
 <223> n equals a,t,g, or c

<400> 44

acccatggat ttccgcccaa ggctcgaaa ttacccttc acttaanggg aacaaaaagc	60
tggagcttca cgcggtggcg gccgctctag aactagtga tccccgggc tgcaggaatt	120
ctcggtcata ggatatgcat attcggttta gtaaaactg ccagtttttg aaagtgattg	180
tactagtttt acattcccag caatagtgtg ataagattc ccttgtttg catttttacc	240
aatacttaaa atggcctgcc ttgagttgtt gatactgtg tcatttttga catctgtcat	300
ccagactcaa cctcctaggg agcttgacce ttcccttttt tcagttttct ctctagccta	360
ggttcagtc gcaagacctc tcagattttt cttttatatt gcctttgtcc ttctccatt	420
gccacagctc aaatattagt catatatgga gtaaatatca ggtgatttgg atatcaggat	480
tatgacagta gtctgccagt tgggtcatct tctagtattt ctgcttttcc aataaatcct	540
gcacagccaa gaaaatgctt catgaaacac cgcaccattg ctctgctcaa aagccgtcaa	600
caacccttca ttgcccattg gatatacagc ttctccccc tcttcccttt ccacctgtac	660
ctctcttctt tcttcccttc ttccgttctt tttttttaat taaagtgtaa tatatatgaa	720
gtgcactatg accgagaatt cgatatcaag cttatcgata ccgtcgacct cgaggggggg	780
cccgttacc aattcgcent gggttccana gaagntcant ag	822

<210> 45
 <211> 2406
 <212> DNA
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (35)
 <223> n equals a,t,g, or c

<400> 45

aattcggcac gaggagaact agtctcgagt ttttcttctt accttttttt tgttaaagag	60
ttacatctct cacaggagga aagaattcaa gagtctatat gattagttac agagaatatt	120
ttcatcccct ctccctgaat agaaaagcag gggtcacat ttgtatcctt acccttgagg	180
tgtttttgaa gatgctgtaa ctcttgaagt tgagctgagg cagaaagggt ggaaaaatgc	240
agccctctgg gwattgtggg gagggatgtg atgtagtaag aggggtgttt gtggtgctag	300
gattcccacg ccaccaactt gcagctttat aasagcgcta ccaagaacca ccrctgggga	360
aaaggttctt attcattgtt tctgttggaa tgtgatcttg ctttctggat ttttaggaatt	420

caggttactc	agtataaaac	tctgagaaat	cagtgtgact	tagtccttca	cctcctaaga	480
taaagtgaat	atttctttac	aaaataattc	atgtccttaa	tgttaaagat	gtaattttat	540
tttcaaaaca	tctataacat	gactttcaga	agcagttcat	ttttccaaga	ttcctcacat	600
tatactagat	aaataatagg	ccctcagtta	atacccttca	gttattgaat	taatctagtt	660
tgtggaatga	ggtgtatcct	gccaacttcc	ctctgctccc	aagtacactc	tgagaggtaa	720
aatgctctgg	gaaatggaac	aagaatcgag	tggaatgctga	ctctgtgtgc	ccacctcctc	780
aactgattga	taatggttga	ccttgggcaa	gtcactttctt	tcaatgcctc	agttcccat	840
ctgtcaaagt	gggttaataa	tactgaccta	cctcacaggg	gtgttgttgt	gaggcattgt	900
aaatcaaagt	taatagaata	cttcagggtc	ctctgtggag	gatgtcttga	gccagagttt	960
aagcctgaca	cacaggcttt	ggtcctcact	gagctgtctc	caagactgga	actacttagt	1020
gactcggcaa	attttctgcc	ccccaccct	catcaaagct	gctagttcag	atgttgacag	1080
tgttttcatg	aatgttgga	tcttactagt	ccagacttac	ttaggatgtt	gttggggaag	1140
gcacttggga	ttttctgtgt	cttgcaattca	cagagggagg	ccatttcaga	ttcaagagca	1200
ttggattagg	gaatcgtgag	gcagggatgc	tactgcgtat	ttctctctgc	aggttgggga	1260
ttaaagttec	tttcccatg	ggtttgaagc	agactcagac	tgtctcagga	tcaaagcaac	1320
cctcaatggt	tttgatttat	gtcattgctt	accactcccc	aaccaatccc	aggacagctg	1380
ggtcactgta	cccccttgtg	gtatctgtac	ctgggcctct	ccttccctcat	agggaccagc	1440
tgattgaata	aatgtgacca	ccttatttcc	acccccacc	cccaaaagct	acattggaat	1500
tatttttctc	agaaatgtgt	ataacactca	gaattgggca	ttgatcctta	aagcttcctc	1560
ccattcaccg	tattcaacat	ctgtcatctc	ttagtgtctg	cagtctgaac	ctaaccttga	1620
ccttttttcc	ctctggtttg	agaaaacttt	ggacactatt	tctacttggc	caggtgtggg	1680
ctcaagagcc	ttactcttcc	catctcagtt	taggggcgca	gcagctcctc	ttcccaatag	1740
ggctctttct	gctttccctc	tccttggccc	tagatttgta	atccatgaaa	aagcacaagg	1800
tccttggtcc	ttgcggtcac	attctgggtc	tctgtgtttt	gtggactctg	ctctcactgt	1860
tcacccagca	ctagcagtac	cagatgggtc	tgtggagtcc	tggggaatgg	agagagcaca	1920
gtctgactcc	ctgccaagta	gccaggagtt	gacttgccca	tgggtccgctg	gctttccac	1980
cacttcctac	aggatgggat	ctaagagact	caagagctgg	gtttctttca	gcactctgta	2040
ctgtcccaaa	tagcaaacaa	atcactttgt	agccagattt	ctgaatggaa	atgagaaatt	2100
gaattctcca	tggactttta	ggtttatggg	ggagttttag	ctgtgtttct	tggttttatt	2160
tcagccaaac	atgtctgctt	ttgatttttt	ttttaaagta	taagtgggtc	atataatgt	2220
tcacctttta	aatgtaaatg	tttaaaaagt	aagcatttat	gtgtttccat	aactgacatc	2280
tgatgcagac	ctcattctct	ccccctcttc	taccctcctc	ttttccccct	tttcatactc	2340
ttgtattggt	tctaataaat	ggttgctttt	caaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	2400
aaaaat						2406

<210> 46

<211> 2455

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (2454)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (2455)

<223> n equals a,t,g, or c

<400> 46

ggcacgagct	tgaagcatg	aagaccagtt	atatagggaa	caggtttctc	tcagtggcac	60
atthttgcttt	ttctgagccc	caaatacatt	gcctgggcat	gaacattgtt	accgtaaatt	120
gcacatgggtc	atggactgaa	ttatgtgact	ttaaaggatg	taactgccc	acatttgacg	180
attctgggtg	gtctatgtga	ccatttgtct	cgtatccaaa	aaccccgggg	ctattggaac	240
ccttccaaca	ctttttcctt	tgcatagac	aagtttatat	ataacttacc	aagatgttgg	300
ctgtcctgggt	gtattgccag	acagctctct	tttgggtccc	attccaaatg	tgctgctgtc	360
cttctttgca	tttcacaata	tcaaagaaac	caccaccctt	cttcctaaca	gcattttatg	420
ccttttatte	cacattaaat	gggaattgtg	cctacttagg	agtgcctctc	caattaatta	480
catgtgtcca	agaataatcc	aagctagaga	cacaagggtg	gaaaacattt	caaaaaaaaa	540
aagtcctctt	aaggccagta	atthtatctga	aaagggtattt	tatcacacct	tgacacctta	600
tatatgagcc	tattaggagc	tgagggtgg	ttcatagggt	aaaatccaag	aaaagagaag	660
gatgtgtggg	gtttctatta	gaagataatt	ttgttctcat	tttacctttt	cttttatgat	720
ccttctctgc	tagaacaggt	taattctcca	aatttgtttt	gttttgtttt	gttatttttt	780
agggaaactct	tttgcaaaag	caatggctcg	atgtaaataa	catttaaagt	atagtgcaca	840
taacttcccc	ggactgttcc	aatctgataa	tttgtaaata	cttttagagt	tttttaatta	900
acacttgtgt	tgctaaattc	tatttatgta	agtctgctaa	agttttttag	cccacttaaa	960
acttaagaca	accattttaa	ataatggatg	ggttactatg	agcaatttcg	ctttcagaac	1020
ccccttggtt	tagtatatga	aaaagcctaa	tgcgcatata	tgagggtgaa	gagactatga	1080
gaaatatgta	tagtgtatat	tttaaaacag	ctttgcttgt	attgtgaaga	tttaaaaaca	1140
aacttgagat	ttttaacgta	actattaaca	cagttttaac	ataagttatc	ccactgggtt	1200
taagagcatc	ttgaatgtat	aatccttttt	gtaaccagag	ttgggttcta	cttttaccag	1260
tcacccaaac	atatttatgt	tttttagttt	atgtactcat	ttccctttgt	tttctcaaaa	1320
cagcatgatt	tttttgca	tgtagaaatt	ttttaaaaga	aagaaattag	tacatcattt	1380
tctctggatt	ttcttcactt	ccctcttcc	ttctactaac	tccttcctta	aaggccatat	1440
cactccattt	gcattatttg	tgcaaatgcc	aggggtgggt	tttattttta	tttttgctat	1500
ttacctaaaa	aaagaaaatg	cttcagtcaa	ttgctttttt	atttaaaaaa	aaagaaaaga	1560
aaaaaagctg	taaccttatc	atthctgagt	agaccattga	gcgatgaatg	cacacctgta	1620
gtagcccagg	accagctgtg	gtggctaaag	ggaatatgtt	aattaagcaa	gagggtcttt	1680
tctaaaagtg	gtatctgtta	tccacaatgt	atthtagtta	ttcccacaag	tcagggttcc	1740
agataaaatg	aggggttatca	gctaactgat	atgctatcat	tgagggttcat	caatgaattt	1800
gtacatttct	agttcccttt	gggaaggga	aaaatgatga	ttttgcaaga	cctagatttt	1860
ggcttggttt	cttgccctct	tttttgccag	ccttcactct	ctcatctccc	aaacccctg	1920
agcccgtagk	ttttcatagt	ggacaaaaga	cttggtgtct	tttaaaactg	ggactgatac	1980
ttttttgaga	gagtatctgt	tcgaaagtgt	gatgttctac	cactttacca	ataactaatt	2040
ttaaatacac	attgtctct	cgatttttgg	accaaacaga	cgctcacagt	ggaggcttat	2100
caagggttgc	attggggaag	aagcctctcc	ctctctgtca	gcaccagctg	gtaaagggtga	2160
ctgtacagat	gtgcattttc	cttttggtat	aaatgggtcca	cagcactaac	tggttaaggct	2220
tattgtacag	tattattgtca	gtattcttct	ggttcagcat	accttatagt	tcatatataa	2280
cctgtattaa	ttgtatagat	tgtgcattaa	aagctgttac	caagttgtca	gaacataaga	2340
gcgaaaacaa	ggcatatgt	aatattttgt	ttgtaagtat	cctttgtatc	atagcaaagg	2400
aatgttttaa	aaaaatcaac	tgtaataaag	taatttttagt	acaaaaaaaa	aaann	2455

<210> 47

<211> 2574

<212> DNA

<213> Homo sapiens

<400> 47

atttatacta	tgaacattgg	ggtaatacat	tttatttttt	cattgctata	tgacagctaa	60
------------	------------	------------	------------	------------	------------	----

ggggcaaatg attcaagtat attttaaate	agaagtattc aaattatattt	tgtataatac	120
tggtcagtag ttccaagaat aagctctgac	aacagccatt gtttctgctt	ccactcatat	180
tctctacaca ttttaataca gaaatttttg	agaggggggtt actttattgc	ttgtggggtta	240
gtatgtctct tacttcaatt aaggttactt	atttggtttg ccttaagcat	tactttttta	300
actttgtgcc atttgggtctt tactttttat	ggatgttttc aaagaaacta	ttttatattc	360
aatctagttt atttagtcta ctgtatttct	atttcgtgga agccttttcc	cctcaaataa	420
tatattatat cattttttgga cttatataaa	tgataattaa ataaattttt	ttcttaatac	480
tgttggactt tgtatataca agttcaaata	acttttttcca agatagtttc	ttatataaat	540
gtaatttaaat ttttttactc ttctatacag	ttcttttagat gtaaaagaat	tagcacaatc	600
tctggcaggt ttataaaagc tggtagagct	cttgctctgc actgtcttta	ggatcatag	660
gtatcagggt tgccttgtgt taatgccact	tcaagtcatt atttggtttc	tgtatttttt	720
ttacctgagg ataagaagaa tgaatattaa	atttgaatat taaatataat	ttactttcca	780
agcactgtat aatgactgtt cagtgaatat	cagacttccg tgcattaaa	agtcatgaga	840
gacagcacag agaggttata ggttgccctg	gtgtactttt gtccaggagt	aacagggaca	900
gaatactttc ttcccttccct tcaagtacaa	gaaggctttc tctaccattt	gcgtctacac	960
tttattttta aagctatcct tttctagtag	tattttatca tggcaatggc	atgatgacaa	1020
caacagtctt tcattacaga ctgaagggaa	gcatgtcctt acttaaaata	gttctgtctac	1080
tttccctcct attataagga aatyttacag	attctaaaaa tacccttaatt	tttctttgat	1140
ttttatttta ccaagtcaca aatgtctttt	tgatgttttg agaattgttc	tcatagaatc	1200
acaaatactg acatttcatt agatgattat	tttccctagaa tcccaaaga	gcagtggcag	1260
tccatggctt ggttgaagct agaaattttc	ctgcccttg tgacctgta	agcctcctgc	1320
tcggaaccgt gtgagtgggt gaggaagatg	agagatgggc agatggaaga	gagraatata	1380
tgaactgtct tggcctctct ggttctgttc	ttggcccaga gtttttgaaa	agcagcggag	1440
catgactgac ttcacatgct cagctttctc	agccttttgt ttattttgtt	gtccttagat	1500
ttccctgttg taaaaggggc aagaaaagta	actcatcatc tctaacacac	catggcagct	1560
tagccaggta gtcttagtgg tgggtgttag	gcataagata tgctgatcat	cagtcctcagg	1620
ccacagtttc cttactaat cgtccagctt	gagtgttctg ttctcttcc	gcccatttcc	1680
ttgaacctcc tgccttagcc ttggcggagg	gagagtgtct tttgcttttg	ttctccctct	1740
gtcttaggaa aagccatctt taatatagtt	cttcaccacy gttgggggtt	ttttgtgatt	1800
ttttttttct tccgaagaac tcttggtgt	tattggattt tgtattttta	tacaaattat	1860
tgaattttat aagcttgtac acaatattta	attagtgtga aaggaaacaa	agaatgcagg	1920
aaaaataatt taatatcaac ctgagttgac	aagggtgtca gattattcaa	ttcgggatcc	1980
tccttttggt aggtttttga gacaacccta	gacctaaact gtgtcacaga	cttctgaatg	2040
tttaggcagt gctagtaatt tcctcgtaat	gattctgtta ttactttcct	attctttatt	2100
cctctttctt ctgaagatta atgaagttga	aaattgaggt ggataaatac	aaaaaggtag	2160
tgtgatagta taagtatcta agtgcagatg	aaagtgtgtt atatayatcc	attcaaaatt	2220
atgcaagtta gtaattactc aggttaact	aaattacttt aatatgctgt	tgaayctact	2280
ctgttccttg gctagaaaaa attataaaca	ggactttgta gtttgggaag	ccaaattgat	2340
aatattctat gttctaaaag ttgggtctata	cataaattat taagaaatat	ggatttttat	2400
tcccaggata tgggtgttcat tttatgatat	tacgcaggat gatgtattga	gtaaaatcag	2460
ttttgtaaat atgtaaatat gtcataaata	aacaatgctt tgacttattt	ccaaaaaaaa	2520
aaaaaaaaa actcgagggg gggcccggta	cccaattttt ccaaaatggg	cgag	2574

<210> 48

<211> 1760

<212> DNA

<213> Homo sapiens

<400> 48

ggaggagctc aacagcggga aggtgatgta cgccttctgc agagtgaagg accccaactc

60

tggactgccc	aaatttgtcc	tcatcaactg	gacaggcgag	gacgtgggac	cccaggcccc	120
agtgggctct	gtgtaccaga	agaccaatgc	cgtgtctgag	attaaaaggg	ttggtaaaga	180
cagcttcttg	gccaaagcag	agaaggagga	ggagaaccgt	cggttgagg	aaaagcggcg	240
ggccgaggag	gcacagcggc	agctggagca	ggagcgcgg	gagcgtgagc	tgctgaggc	300
tgcacgccgg	gagcagcgt	atcaggagca	gggtggcgag	gccagcccc	agaggacgtg	360
ggagcagcag	caagaagtgg	tttcaaggaa	ccgaaatgag	caggagtctg	ccgtgcaccc	420
gagggagatt	ttcaagcaga	aggagagggc	catgtccacc	acctccatct	ccagtccctca	480
gcctggcaag	ctgaggagcc	ccttcctgca	gaagcagctc	acccaaccag	agaccactt	540
tggcagagag	ccagctgctg	ccatctcaag	gcccagggca	gatctccctg	ctgaggagcc	600
ggcgccacg	actcctccat	gtctggtgca	ggcagaagag	gaggctgtgt	atgaggaacc	660
tccagagcag	gagaccttct	acgagcagcc	ccactggtg	cagcagcaag	gtgctggctc	720
tgagcacatt	gaccaccaca	ttcagggcca	ggggtcagct	gggcaagggc	tctgtgcccg	780
tgccctgtac	gactaccagg	cagccgacga	cacagagatc	tcctttgacc	ccgagaacct	840
catcacgggc	atcgaggtga	tcgacgaagg	ctggtggcgt	ggctatgggc	cggatggcca	900
ttttggcatg	ttccctgcca	actacgtgga	gtcattgag	tgaggctgag	ggcacatctt	960
gcccctcccc	tctcagacat	ggcttcctta	ttgctggaag	aggaggcctg	ggagttgaca	1020
ttcagcactc	ttccaggaat	aggaccccca	gtgaggatga	ggcctcaggg	ctccctccgg	1080
cttgccagac	tcagcctgtc	accccaaatg	cagcaatggc	ctggtgatcc	ccacacatcc	1140
ttctctgcatc	ccccgacct	cccagacagc	ttggctcttg	cccctgacag	gatactgagc	1200
caagccctgc	ctgtggccaa	gccctgagtg	gccactgcca	agctgcgggg	aagggtcctg	1260
agcaggggca	tctgggaggc	tctggtgccc	ttctgcattt	atttgccttt	tttctttttc	1320
tcttgcttct	aaggggtggt	ggccaccact	gtttagaatg	acccttgggg	acagtgaacg	1380
tagagaattg	tttttagcag	agtgtgtgac	caaagtcaga	gtggatcatg	gtggtttggc	1440
agcagggaat	ttgtcttggt	ggagcctgct	ctgtgctccc	cactccattt	ctctgtccct	1500
ctgctgggc	tatgggaagt	gggatgcag	atggccaagc	tcccaccctg	ggtattcaaa	1560
aacggcagac	acaacatggt	cctccacgcg	gtcactcga	tgctgcagg	cccagtggtg	1620
tgctcaact	gattctgact	tcaggaaaag	taacacagag	tggccttggc	ctgttgtctt	1680
ccctatattt	ctgtcccagc	tcatccgtgt	ctctgaagaa	caaatatgct	tttggaccac	1740
gaaaaaaaa	aaaaaaaaa					1760

<210> 49

<211> 1023

<212> DNA

<213> Homo sapiens

<400> 49

acgagggact	gctgaccttc	gggtacctgg	tgtgtctgtc	ccacgttggc	gagcgcattg	60
ctgtggacat	gcggagggcc	ctcttcagct	ccctgctccg	acaagacatc	accttctttg	120
acgccaataa	gacagggcag	ctggtgagcc	gcttgacaac	tgacgtgcag	gagtttaagt	180
catccttcaa	gcttgtcatc	tcccaggggc	tgcgaagctg	caccaggtg	gcaggctgcc	240
tgggtgccct	gtccatgctg	tcgacacgcc	tcacgctgct	gctgatgggtg	gccacaccag	300
ccctgatggg	agtgggcacc	ctgatgggct	caggcctccg	aaaattgtct	cgccagtgtc	360
aggagcagat	cgccagggca	atgggcgtag	cagacgaggc	cctgggcaat	gtgcggactg	420
tgcgagcctt	cgccatggag	caacgggaag	aggagcgcta	tggggcagag	ctggaagcct	480
gccgtgccc	ggcagaggag	ctgggccgcg	gcacgcctt	gttccaaggg	cttccaaca	540
tcgccttcaa	ctgatgggtc	ttgggtaccc	tatttatttg	gggtccctt	gtggccggac	600
agcagctgac	agggggagac	ctcatgtcct	tcctggtggc	ctcccagaca	gtgcaaagct	660
tcctccgtgt	tgaccctgt	ccgaattccc	ttccgctgca	ggctgtgaca	ctccatgcat	720
ggaaggacca	tccttgacag	gctgtgtgag	ctgcccttcc	ccatgcctgc	cacttccagg	780
gatgacaagc	tgaccctgt	ccccacacac	cccaccctta	tagcttattg	ctttgcgttg	840

```

gtccaaaacc acccgtagct gaacctctgg gatgaccaga gctgatcacc agacagctca      900
aggcgggcct tcccggtcct atctcttttc aaagcttaac acaagcagtt ctacataaat      960
atgttatggg aaataatgag atagtaaata tgctgtaaca gataaaaaaa aaaaaaaaaa     1020
aaa                                                    1023

```

<210> 50

<211> 617

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (1)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (9)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (29)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (39)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (41)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (154)

<223> n equals a,t,g, or c

<400> 50

```

nccccatnc ctggctaatt tttgtagana ggggggtccnc nctttgttcc ccagactggg      60
agatTTTTct gtacttggtc gtatgcttcc cattgatctg ctgctgtttt cactattatt     120
ccttcttttg tgtgggtatt ttcttttgat tttnagaatt ttacttgtaa acatgctaca     180
tatacatata atttggtgcc ctgtttttcc atttacatat tatactttcc atattagtag     240
attgtctgat atttctgcat aatactcaat tcaacttacc tgctattgtt ttatcatat      300
ctctattaca aacattaggc ccatttccct tttttaaaag aggaaagttt gaggttatgg      360
gcggtgttct gataaaataa ataatatTTT gtcatgtttg ttttttcatt gattaggaaa     420
cattgttttg aatttaaatgc ctcaaatTTg gtgcacaata atttgaaggg aaaaactgac     480
aagtttgaaa tgaacattga tattacataa tttacattaa aatgatacat cttttgtaaa     540

```

tttgaagaa gaataaataa atgaaaacct gattaccttt caaaaaaaaa aaaaaaaaaa 600
aaaaaaaaaa actcgag 617

<210> 51
<211> 878
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (219)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (222)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (862)
<223> n equals a,t,g, or c

<400> 51
ctattatata gcggcctctc gacttttgag actcgcggtt cettggccag yggtaacaca 60
ggacgtgtgt gcgcatgtgc aagtgtggat gtatgtgtgt gcgtgtgttt tgctcatttc 120
tttagggaac ttgggagtcg ggggttgagg tgctgggcaa tggaacttca aattcaatgt 180
cgcccagcag tgaggggagt cgggaggtga ggcctgtang cnaaccaatt ggtggagtct 240
cagcgatacc caggtgagaa gtggttcacc cagagggcag ggtgggggcc tcgggcagat 300
ctgtccctct tggccctct gtccctcaaat gtccaaaatg ttggaggacc tctgttcata 360
tcccacgcct gggctcttgc cagcagtggg gttactgtag agggatgtcc caagcttggt 420
ttccaatcag tgtaagctg tttgaaactc tectgtgtct gtgttttggt tgtgcgtgtg 480
tgtgagagca catcagtgtg tgcaggctgt gtttcccat ttctctctc cttcagacc 540
catcattgag aacaaatgta agaaatccct tcccaccacc ctccctgcct cccaggccct 600
ctgcggggga aacaagatca cccagcatcc ttccccaccc cagctgtgta tttatataga 660
tggaatatata ctttatattt tgtatcatcg tgcctatagc cgtgccacc gtgtataaat 720
cctggtgtmt gctccttata ctggacatga atgtattgta cactgacgag tccccactcc 780
tgtacagctg ctttgtttct ttgcaatgca ttgtatggct ttataaatga taaagttaa 840
gaaaaaaaa aaaaaaaagg gnggccgctc taaggggt 878

<210> 52
<211> 4561
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (99)
<223> n equals a,t,g, or c

<220>
 <221> SITE
 <222> (105)
 <223> n equals a,t,g, or c

<220>
 <221> SITE
 <222> (106)
 <223> n equals a,t,g, or c

<220>
 <221> SITE
 <222> (1358)
 <223> n equals a,t,g, or c

<400> 52

gcacaccctg	acctaaagac	atagccccc	atcactttca	ccatgtaggg	tctgagcctc	60
tttaaatacca	tattcccgtc	catccagtg	tgtgcaaant	gaganngagt	gtgctttggt	120
ccttccttgg	agtcagcgtc	gcctgtggcc	ccctccgtta	ttgtctcgtg	gccttttgtg	180
ctaaactcgg	ggcctctgct	gtggagtaaa	gaatgtgggt	ttgtgtccct	acctctgtca	240
ctgctggttc	tgcaaccag	gacsattctc	attctactat	ggtgatgccc	ctgayttcgt	300
tgacagcaca	cagacrtgac	ttcagagttc	cgtgcacatg	tgtgcatctt	ctttcccttc	360
tctagagatg	tttggcatct	tcctcctgct	gggttgcaac	rcaggctgct	acagcattct	420
cttatcttcc	tttgccctta	cacagactcc	aagccacg	tagagacgct	gggaccact	480
gtgaagagcg	aagagacaac	cacccctac	cccaccgaag	aggaggccac	agagtgtggg	540
gagaactgca	gctttgagga	tgacaaagat	ttgcagctcc	ttcgggattc	aattgcaact	600
tcgatttcct	cgaggagccc	tgtggttgg	tgtatgacca	tgccaagtgg	ctccggacca	660
cctggggcag	cagctccagc	ccaaacgacc	ggacgtttcc	agatgacagg	aatttcttgc	720
ggctgcagag	tgacagccag	agagagggcc	agtatgccg	gctcatcagc	ccccctgtcc	780
acctgccccg	aagcccggtg	tgcattggag	tccagtacca	ggccacgggc	ggccgcgggg	840
tggcgctgca	ggtggtgcgg	gaagcagcca	ggagagcaag	ttgctgtggg	tcattccgtga	900
gaccagggcg	gcgagtggaa	gcacgggcgg	atcatcctgc	ccagctacga	catggagtac	960
cagatttgtg	tcgagggagt	gatagggaaa	ggacgttccg	gagagattgc	cattgatgac	1020
attcggataa	gcactgatgt	cccactggag	aactgcatgg	aacctatctc	ggcttttgc	1080
gtggacatcc	cagaaataca	tgagagagaa	ggatatgaag	atgaaattga	tgatgaatac	1140
gaggtggact	ggagcaattc	ttcttctgca	acctcaggg	ctggcgcccc	ctcgaccgac	1200
aaagaaaaga	gctggctgta	caccctggat	cccatcctca	tcaccatcat	cgccatgagc	1260
tcactgggcg	tcctcctggg	ggccacctgt	gcaggcctcc	tgctctactg	cacctgttcc	1320
tactcgggcc	tgagctcccc	aagctgcacc	acactgggag	aactacaact	tcgagctcta	1380
cgatggcctt	aagcacaagg	tcaagatgaa	ccaccaaagg	tgctgctccg	aggcatgacg	1440
gattgcacct	gaatcctatc	tgacgtttca	ttccagcaag	aggggctggg	gaagattaca	1500
ttttttttcy	tttgaaact	gaatgccata	atctcgatca	aaccgatcca	gaataccgaa	1560
grtakggaca	ggacagaaaa	gcgagtcgca	ggaggaagg	agatgcagcc	gcacagggga	1620
tgattaccct	cctaggaccg	cggtggctaa	gtcattgcag	gaacggggct	gtgttctctg	1680
ctgggacaaa	acaggagctc	atctcttttg	ggtcacagtt	ctattttgtt	tgtgagtttg	1740
tattattatt	attattatta	ttattattat	tatatattat	ttctttggtc	tgtgagcaac	1800
tcaaagaggc	agaagaggag	aatgactttt	ccagaataga	agtggagcag	tgatcattat	1860
tctccgcttt	ctctttctaa	tcaacacttg	aaaagcaaag	tgtcttttca	gcctttccat	1920
ctttacaaat	aaaactcaaa	aaagccgtcc	agcttatccc	atcctctgat	tgtcttctga	1980
cttaagggat	ttactgtggg	gtaggttctg	ccagccaacc	ctacaagctg	ccatttccag	2040

tcctagcatt	taagtaggat	gttgttgcc	ttaacttttc	ttatccagg	gaaaattgcc	2100
attttaggg	cagcatgaac	agctctttct	tgtatgcgat	ttaaaacaaa	ctggaaagga	2160
aacttcacac	gtcaaaatcc	atagaagcgc	ctggacgagg	cttaaagtgc	tttgtgagtg	2220
aataggagcc	attcgcta	tctagacca	cagtgtctgg	tgggtgggct	tcccttgtgg	2280
ggcttctgg	ggtgggtttg	ccttttcttt	tccctcctcc	atgttcttct	aaaacatata	2340
catatataca	tacacacata	cacatattct	tcagggtctct	aagcccctgg	aagcagcatt	2400
gtgtgatatt	ctcagaggca	ggggaaaata	gagggaaaaa	tagagactat	tgggtatgttc	2460
tcccatcag	cgagttattg	taactgggtca	ccactggacg	ggaaggagaa	cagaggagag	2520
ggaaagagaa	gccccacctc	tgtratcata	tgagggccaa	ggctgagcag	tgtagacaga	2580
gaccctttga	aatgcatttg	tctctcaaat	agactagtaa	acaccgactt	ctcctttggg	2640
ttacaaacac	catttcaacc	tttcgggaga	gtcagagcta	ggatgtacaa	gaactgattc	2700
taaccagaag	tccgcaagta	ctgtggacaa	gaatgcttaa	ccatgctgct	tcagccttga	2760
gagacctagg	ttcttacaca	tatgcacaca	cgcatacaca	catgcacgca	cacacacata	2820
cacacatgca	cgcacgcacg	catgcacacc	aatttatgtt	tttattaagt	gccttgaaaa	2880
aatgaagaaa	aatgtatttt	ccctttatgt	aaaaattagt	gaatatctta	tgaattaagg	2940
cattcctctt	tccctaaccc	cgatggctcc	attcccaagt	accccaactc	actgctgac	3000
ctattaaagg	aatgagtcct	gctacccgag	tggtagtcct	agccctagat	gactctcaac	3060
tactcttcaa	agggaggcat	caggaataga	atgaaactgt	gtgaaggata	agattgttcg	3120
catcaagatc	caaatcttga	tttcatatta	acgcctaagg	attgcctgtg	tgttggaat	3180
atatttgaaa	ctcaaccagt	atgccagcc	tattgcata	cattgtcaga	ccatttttgc	3240
tgtgtgtgtc	acccacgatt	tcatttgtct	tataccagg	tgaaggggga	aggggtgaatg	3300
ggactggctg	gttccttta	atgttaactt	atggaaatgc	tagttcaaat	ggtaatgtca	3360
cagtgttttg	tatgcagaga	gcaagagttc	aaccaacagc	tgtttattca	tgtgtgtgtg	3420
tctttgtctg	tttgagttct	ctgtatctac	tgtgtatgtg	aatggctcatg	tgggactcag	3480
tgggtgtgtt	gtgactttga	cctagggctc	gagtgtcaca	gctgatcttg	gcactcggca	3540
ctcattggca	cagtggtagt	tagaggtgaa	aagtagagct	gtcaagccca	agggcttagc	3600
tttagggctc	ctcctgagtt	cggcccacag	tagaagcaag	attttaacta	gccccctttc	3660
ctcttcaccc	tcccatgatg	cgcagtgttc	agaaagctgg	taagtcctag	ggatttccag	3720
aagtagcctg	cagaagaagg	taagtttgaa	agccactcca	gggttcctga	tgtgtctatg	3780
ctcagtgagc	cattttacag	ttctccaaag	tctagccctg	tttcggacct	gcacttcacc	3840
tctaagttat	gtacaactca	acctgcatcc	ctctaaaagt	cctatatcca	tattcaccat	3900
tggctaattt	gaggccctga	gtgggcyttg	aatgctaaaa	agaagcaggg	tacgsagggc	3960
tacatgtaga	taccacacca	aggctggagg	ctgstctgtc	rtaagacaga	aagaaagacg	4020
ctgggcccac	ttttgacttg	gccaggggac	accttggtgt	gtttgttatc	tttatctgtg	4080
ggtaggctag	ctgacccatc	tccttgagtc	attccctttg	ggaaacccca	ctgccagtat	4140
tgatctcctt	tttgccctgt	actgaatgac	acattacctc	cacactctcc	cggactaggt	4200
ggtcaacagg	gccacaggg	tgctttctgt	ctttgggtgg	gcaggggagt	tgacagggat	4260
gagggtcaca	ggaataagca	tgaatgacaa	gaaaacaagg	gaaagagtta	acctgtcaca	4320
tagcagggtta	actttttcag	ggtttgcagt	tagaggtatt	cgaccattca	ctggctgagc	4380
cagatcacgg	gaacttgaga	gcttttactg	tgattcttca	atgtaaaaaa	taaacaacaa	4440
tgtcaaactg	tgtttatatg	atttgtataa	agccttttta	agattactat	ttaaataaac	4500
attataccag	agaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	agggcgggcg	4560
c						4561

<210> 53

<211> 1317

<212> DNA

<213> Homo sapiens

<400> 53

gctcagtcctg aatgatcatc ttcaatatcc tatctagtga tggagtgaga aaattctcct	60
gaactctggg caggaagttc atattgctca gggtagacca ccatgataaa aataactcac	120
acaggctaata tacaattaat ctaggctctt gacctttaa aaatgtatat aatgtttaca	180
tatgtttata atgtcacgcc atttatttca tttaaaattt taaatgattt tatctttggt	240
cctctcttac aacttattct tggtagaact tattctttgt actataacag cagagatgag	300
taattgggac agactagcct ccaaagcata aacttattta tgatttgcc ctttacagta	360
aaagggccaa atcataaata agtttatgcc cacgcgtccg aacttattta tgatttgcc	420
ctttacagta aaagtctgct catcccaggt tttgcttgct aatttatata ctggcgtttg	480
ttctgatcc tttttattta tttctggcat ccaactctgg tagttcttct tgaatcagtt	540
taatgaagtt tgtaaatgat gtaattaaac gttatttatt acttttattt ttttctagag	600
atagggctctt gctgtgttgc ccaggctggt ctgaaactcc tggcctcaag tgattctcct	660
gctttggcct cccagagttt tgggattaca cgtctgaggg attgcaactca gacactttta	720
tctaaagttt atatactgtt aaactaaaga aaccatatac aaatttcaag tcagggtgctt	780
ttactcatctt tataccttga ttcttgaatg gccagatttt ctgaaaatac ccagttaatg	840
attagattat gctacttcag tcaccacgtg tttgaaggct gatcacagaa aactagaagc	900
aatgtaacta gtttcaaaat ataattaaat ggaggaggaa gtgtttggct ttttccctc	960
cagaccacaa attggtaggt aaagtaaaag tttagatttga aaattgggccc kgggtgtggt	1020
ggcttacacc tctcagcacg ttgggaggcc aagggtgagt gatctgttga gtcccagagt	1080
tttagaccag cctgggcaac atggcaaaat gccattttta ctaaaaatac aaaaatgtag	1140
ctgaatgtgg tggcgcatgc ctgtagtccct agctaccag gaggtgagg tgggaggatc	1200
atctaagccc aggaagttga ggctgcagt agccatgata atgccactgt atgccatcct	1260
gggcaatgga aatgagagac ccccgctcct aaaaaaaaaa aaaaaaaggc cggccgc	1317

<210> 54

<211> 1681

<212> DNA

<213> Homo sapiens

<400> 54

gtcagaatca ccatggccag ctatccttac cggcagggct gccaggagc tgcaggacaa	60
gcaccaggag cccctccggg tagctactac cctggacccc ccaatagtgg agggcagtat	120
ggtagtgggc taccctctgg tgggtggtat gggggctctg cccctggagg gccttatgga	180
ccaccagctg gtggagggcc ctatggacac cccaatcctg ggatgttccc ctctggaact	240
ccaggaggac catatggcgg tgcagctccc gggggccccc atggtcagcc acctccaagt	300
tcctacggtg cccagcagcc tgggctttat ggacagggtg gcgcccctcc caatgtggat	360
cctgaggcct actcctggtt ccagtcggtg gactcagatc acagtggcta tatctccatg	420
aaggagctaa agcaggccct ggtcaactgc aattggtctt cattcaatga tgagacctgc	480
ctcatgatga taaacatggt tgacaagacc aagtcaggcc gcatcgatgt ctacggcttc	540
tcagccctgt ggaaattcat ccagcagtg aagaacctct tccagcagta tgaccgggac	600
cgtcgggct ccattagcta cacagagctg cagcaagctc tgtcccaaat gggctacaac	660
ctgagcccc agttcaccca gcttctggtc tcccgtact gccacgctc tgccaatcct	720
gccatgcagc ttgaccgctt catccaggtg tgcacccagc tgcagggtgct gacagaggcc	780
ttccgggaga aggacacagc tgtacaaggc aacatycggc tcagcttcga ggacttcgtc	840
accatgacag cttctoggat gctatgacct aacctctgt ggagagtgga gtgcaccagg	900
gacctttcct ggcttcttag agtgagagaa gtatgtggac atctcttctt ttcctgtccc	960
tctagaagaa cattctccct tgcttgatgc aacctgttc caaaagaggg tggagagtcc	1020
tgatcatag ccaccaaata gtgaggaccg gggctgaggc cacacagata ggggcctgat	1080
ggaggagagg atagaagttg aatgtcctga tggccatgag cagttgagtg gcacagcctg	1140
gcaccaggag caggctcttg taatggagtt agtgtccagt cagctgagct ccacctgat	1200
gccagtggtg agtgttcatc ggcctgttac cgtagtacc tgtgttccct caccaggcca	1260

tcctgtcaaa	cgagcccatt	ttctccaaag	tggaatctga	ccaagcatga	gagagatctg	1320
tctatgggac	cagtggcttg	gattctgcca	caccataaaa	tccttgtgtg	ttaacttcta	1380
gctgcctggg	gctggccctg	ctcagacaaa	tctgtocct	gggcatcttt	ggccaggctt	1440
ctgccctctg	cagctgggac	ccctcacttg	cctgccatgc	tctgctcggc	ttcagtctcc	1500
aggagacagt	ggtcacctct	ccctgccaat	acttttttta	atttgcattt	tttttcattt	1560
ggggccaaaa	gtccagtga	attgtaagct	tcaataaaaag	gatgaaactc	tggaaaaaaa	1620
aaaaaaaaaa	aaaaaaaaaa	aaaaaaactc	gtaggggggg	cccgtaccca	atcgcctcat	1680
c						1681

<210> 55

<211> 1595

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (1284)

<223> n equals a,t,g, or c

<400> 55

gcgcgcgggc	ccccacctct	gcctccttct	actcgggggc	cccgcccgcc	gccacctctc	60
cccagcccag	gagaggctgc	ggagccgcag	ccgcccagac	cgcgcagcgg	ggaggcagggt	120
tccgcacgaa	ataaatcaga	atgagttatg	cagaaaaaac	cgatgaaatc	acgaaagatg	180
agtggatgga	aaagctcaat	aacttgcatg	tccagagagc	agacatgaac	cgctcatca	240
tgaactacct	ggtcacagag	ggctttaagg	aagcagcgga	gaagtttcga	atggaatctg	300
gaatcgaacc	tagtgtggat	ctggaaacac	ttgatgaacg	aatcaagatc	cgggagatga	360
tactgaaagg	tcagattcag	gaggccatcg	ccttgatcaa	cagcctccac	ccagagctct	420
tggaacacaaa	ccggtatctt	tacttccatt	tgcagcaaca	gcatttgatc	gagctgatcc	480
gccagcggga	gacagaggcg	gcgctggagt	ttgcacagac	tcagctggcg	gacagggcga	540
ggagagccga	gagtgcctca	cagagatgga	gcgtaccctg	gcactgctgg	cctttgacag	600
tcccagaggag	tcgcccttcg	gagacctcct	ccacaccatg	cagaggcaga	aggtgtggag	660
tgaagttaac	caagctgtgc	tagattatga	aaatcgcgag	tcaacaccca	aactggcaaa	720
attactgaaa	ctactacttt	gggctcagaa	cgagctggac	cagaagaaag	taaaatatcc	780
caaaatgaca	gacctcagca	aggggtgtgat	tgaggagccc	aagtagcgcc	tgcgcttgcg	840
tggtggatcc	aacaccagcc	ctgcgtcgtg	ggacttgctt	cagatcagcc	tgcgactgca	900
agattctttac	tgcagtagag	aactcttttt	ctcccttgta	cttttttttg	acctggcatc	960
tttttatagg	gaaaaatggc	ctttgtaggc	agtggaaaac	ttgcaaggaa	agctgccgtc	1020
tctttggcag	tctgatgcag	agcctgcact	ctggcactcg	ctgaagaatc	tggaaggttg	1080
cggtttgctc	ttccagtgtt	cgggggcctc	tggtctgtga	aggattcggg	ctaccacgga	1140
gggctgtgct	gttaggctgc	atccactca	aaatacagga	aaagcacgaa	tcattgattct	1200
gctttctgtt	agcttaggca	gacattgggc	cttcacctac	aagtttttcc	ttacctctgt	1260
ggtttttgtg	tttttttttt	tttntttttt	ccataggaaa	gaatatataa	atttgtaa	1320
cctaattcaa	agatggctca	tgtgtgaggg	cattgagttt	gatttgtttt	ccctttggtc	1380
tgggttgtgt	ggcttttggg	ggatgcgtgt	gagggggcta	tgtgtttttt	aattttttaa	1440
atatatatatt	tgggtgctgt	tgtggtaaga	gacttgttcc	tagtggatca	atgaaccatc	1500
tcttctgggc	agttttgttg	aaaataaagg	tttctctttg	atttcaaraa	wraaaaaaaa	1560
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaac	tcgag			1595

<210> 56

<211> 953

<212> DNA

<213> Homo sapiens

<400> 56

```

ggcacgagca gaattcctgt tgggacaaga gtaggaagag gcaagactga atgagtggtc      60
ctctgcatgg acaccactca ctctgagggc tgcctggcagc atgtaccctc atcctgcctc      120
actccttagc agctagtgtg aacgtgaaga attgagaaat atagtgatca catcagtgtg      180
tattcattct ggtcagcaaa ctaggcatat cttaagtttt ttaggaaatc actggtggcc      240
tccttttgtg tatcatagtg caaaacagtt ttaattagtt gaattattat agatacacia      300
gaatttagaa aatgcgtctg ggcgtggtag ctacacactg tagtcccggc actttgggag      360
tccaaggcga atggatctgc ttaagtccag gagtttgaga ccagcctggg caacatgggt      420
aaaccctgtg tctacaaaaa ctaccgtgtc tacaaaaaaa ttagccaatc atgggtgttg      480
atgtctatgg ttccaactac tttgagaggc tgtggttggg aagatcactt gagcccagga      540
gtagagggtt gcagtgaacc gagatcacac cactgcactc cagcatgggc aaaaaaaat      600
gagactcttg tttaaagaaa aaaaaaaaga gtttagaaat ggccattacg ggccgggcgt      660
ggtgctcacg cctgtaatcc cagcactttg ggaggctgag gtgggtggat catgagggtca      720
ggagatcgag accatcctgg ctaatacggc caaacccmgc ctctactaaa aatacaaaaa      780
atcagctggg cgtggtggca ggtgcctgta gtcccaacta ctctgagggc tgaggcggga      840
gaatgggtgtg aaccggggag gcagagcttg cagtgaaccg agattgcgtc actgcaactcc      900
agcctggggc acagagcgag actccatctc aaaaaaaaaa aaaaaaactc gag          953

```

<210> 57

<211> 1252

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (243)

<223> n equals a,t,g, or c

<400> 57

```

gagaagaagt actactccaa aaacttttgt aaagtgttta ttcttcctta gcagtaggct      60
gttgctgagt ttagactggg tggttttatg aaaaaaaaaa aggttgggga ggtgtgaaga      120
tggaatatgag ggctgtgtta tgtatatctg gtatctactt ctgttccagg tgcttaattc      180
accctcatalc tgatgtttta agttagagga ttcttgtcca tttgtcttgt cttctgtttg      240
canggtcaca tgcaggtaat aggctatggg aagggggaaga tgcctagatt acttctaggc      300
tgggtctccaa gcccgaagtt caagcctcct gagtagctga gactacaggc acacaccatc      360
gttctcaact tttctttttt aacataggct agctagctcc caccttagcc ttctagacct      420
ctccattata attcttattc aattgccttg gcctcccaaa gtgctggaat tacagggtgtg      480
agccactgca cccagctatt ttttctatat ttttatgtag ttcattgagg gtaataattt      540
tatcctacaa caaacatgta agttattgaa gaattattgga gttttatgat aatgctgtca      600
taaatataaaa aggtagggta agagggatcc aaatagagct cacttatatt gtcactgata      660
ggcagtcacg ctgtgctgat agaattgtggc ctgacacttg atggagtgca gcatatgtat      720
acttgggcaa tttgagcaga tatatacggt cccgagttta aagaagagaa caaacaccag      780
tgcacagcta tagtattcct aatataggat gcatttttaa gaatttcaca ttctacaaat      840
ggagagagat ggcaggagaa gccttatttt aagtcctgca ctaaggcagg ttaacctcat      900
gggtgtaatt acctggacct ttttgtaagg acaaaatatt taatcattaa aaggccctct      960
gtaggggtttg aaatatctat attttatata tgaatgcttc ttttattaat atttatggta      1020

```

agatatTTTta	tactgctgat	aaacggacat	taatgatata	tagcctattg	tttgaaaaaa	1080
gcatttttga	ttatagccca	aaactggaaa	taaccaacag	ataaataaat	ggtgggtatat	1140
tcatacaata	aaatactact	cagataaaaa	agatgaactt	aatctcataa	acattatggg	1200
caacatagtg	agaacccatc	tcttttaaaa	aaaaaaaaaa	aaaaaactcg	aa	1252

<210> 58

<211> 1049

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (8)

<223> n equals a,t,g, or c

<400> 58

taccgggncc	ccccccgrgt	tttttttttt	ttttttttta	atattgctcc	cattatgccc	60
aagaatcaaa	gattcttttg	tttgggtgga	ggactctctg	tccacttagc	tccttcccaa	120
ctcagctaca	gattagggtt	gtttcaataa	cataaggact	gttctccaaa	agctctggca	180
actgtggaca	aaaagggtt	cttcgagcta	ttacacaaca	tgtgactttg	ctaaatcaaa	240
cctttattta	taagatatgg	aagaatcagt	tatttgtgtg	ataagacatg	cgaattctag	300
gatagtagga	cctaggcaga	tgtccacatg	aacttgaggg	actttaaaaa	tcttaggatt	360
ttaaactata	cccactttac	tccaacaaaa	tagaccaaat	agctaatact	tacagaatac	420
ttaccctgta	ccaggcacta	agtactttat	atgtgcgaaa	ttaatcctct	cagctctaac	480
tttacaaaacg	aggagacgga	gacacaaagc	agataaggaa	cttgcccagg	atcacagggtg	540
aagtggcaga	ggctcgccct	agctgccaac	agacaccgcc	cccatgccag	gctgctgccc	600
atcgtgagca	gcagtcgccat	gctaccaggc	tccgggtagt	caagaggcca	gcagtgttac	660
aggtaggctg	catcatacag	tcggcaggct	tttgtgagct	agcctgagaa	tctttcacaa	720
cactaaaatt	tgatgcgtct	tcacacagga	agaaacactg	gacttccaat	actgataata	780
acagcagtag	ctaaccattct	aagagcatta	cctacgttaa	ttctttgaat	cctcagaata	840
ccatgaggta	ggtgttatta	ttacccttat	tttacagatg	aagaaactga	ggcacagaga	900
gtctttgtaa	gtaaccaaca	gtttagtaag	tgggagattt	gagattccaa	cccaggcagc	960
ctggcttcag	agtcttggtt	accggagttt	ttaaccctca	cattatgctg	ccctcagaat	1020
gcttatttaa	cctttccgga	cgcgtgggt				1049

<210> 59

<211> 1623

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (1333)

<223> n equals a,t,g, or c

<400> 59

gaattcggca	cgagcagaga	ttgggattgt	ttgattgggt	ctttagcagt	ggtactaata	60
gcaacttctg	tctctagaac	attggaaaat	taaaatgtgt	ttatctaccg	tttttttcct	120
cgaggttata	tgaaggtaga	aatgaatcag	actagatgat	tagctaagcg	agactattaa	180

```

ccctcatccc ttccccctcta gacaactatg aaattagtc aattatgtatkc satccttctw 240
gcagtctctt ctctgacagt tataaaagtg atttaggctg cataaatgttg tttgaatgaa 300
atgaaaatat agactagagc tgtttttttt tttatttcca tcagtctctt cagtgaaaac 360
taacatttga gcatgattct ttttttaaat cattttgtga cagtttagca agggttgtga 420
taagcaagtt atggatatgt aatattttcta gtgtccacgt ttcytcacat gtctgggtga 480
tggaactac taactccatc rggaccttgc ctatagtagg tacycmacat ttactgaatt 540
aatcaataa acatttttaa tgaattacag tacaagtcag acctctgtat ctgtgggctc 600
tgcattctgca aattcagcca accatggatc agaaatatta gaaaaatgga agaacagtcc 660
agcaatacaa gtaatatgaa taaaaacaat acaacaacta tgtacattgt atcagggtatt 720
ataagtaatt tagagatgct ttaagtatac tgaaggattt gcgtagggtta tatgcagata 780
ctgtaccatt ttatataagg aacttgagca tctgtggatt ttgggtattg catggttcct 840
ggaaccaatc ccccagggat actgagggac tatagttgat cataccacct gatttttagag 900
attttctgag tctcagaagt taattaagta aactacaata gtctgttctt aacctcggag 960
gatacattcc aagaacctca gtgaatatct gaaaccacag atagtattga atccaatata 1020
tacacggtaa tattttttcc tatacatatg tatctataaa gtttaaattc taaatcagac 1080
acagtattaa cgataataat aaattartgc aagactgggc atagtgggtc acacctataa 1140
tcttaacact ttaactatga cgttgtctyt gaaaagaaat cagctagccc aagggtgctc 1200
atggctgtaa tcctagtgtt ttgagaagct aagtcaggaa gattgcttga gccaggagt 1260
ctgagaccac cctaggcaac atgggtgaaac cctgtttcta taaaaaatac caaaaaatag 1320
gctgggcgcg gtngctcacg cctgtaatct cagcactttg ggaggctgag gcgggtgat 1380
cacgaggtea ggagattgag accgtcctgg ctaacacggg gaaacccgt ctctactaaa 1440
aatacaaaaa attagccggg agtagtgggc gcctgtagtc ccagctactc aggagactga 1500
ggcaggagaa tggcgtgaac ccgggaggtg gagcttgacg tgaaccgaga tcgcgccact 1560
gcatgccagc ctgggcaaca gagcgagact ccatctcaaa aaaaaaaaaa aaaaaaactc 1620
gaa 1623

```

<210> 60

<211> 15

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (15)

<223> Xaa equals stop translation

<400> 60

Met Leu His Ser Arg Leu Tyr Ser Leu Val Gly Trp Leu Leu Xaa

1 .

5

10

15

<210> 61

<211> 27

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (27)

<223> Xaa equals stop translation

<400> 61

Met Arg Thr Tyr Leu Trp Ile Leu Thr Cys Ile Arg Thr Ser Val Gln
1 5 10 15

Gly Pro Leu Met Thr Met Ala Cys Pro Gly Xaa
20 25

<210> 62

<211> 48

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (48)

<223> Xaa equals stop translation

<400> 62

Met Arg Asn Thr Ala Tyr Leu Pro Ile Ser Leu Leu Leu Val Gly Ser
1 5 10 15

Gly Leu Cys Leu Ala Gln Arg Ile Thr Leu Phe Thr Ser Gly Thr Phe
20 25 30

Arg Arg Lys Arg Leu Tyr Arg Asn Tyr Lys Ala Thr Gln Met Ser Xaa
35 40 45

<210> 63

<211> 72

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (72)

<223> Xaa equals stop translation

<400> 63

Met Asn Gly Lys Trp Ser Leu Met Cys Ser Val Ser Leu Val Ala Leu
1 5 10 15

Gln Leu Thr Val Ala Pro Ala Gly His Pro Ala Gln Asn Ala Gln Lys
20 25 30

Arg Thr Met His Thr Cys Thr Ala Phe Glu Ser His Glu Leu Glu Ala

35 40 45
 Val Val Arg Ala Ser Lys Glu Pro Thr Val Trp Cys Ala Val Gly Ile
 50 55 60
 Trp Arg Gly Arg Gly Pro Gly Xaa
 65 70

<210> 64
 <211> 11
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (11)
 <223> Xaa equals stop translation

<400> 64
 Met Pro Gly Ala Ser Arg Ser Val Cys Leu Xaa
 1 5 10

<210> 65
 <211> 27
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (27)
 <223> Xaa equals stop translation

<400> 65
 Met Leu Pro Glu Cys Leu Leu Cys Cys Val Val Val Gly Met Leu Leu
 1 5 10 15

His Leu Ser Val Pro Gln Phe Pro Gln Leu Xaa
 20 25

<210> 66
 <211> 20
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (20)
 <223> Xaa equals stop translation

<400> 66

Met Ser Phe Thr Ala His Ser Gly Trp Trp Val Ser Leu Leu Phe Trp
1 5 10 15

Val Leu Asp Xaa
20

<210> 67

<211> 95

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (95)

<223> Xaa equals stop translation

<400> 67

Met Arg Thr Ile Tyr Ser Ala Phe Phe Phe Leu Ser Leu Cys Leu Ser
1 5 10 15

Val Leu Leu Ser Ser Thr Val Phe Asp Asp Trp His Pro Ile Ser Ile
20 25 30

Ser Trp Val Gln Asn Phe Gly Leu Thr Pro Ser Phe Asp Val Gln Val
35 40 45

Pro Gln Thr Leu Arg Cys Phe Phe Arg Ser Gly Cys Arg Trp His Pro
50 55 60

Leu Asn Leu Leu Gln Phe Lys Leu Ser Thr Phe Leu Arg Ile Ile Ser
65 70 75 80

Phe Tyr Leu Ser Phe Cys Ser Glu Lys Arg Leu Gln His Glu Xaa
85 90 95

<210> 68

<211> 28

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (28)

<223> Xaa equals stop translation

<400> 68

Met Phe Tyr Trp Gln Arg Leu Gly Leu Ala Leu Leu Ala Ser Val Leu

51

1 5 10 15
Gly Phe Phe Leu Cys Thr Ala Asp Trp Leu Ser Xaa
20 25

<210> 69

<211> 15

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (15)

<223> Xaa equals stop translation

<400> 69

Met Leu Leu Met Phe Phe Thr Phe Trp Thr Arg Glu Arg Leu Xaa
1 5 10 15

<210> 70

<211>

24MFQWFFLFVVFVFLPFSFTGLF*NL*GINS*EQQEKFRIYL*KLHMMMVHTSREKDWIWGY***GDSLVR
EMQNKITLN*FKIITLAKALECQLLERCGAIGTLIRCYRK*LCXA*FGNV**S*RCE*SLTQQFHV*TSTXSLLV
FQGXTYDGPLQNCENEKLKAI*PLG*IQDRMQTKMNN*RYFCQHG*TSKIVLMKLNRYLFYIIQYNVQFQNMQIS
VMYFCHG*ILYKKDLKELIK*SSDSEQW*PAGRKTTEIGERMQMKIPLIIHFF*K*ANTV*PILKI**SWL*VYE
SVLTLCIFLYKLFHNAKK*RIFK*KKKKKKTR

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (24)

<223> Xaa equals stop translation

<400> 70

Met Phe Gln Trp Phe Phe Leu Phe Val Val Phe Val Phe Val Leu Pro
1 5 10 15

Phe Ser Phe Thr Gly Leu Phe Xaa
20

<210> 71

<211> 80

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (80)

<223> Xaa equals stop translation

<400> 71

Met	Gly	Leu	Arg	Pro	Pro	Gln	Ala	Gln	Met	Pro	Pro	Pro	Met	Pro	Ala
1				5					10					15	

Leu	Gly	Ser	Ser	Gly	Pro	His	Pro	Pro	Val	Pro	Pro	Thr	His	Pro	Asn
			20					25					30		

Met	Glu	Gly	Leu	Cys	Leu	Pro	Arg	Ala	Cys	Leu	Ser	Gly	Ala	Cys	Arg
			35					40					45		

Thr	Leu	Pro	Glu	Thr	Leu	Arg	Thr	Ala	Pro	Arg	Lys	Ser	Ser	Leu	Met
	50						55					60			

Pro	Thr	Lys	Ala	Ser	Arg	Thr	Val	Arg	Arg	Ser	Ser	Pro	Arg	Arg	Xaa
65						70				75					80

<210> 72

<211> 135

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (135)

<223> Xaa equals stop translation

<400> 72

Met	Leu	Lys	Leu	Ile	Leu	Leu	Leu	Leu	Phe	Ser	Gly	Ala	Thr	Leu	Ser
1				5					10					15	

Ser	Thr	Trp	Phe	Thr	Leu	Asn	Cys	Leu	Asn	Ser	Ile	Thr	His	Leu	Pro
			20					25					30		

Leu	Thr	Thr	Val	Thr	Leu	Tyr	Ala	Ser	Cys	Ile	Leu	Leu	Gly	Val	Phe
			35				40					45			

Leu	Asn	Ser	Ser	Val	Pro	Ile	Phe	Phe	Glu	Leu	Phe	Val	Glu	Thr	Val
	50					55					60				

Tyr	Pro	Val	Pro	Glu	Gly	Ile	Thr	Cys	Gly	Val	Val	Thr	Phe	Leu	Ser
65						70				75					80

Asn	Met	Phe	Met	Gly	Val	Leu	Leu	Phe	Phe	Leu	Thr	Phe	Tyr	His	Thr
				85						90					95

Glu Leu Ser Trp Phe Asn Trp Cys Leu Pro Gly Ser Cys Leu Leu Ser
100 105 110

Leu Leu Leu Ile Leu Cys Phe Arg Glu Ser Tyr Asp Arg Leu Tyr Leu
115 120 125

Asp Val Val Val Ser Val Xaa
130 135

<210> 73
<211> 42
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (42)
<223> Xaa equals stop translation

<400> 73
Met Glu Glu Val Lys Pro Ala Ser Trp Trp Val Leu Val Ser Tyr Gly
1 5 10 15

Val Leu Leu Val Thr Leu Gly Ala Phe Ile Phe Gly Gln Thr Thr Ala
20 25 30

Asn Ala Ile Phe Val Asp Leu Leu Ala Xaa
35 40

<210> 74
<211> 40
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (40)
<223> Xaa equals stop translation

<400> 74
Met Ser Glu Ala Gly Trp Trp Ala Trp Leu Phe Val Ile Leu His Pro
1 5 10 15

Phe Gly Met Pro Asp Thr Phe His Asn Asn Phe Lys Lys Asp Lys Thr
20 25 30

Thr Ala Glu Lys Cys Ile Glu Xaa
35 40

<210> 75
<211> 29
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (29)
<223> Xaa equals stop translation

<400> 75
Met Ser Pro Asn Cys His Leu Leu Glu Thr Arg Pro Ser Ala Ser Leu
1 5 10 15

Leu Leu Leu Gly Ile Pro Leu Leu Arg Gly Ala Ser Xaa
20 25

<210> 76
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (48)
<223> Xaa equals stop translation

<400> 76
Met Cys Gly Arg Gln Pro Met Arg Leu Trp Val Ser Phe Ala Val His
1 5 10 15

Cys Thr Arg Pro Val Lys Ala Ala Pro Arg Asn Pro Thr Leu Leu Leu
20 25 30

Cys Arg Leu Pro Trp Pro Glu Ser Cys His Pro Thr Cys Arg Gln Xaa
35 40 45

<210> 77
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> SITE

55

<222> (39)

<223> Xaa equals stop translation

<400> 77

Met Arg Val Val Leu Pro Ser Trp Leu Gly Ser Ser Gly Cys Trp Asp
 1 5 10 15

Ile Leu Ser Leu Leu Cys Phe Asn Ile Phe Thr Ala Leu Phe Leu Asn
 20 25 30

Gly Pro Val Thr Arg Asp Xaa
 35

<210> 78

<211> 124

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (124)

<223> Xaa equals stop translation

<400> 78

Glu Leu Leu Ile Leu Asn Phe Cys Lys Cys Phe Leu Leu Gln Ser Met
 1 5 10 15

Val Phe Ala Lys Thr Cys Gly Ser Trp Arg Ser Gln Ala Cys Leu Val
 20 25 30

Gly Thr Ser Met Arg Ser Val Leu Asn Pro Arg Val Lys Ser Gly Arg
 35 40 45

Phe Val Lys Ile Leu Pro Asp Tyr Glu His Met Ala Tyr Arg Asp Val
 50 55 60

Tyr Thr Cys Leu Leu His Arg Tyr Arg His Ile Leu Gly Leu Trp Gln
 65 70 75 80

Pro Asp Ile Gly Pro Tyr Gly Gly Leu Leu Asn Val Val Val Asp Gly
 85 90 95

Leu Phe Ile Ile Val Met Arg Arg Ala Pro Pro Ile Cys Thr Val His
 100 105 110

Ser Thr Ser Ile Ala Phe Leu Phe Tyr Phe Phe Xaa
 115 120

<210> 79

<211> 34
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (13)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (16)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (30)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (34)
 <223> Xaa equals stop translation

<400> 79
 Ser Leu Gly Gly Trp Gly Gly Gly Gln Glu Gly Lys Xaa Gly Gly Xaa
 1 5 10 15

Lys Leu Gly Asp Ser Leu Arg Asp Phe Cys Phe Lys Pro Xaa Val Phe
 20 25 30

Leu Xaa

<210> 80
 <211> 52
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (52)
 <223> Xaa equals stop translation

<400> 80
 Met Arg Leu Gly Pro Asn Arg Met Arg Gly Arg Val Leu His Ala Trp
 1 5 10 15

Leu Pro Leu Leu Leu Leu Leu Leu Leu Gln Cys Thr His His Ser
 20 25 30

Ser Gln Leu Leu Leu Leu Leu Ala Tyr Ser Leu Arg Asn Leu Ser
35 40 45

Leu Val Leu Xaa
50

<210> 81
<211> 16
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (16)
<223> Xaa equals stop translation

<400> 81
Met Phe Ser Ile Ile Ala Phe Pro Leu Ile Leu Leu Thr Cys Cys Xaa
1 5 10 15

<210> 82
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (51)
<223> Xaa equals stop translation

<400> 82
Met Asp Val Leu Thr Val Ala Phe Leu Ser Ile Leu Ile Thr Ala Pro
1 5 10 15

Ile Gly Ser Leu Leu Ile Gly Leu Leu Gly Pro Arg Leu Leu Gln Lys
20 25 30

Val Glu His Gln Asn Lys Asp Glu Glu Val Gln Gly Glu Thr Ser Val
35 40 45

Gln Val Xaa
50

<210> 83

<211> 66
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (66)
<223> Xaa equals stop translation

<400> 83
Met Ser Gly Ala Pro Thr Ala Gly Ala Ala Leu Met Leu Cys Ala Ala
1 5 10 15
Thr Ala Val Leu Leu Ser Ala Gln Gly Gly Pro Val Gln Ser Lys Ser
20 25 30
Pro Arg Phe Ala Ser Trp Asp Glu Met Asn Val Leu Ala His Gly Leu
35 40 45
Leu Gln Leu Gly Gln Gly Leu Arg Glu His Ala Glu Ala Pro Ala Val
50 55 60
Ser Xaa
65

<210> 84
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (39)
<223> Xaa equals stop translation

<400> 84
Met Ile Gly Thr Leu His Leu Ser Leu Ser Val Ile Leu Ala Ser Val
1 5 10 15
Leu Phe Ala Tyr Gln Asn Ala Val Cys Phe Cys Gln Arg Ile Thr Ile
20 25 30
Lys Pro Leu Arg Pro Asn Xaa
35

<210> 85
<211> 32
<212> PRT
<213> Homo sapiens

<220>

<221> SITE

<222> (32)

<223> Xaa equals stop translation

<400> 85

Glu Trp Thr Leu Arg Tyr Phe Arg Cys Val Leu Phe Ser Ile Ala Ala

1

5

10

15

Val Phe Val Thr Val Leu Val Met Val His Val His Ile Leu Leu Xaa

20

25

30

<210> 86

<211> 10

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (10)

<223> Xaa equals stop translation

<400> 86

Asn Leu Gln Phe Ser Met Thr Gln Leu Xaa

1

5

10

<210> 87

<211> 19

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (19)

<223> Xaa equals stop translation

<400> 87

Met Leu Cys Phe Ser Phe Leu Cys Leu Ser Leu Leu Val Ser Ala

1

5

10

15

Gln Gly Xaa

<210> 88

<211> 70
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (70)
<223> Xaa equals stop translation

<400> 88
Met Lys Leu Leu Leu Cys Phe Trp Val Asn Arg Cys Ala Cys Gln Leu
1 5 10 15
Ala Cys Val Leu Ser Lys Phe His Lys Leu Lys Val Phe Lys Gly Cys
20 25 30
Val Val Ser Glu Leu Tyr Val Ser Phe Leu Ser Leu Tyr Leu Gln Arg
35 40 45
Val Arg Asn Glu Ile Tyr Thr Ser Lys Val Ser Leu Ile Asn Met Ala
50 55 60
Phe Cys Phe Ser Met Xaa
65 70

<210> 89
<211> 4
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (4)
<223> Xaa equals stop translation

<400> 89
Met Phe Pro Xaa
1

<210> 90
<211> 62
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (62)
<223> Xaa equals stop translation

<400> 90

Met Trp Leu Phe Arg Ser Leu Ser Gly Leu Phe Thr Asp Ile Leu Ala
 1 5 10 15

Ser Pro Gln Leu Ser Leu Thr Lys Gly Tyr Ser Gln Lys Trp Ser Pro
 20 25 30

Tyr Phe Pro Ser Ser Asn Asp Tyr Leu Pro Gly Gly Arg Ser Ser Ser
 35 40 45

Val His Ser Ile Cys Phe Arg Thr Tyr Ala Gln Arg Leu Xaa
 50 55 60

<210> 91

<211> 55

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (55)

<223> Xaa equals stop translation

<400> 91

Met Leu Gln Tyr Lys Ala Leu Ser Met Ser Gly Lys Ser Leu Leu Gln
 1 5 10 15

Lys Arg Leu Gln Ile Thr Leu Thr Cys Ala Trp Leu Cys Trp Met Val
 20 25 30

Tyr Ser Val Ser Phe Phe Phe Met Gly Glu Thr Ala His Arg Ala His
 35 40 45

Gln Gln Val Leu Gln Asn Xaa
 50 55

<210> 92

<211> 32

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (32)

<223> Xaa equals stop translation

<400> 92

Met Tyr Asn Leu Leu Tyr Phe Pro Leu Cys Ile Leu Leu Trp Val Phe
 1 5 10 15

Cys Gly Ser Gln Asp Ser Ser Leu Arg Phe Ile Ser His Glu Ser Xaa
20 25 30

<210> 93
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (37)
<223> Xaa equals stop translation

<400> 93
Met Ala Cys Leu Glu Leu Leu Ile Leu Val Ser Phe Leu Thr Ser Val
1 5 10 15

Ile Gln Thr Gln Pro Pro Arg Glu Leu Asp Pro Ser Leu Phe Ser Val
20 25 30

Phe Ser Leu Ala Xaa
35

<210> 94
<211> 41
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (41)
<223> Xaa equals stop translation

<400> 94
Gly Ile Leu Leu Val Gln Thr Tyr Leu Gly Cys Cys Trp Gly Arg His
1 5 10 15

Leu Gly Phe Ser Val Ser Cys Ile His Arg Gly Arg Pro Phe Gln Ile
20 25 30

Gln Glu His Trp Ile Arg Glu Ser Xaa
35 40

<210> 95

<211> 109
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (109)
<223> Xaa equals stop translation

<400> 95

Ile Thr Tyr Gln Asp Val Gly Cys Pro Gly Val Leu Pro Asp Ser Ser
1 5 10 15
Leu Leu Val Pro Ile Pro Asn Val Leu Leu Ser Phe Phe Ala Phe His
20 25 30
Asn Ile Lys Glu Thr Thr Thr Leu Leu Pro Asn Ser Ile Leu Cys Leu
35 40 45
Leu Phe His Ile Lys Trp Glu Leu Cys Leu Leu Arg Ser Ala Pro Pro
50 55 60
Ile Asn Tyr Met Cys Pro Arg Ile Ile Gln Ala Arg Asp Thr Arg Trp
65 70 75 80
Glu Asn Ile Ser Lys Lys Lys Ser Pro Leu Lys Ala Ser Asn Leu Ser
85 90 95
Glu Lys Val Phe Tyr His Thr Leu Thr Pro Tyr Ile Xaa
100 105

<210> 96
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (39)
<223> Xaa equals stop translation

<400> 96

Met Phe Ser Lys Lys Leu Phe Tyr Ile Gln Ser Ser Leu Phe Ser Leu
1 5 10 15
Leu Tyr Phe Tyr Phe Val Glu Ala Phe Ser Pro Gln Ile Ile Tyr Tyr
20 25 30
Ile Ile Phe Gly Leu Ile Xaa
35

<210> 97
<211> 81
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (81)
<223> Xaa equals stop translation

<400> 97
Met Gly Arg Met Ala Ile Leu Ala Cys Ser Leu Pro Thr Thr Trp Ser
1 5 10 15
Ser Leu Ser Glu Ala Glu Gly Thr Ser Cys Pro Ser Pro Leu Arg His
20 25 30
Gly Phe Leu Ile Ala Gly Arg Gly Gly Leu Gly Val Asp Ile Gln His
35 40 45
Ser Ser Arg Asn Arg Thr Pro Ser Glu Asp Glu Ala Ser Gly Leu Pro
50 55 60
Pro Ala Trp Gln Thr Gln Pro Val Thr Pro Asn Ala Ala Met Ala Trp
65 70 75 80

Xaa

<210> 98
<211> 161
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (161)
<223> Xaa equals stop translation

<400> 98
Met Leu Ser Thr Arg Leu Thr Leu Leu Leu Met Val Ala Thr Pro Ala
1 5 10 15
Leu Met Gly Val Gly Thr Leu Met Gly Ser Gly Leu Arg Lys Leu Ser
20 25 30
Arg Gln Cys Gln Glu Gln Ile Ala Arg Ala Met Gly Val Ala Asp Glu
35 40 45

Ala Leu Gly Asn Val Arg Thr Val Arg Ala Phe Ala Met Glu Gln Arg
 50 55 60

Glu Glu Glu Arg Tyr Gly Ala Glu Leu Glu Ala Cys Arg Cys Arg Ala
 65 70 75 80

Glu Glu Leu Gly Arg Gly Ile Ala Leu Phe Gln Gly Leu Ser Asn Ile
 85 90 95

Ala Phe Asn Cys Met Val Leu Gly Thr Leu Phe Ile Gly Gly Ser Leu
 100 105 110

Val Ala Gly Gln Gln Leu Thr Gly Gly Asp Leu Met Ser Phe Leu Val
 115 120 125

Ala Ser Gln Thr Val Gln Ser Phe Leu Arg Val Ala Pro Cys Pro Asn
 130 135 140

Ser Leu Pro Leu Gln Ala Val Thr Leu His Ala Trp Lys Asp His Pro
 145 150 155 160

Xaa

<210> 99

<211> 60

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (24)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (60)

<223> Xaa equals stop translation

<400> 99

Met Leu Ser Ile Asp Leu Leu Leu Phe Ser Leu Leu Phe Leu Leu Leu
 1 5 10 15

Cys Gly Tyr Phe Leu Leu Ile Xaa Arg Ile Leu Leu Val Asn Met Leu
 20 25 30

His Ile His Ile Ile Trp Cys Pro Val Phe Pro Phe Thr Tyr Tyr Thr
 35 40 45

Phe His Ile Ser Thr Leu Ser Asp Ile Ser Ala Xaa
50 55 60

<210> 100
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (27)
<223> Xaa equals stop translation

<400> 100
Met Ser Gln Ala Cys Phe Pro Ile Ser Val Lys Leu Phe Glu Thr Leu
1 5 10 15

Leu Cys Leu Cys Phe Val Cys Ala Cys Val Xaa
20 25

<210> 101
<211> 40
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (40)
<223> Xaa equals stop translation

<400> 101
Met Pro Ser Leu Leu His Ile Ile Val Arg Pro Phe Leu Leu Leu Trp
1 5 10 15

Ser Pro Thr Ile Ser Phe Val Leu Tyr Pro Gly Glu Arg Gly Arg Val
20 25 30

Asn Gly Thr Gly Trp Phe Leu Xaa
35 40

<210> 102
<211> 36
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (36)

<223> Xaa equals stop translation

<400> 102

Met Ile Leu Ser Leu Val Leu Ser Tyr Asn Leu Phe Leu Val Gln Leu
1 5 10 15

Ile Leu Cys Thr Ile Thr Ala Glu Met Ser Asn Trp Asp Arg Leu Ala
20 25 30

Ser Lys Ala Xaa
35

<210> 103

<211> 73

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (73)

<223> Xaa equals stop translation

<400> 103

Met Gly Tyr Asn Leu Ser Pro Gln Phe Thr Gln Leu Leu Val Ser Arg
1 5 10 15

Tyr Cys Pro Arg Ser Ala Asn Pro Ala Met Gln Leu Asp Arg Phe Ile
20 25 30

Gln Val Cys Thr Gln Leu Gln Val Leu Thr Glu Ala Phe Arg Glu Lys
35 40 45

Asp Thr Ala Val Gln Gly Asn Ile Arg Leu Ser Phe Glu Asp Phe Val
50 55 60

Thr Met Thr Ala Ser Arg Met Leu Xaa
65 70

<210> 104

<211> 42

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (31)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE
<222> (42)
<223> Xaa equals stop translation

<400> 104

Met Ile Leu Leu Ser Val Ser Leu Gly Arg His Trp Ala Phe Thr Tyr
1 5 10 15

Lys Phe Phe Leu Thr Pro Val Val Phe Val Phe Phe Phe Xaa Phe
20 25 30

Phe His Arg Lys Glu Tyr Ile Asn Leu Xaa
35 40

<210> 105
<211> 35
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (35)
<223> Xaa equals stop translation

<400> 105

Met Ser Gly Pro Leu His Gly His His Ser Leu Leu Arg Leu Leu Ala
1 5 10 15

Ala Cys Thr Leu Ile Leu Pro His Ser Leu Ala Ala Ser Val Asn Val
20 25 30

Lys Asn Xaa
35

<210> 106
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (17)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (48)
<223> Xaa equals stop translation

<400> 106

Met Phe Lys Val Arg Gly Phe Leu Ser Ile Cys Leu Val Phe Cys Trp
1 5 10 15

Xaa Gly His Met Gln Val Ile Gly Tyr Gly Lys Gly Lys Met Pro Arg
20 25 30

Leu Leu Leu Gly Trp Ser Pro Ser Pro Lys Phe Lys Pro Pro Glu Xaa
35 40 45

<210> 107

<211> 6

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (6)

<223> Xaa equals stop translation

<400> 107

Phe Cys Glu Leu Ala Xaa
1 5

<210> 108

<211> 23

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (8)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (23)

<223> Xaa equals stop translation

<400> 108

Met Lys Leu Val Ile Met Tyr Xaa Ile Leu Leu Ala Val Ser Ser Leu
1 5 10 15

Thr Val Ile Lys Val Ile Xaa
20

70

<210> 109
 <211> 141
 <212> PRT
 <213> Homo sapiens

<400> 109

Tyr Cys Glu Lys Tyr Asp Ser Arg Thr Asn Ser Phe Cys Lys Arg Leu
 1 5 10 15

Lys Ser Leu Cys Pro Glu His Arg Lys Leu Gly Asp Glu Gln His Leu
 20 25 30

Lys Val Cys Gly Tyr Pro Lys Lys Trp Glu Asp Gly Met Ile Glu Thr
 35 40 45

Ala Lys Thr Val Ser Glu Leu Ile Glu Met Glu Asp Pro Phe Gly Glu
 50 55 60

Glu Gly Cys Arg Thr Lys Lys Asp Ala Cys His Lys His His Lys Trp
 65 70 75 80

Ile Pro Ser Leu Arg Gly Thr Ile Glu Leu Glu Gln Ala Cys Leu Phe
 85 90 95

Gln Lys Met Tyr Glu Leu Cys His Glu Met His Lys Leu Asn Ala His
 100 105 110

Ala Glu Trp Thr Thr Asn Ala Leu Ser Ile Met Met His Lys Gln Pro
 115 120 125

Ser Thr Glu Lys Cys Ser Phe Phe Leu Arg Asn Phe Ala
 130 135 140

<210> 110
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 110

Phe Cys Asp Val Tyr Asn Pro Gln Ser Lys Thr Tyr Cys Lys Arg Leu
 1 5 10 15

Gln Val Leu Cys Pro Glu His Ser Arg Asp Pro Lys Val Pro Ala Asp
 20 25 30

Glu Val Cys Gly Cys Pro Leu Val Arg Asp Val Phe Glu Leu Thr Gly
 35 40 45

Asp Phe Cys Arg Leu Pro Lys Arg Gln Cys Asn Arg His Tyr Cys Trp

50 55 60
 Glu Lys Leu Arg Arg Ala Glu Val Asp Leu Glu Arg Val Arg Val Trp
 65 70 75 80
 Tyr Lys Leu Asp Glu Leu Phe Glu Gln Glu Arg Asn Val Arg Thr Ala
 85 90 95

 Met Thr Asn Arg Ala Gly Leu Leu Ala Leu Met Leu His Gln Thr Ile
 100 105 110
 Gln His Asp Pro Leu Thr Thr Asp Leu Arg Ser Ser Ala
 115 120 125

 <210> 111
 <211> 323
 <212> PRT
 <213> Homo sapiens

 <400> 111
 Pro Ala Pro Gly Ala Ser Ala Gln Thr Pro Asn Pro Asn Ala Ala Gly
 1 5 10 15
 Ala Ser Ala Ser Gly Ser Ala Asn Tyr Lys Leu Met Cys Thr Leu Glu
 20 25 30
 Gly His Thr Lys Ser Ile Ser Ser Ala Lys Phe Ser Pro Cys Gly Lys
 35 40 45
 Tyr Leu Gly Thr Ser Ser Ala Asp Lys Thr Val Lys Ile Trp Asn Met
 50 55 60
 Asp His Met Ile Cys Glu Arg Thr Leu Thr Gly His Lys Leu Gly Val
 65 70 75 80
 Asn Asp Ile Ala Trp Ser Ser Asp Ser Arg Cys Val Val Ser Ala Ser
 85 90 95
 Asp Asp Lys Thr Leu Lys Ile Phe Glu Ile Val Thr Ser Arg Met Thr
 100 105 110
 Lys Thr Leu Lys Gly His Asn Asn Tyr Val Phe Cys Cys Asn Phe Asn
 115 120 125
 Pro Gln Ser Ser Leu Val Val Ser Gly Ser Phe Asp Glu Ser Val Arg
 130 135 140
 Ile Trp Asp Val Lys Thr Gly Met Cys Ile Lys Thr Leu Pro Ala His
 145 150 155 160

Ser Asp Pro Val Ser Ala Val Ser Phe Asn Arg Asp Gly Ser Leu Ile
 165 170 175
 Ala Ser Gly Ser Tyr Asp Gly Leu Val Arg Ile Trp Asp Thr Ala Asn
 180 185 190
 Gly Gln Cys Ile Lys Thr Leu Val Asp Asp Glu Asn Pro Pro Val Ala
 195 200 205
 Phe Val Lys Phe Ser Pro Asn Gly Lys Tyr Ile Leu Ala Ser Asn Leu
 210 215 220
 Asp Ser Thr Leu Lys Leu Trp Asp Phe Ser Lys Gly Lys Thr Leu Lys
 225 230 235 240
 Gln Tyr Thr Gly His Glu Asn Ser Lys Tyr Cys Ile Phe Ala Asn Phe
 245 250 255
 Ser Val Thr Gly Gly Lys Trp Ile Ile Ser Gly Ser Glu Asp Cys Lys
 260 265 270
 Ile Tyr Ile Trp Asn Leu Gln Thr Arg Glu Ile Val Gln Cys Leu Glu
 275 280 285
 Gly His Thr Gln Pro Val Leu Ala Ser Asp Cys His Pro Val Gln Asn
 290 295 300
 Ile Ile Ala Ser Gly Ala Leu Glu Pro Asp Asn Lys Ile His Ile Trp
 305 310 315 320
 Arg Ser Asp

<210> 112

<211> 317

<212> PRT

<213> Homo sapiens

<400> 112

Pro Thr Pro Ser Ser Ser Ala Thr Gln Ser Lys Pro Thr Pro Val Lys
 1 5 10 15
 Pro Asn Tyr Ala Leu Lys Phe Thr Leu Ala Gly His Thr Lys Ala Val
 20 25 30
 Ser Ser Val Lys Phe Ser Pro Asn Gly Glu Trp Leu Ala Ser Ser Ser
 35 40 45
 Ala Asp Lys Leu Ile Lys Ile Trp Gly Ala Tyr Asp Gly Lys Phe Glu
 50 55 60

Lys Thr Ile Ser Gly His Lys Leu Gly Ile Ser Asp Val Ala Trp Ser
65 70 75 80

Ser Asp Ser Asn Leu Leu Val Ser Ala Ser Asp Asp Lys Thr Leu Lys
85 90 95

Ile Trp Asp Val Ser Ser Gly Lys Cys Leu Lys Thr Leu Lys Gly His
100 105 110

Ser Asn Tyr Val Phe Cys Cys Asn Phe Asn Pro Gln Ser Asn Leu Ile
115 120 125

Val Ser Gly Ser Phe Asp Glu Ser Val Arg Ile Trp Asp Val Lys Thr
130 135 140

Gly Lys Cys Leu Lys Thr Leu Pro Ala His Ser Asp Pro Val Ser Ala
145 150 155 160

Val His Phe Asn Arg Asp Gly Ser Leu Ile Val Ser Ser Ser Tyr Asp
165 170 175

Gly Leu Cys Arg Ile Trp Asp Thr Ala Ser Gly Gln Cys Leu Lys Thr
180 185 190

Leu Ile Asp Asp Asp Asn Pro Pro Val Ser Phe Val Lys Phe Ser Pro
195 200 205

Asn Gly Lys Tyr Ile Leu Ala Ala Thr Leu Asp Asn Thr Leu Lys Leu
210 215 220

Trp Asp Tyr Ser Lys Gly Lys Cys Leu Lys Thr Tyr Thr Gly His Lys
225 230 235 240

Asn Glu Lys Tyr Cys Ile Phe Ala Asn Phe Ser Val Thr Gly Gly Lys
245 250 255

Trp Ile Val Ser Gly Ser Glu Asp Asn Leu Val Tyr Ile Trp Asn Leu
260 265 270

Gln Thr Lys Glu Ile Val Gln Lys Leu Gln Gly His Thr Asp Val Val
275 280 285

Ile Ser Thr Ala Cys His Pro Thr Glu Asn Ile Ile Ala Ser Ala Ala
290 295 300

Leu Glu Asn Asp Lys Thr Ile Lys Leu Trp Lys Ser Asp
305 310 315

<210> 113

<211> 83

<212> PRT

<213> Homo sapiens

<400> 113

Val Gln Ala Val Leu Asn Asp Glu Arg Tyr Gln Ser Phe Lys Leu Phe
1 5 10 15

Thr Ser Val Phe Gly Val Gly Leu Lys Thr Ala Asp Lys Trp Tyr Arg
20 25 30

Met Gly Phe Arg Thr Leu Asn Lys Ile Arg Ser Asp Lys Thr Leu Lys
35 40 45

Leu Thr Lys Met Gln Lys Ala Gly Leu Cys Tyr Tyr Glu Asp Leu Ile
50 55 60

Asp Cys Val Ser Lys Ala Glu Ala Asp Ala Val Ser Leu Leu Val Gln
65 70 75 80

Asp Ala Val

<210> 114

<211> 82

<212> PRT

<213> Homo sapiens

<400> 114

Val Glu Arg Val Arg Arg Ser Glu Arg Tyr Gln Thr Met Lys Leu Phe
1 5 10 15

Thr Gln Ile Phe Gly Val Gly Val Lys Thr Ala Asp Arg Trp Tyr Arg
20 25 30

Glu Gly Leu Arg Thr Leu Asp Asp Leu Arg Glu Gln Pro Gln Lys Leu
35 40 45

Thr Gln Gln Gln Lys Ala Gly Leu Gln His His Gln Asp Leu Ser Thr
50 55 60

Pro Val Leu Arg Ser Asp Val Asp Ala Leu Gln Gln Val Val Glu Glu
65 70 75 80

Ala Val

<210> 115

<211> 504

<212> PRT

<213> Homo sapiens

<400> 115

Glu Lys Ile Glu Arg Lys Gln Pro Lys Thr Phe Ala Phe Asp His Cys
 1 5 10 15

Phe Tyr Ser Leu Asn Pro Glu Asp Glu Asn Phe Ala Ser Gln Glu Thr
 20 25 30

Val Phe Asp Cys Val Gly Arg Gly Ile Leu Asp Asn Ala Phe Gln Gly
 35 40 45

Tyr Asn Ala Cys Ile Phe Ala Tyr Gly Gln Thr Gly Ser Gly Lys Ser
 50 55 60

Tyr Thr Met Met Gly Thr Gln Glu Ser Lys Gly Ile Ile Pro Arg Leu
 65 70 75 80

Cys Asp Gln Leu Phe Ser Ala Ile Ala Asn Lys Ser Thr Pro Glu Leu
 85 90 95

Met Tyr Lys Val Glu Val Ser Tyr Met Glu Ile Tyr Asn Glu Lys Val
 100 105 110

His Asp Leu Leu Asp Pro Lys Pro Asn Lys Gln Ser Leu Lys Val Arg
 115 120 125

Glu His Asn Val Met Gly Pro Tyr Val Asp Gly Leu Ser Gln Leu Ala
 130 135 140

Val Thr Ser Tyr Gln Asp Ile Asp Asn Leu Met Thr Glu Gly Asn Lys
 145 150 155 160

Ser Arg Thr Val Ala Ala Thr Asn Met Asn Ala Glu Ser Ser Arg Ser
 165 170 175

His Ala Val Phe Ser Val Val Leu Thr Gln Ile Leu Thr Asp Gln Ala
 180 185 190

Thr Gly Val Ser Gly Glu Lys Val Ser Arg Met Ser Leu Val Asp Leu
 195 200 205

Ala Gly Ser Glu Arg Ala Val Lys Thr Gly Ala Val Gly Asp Arg Leu
 210 215 220

Lys Glu Gly Ser Asn Ile Asn Lys Ser Leu Thr Thr Leu Gly Leu Val
 225 230 235 240

Ile Ser Lys Leu Ala Asp Gln Ser Asn Gly Lys Lys Ser Gly Asn Asp
 245 250 255

Lys Phe Val Pro Tyr Arg Asp Ser Val Leu Thr Trp Leu Leu Lys Asp
260 265 270

Asn Leu Gly Gly Asn Ser Arg Thr Val Met Val Ala Thr Ile Ser Pro
275 280 285

Ser Ala Asp Asn Tyr Glu Glu Thr Leu Ser Thr Leu Arg Tyr Ala Asp
290 295 300

Arg Ala Lys Arg Ile Val Asn His Ala Val Val Asn Glu Asp Pro Asn
305 310 315 320

Ala Arg Ile Ile Arg Glu Leu Arg His Glu Val Glu Thr Leu Arg Ser
325 330 335

Met Leu Lys His Ala Thr Gly Ser Pro Val Gly Asp Val Gln Asp Lys
340 345 350

Leu Ala Glu Ser Glu Asn Leu Met Lys Gln Ile Ser Gln Thr Trp Glu
355 360 365

Glu Lys Leu Val Lys Thr Glu Arg Ile Gln Asn Glu Arg Gln Gln Ala
370 375 380

Leu Glu Lys Met Gly Ile Ser Val Gln Ala Ser Gly Ile Lys Val Glu
385 390 395 400

Lys Asn Lys Tyr Tyr Leu Val Asn Leu Asn Ala Asp Pro Ser Leu Asn
405 410 415

Glu Leu Leu Val Tyr Tyr Leu Lys Asp Arg Thr Leu Ile Gly Gly Arg
420 425 430

Thr Ile Ser Gly Gln Gln Pro Asp Ile Gln Leu Ser Gly Leu Gly Ile
435 440 445

Gln Pro Glu His Cys Val Ile Thr Ile Glu Asp Ser Gly Leu Tyr Met
450 455 460

Glu Pro Val Gln Gly Ala Arg Cys Phe Val Asn Gly Ser Ala Ala Val
465 470 475 480

Glu Lys Thr Pro Leu Gln Asn Gly Asp Arg Ile Leu Trp Gly Asn His
485 490 495

His Phe Phe Arg Val Asn Ser Pro
500

<211> 503
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (51)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (207)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (213)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (257)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (282)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 116

Glu	Ser	Phe	Gln	Arg	Arg	Cys	Pro	Gly	Pro	Ala	Glu	Val	Phe	Ala	Tyr
1				5				10						15	
Asp	His	Cys	Phe	Trp	Ser	Met	Asp	Glu	Ser	Val	Lys	Glu	Lys	Tyr	Ala
			20					25					30		
Gly	Gln	Asp	Ile	Val	Phe	Lys	Cys	Leu	Gly	Glu	Asn	Ile	Leu	Gln	Asn
		35					40					45			
Ala	Phe	Xaa	Gly	Tyr	Asn	Ala	Cys	Ile	Phe	Ala	Tyr	Gly	Gln	Thr	Gly
	50					55					60				
Ser	Gly	Lys	Ser	Tyr	Thr	Met	Met	Gly	Thr	Ala	Asp	Gln	Pro	Gly	Leu
65					70					75				80	
Ile	Pro	Arg	Leu	Cys	Ser	Gly	Leu	Phe	Glu	Arg	Thr	Gln	Lys	Glu	Gly
			85						90					95	
Asn	Glu	Glu	Gln	Ser	Phe	Lys	Val	Glu	Val	Ser	Tyr	Met	Glu	Ile	Tyr
			100						105					110	

Asn Glu Lys Val Arg Asp Leu Leu Asp Pro Lys Gly Ser Arg Gln Thr
115 120 125

Leu Lys Val Arg Glu His Ser Val Leu Gly Pro Tyr Val Asp Gly Leu
130 135 140

Ser Lys Leu Ala Val Thr Ser Tyr Lys Asp Ile Glu Ser Leu Met Ser
145 150 155 160

Glu Gly Asn Lys Ser Arg Thr Val Ala Ala Thr Asn Met Asn Glu Glu
165 170 175

Ser Ser Arg Ser His Ala Val Phe Lys Ile Thr Leu Thr His Thr Leu
180 185 190

Tyr Asp Val Lys Ser Gly Thr Ser Gly Glu Lys Val Gly Lys Xaa Ser
195 200 205

Leu Val Asp Leu Xaa Gly Ser Glu Arg Ala Thr Lys Thr Gly Ala Ala
210 215 220

Gly Asp Arg Leu Lys Glu Gly Ser Asn Ile Asn Lys Ser Leu Thr Thr
225 230 235 240

Leu Gly Leu Val Ile Ser Ala Leu Ala Asp Gln Ser Ala Gly Lys Ser
245 250 255

Xaa Asn Lys Phe Val Pro Tyr Arg Asp Ser Val Leu Thr Trp Leu Leu
260 265 270

Lys Asp Ser Leu Gly Gly Asn Ser Lys Xaa Ala Met Val Ala Thr Val
275 280 285

Ser Pro Ala Ala Asp Asn Tyr Asp Glu Thr Leu Ser Thr Leu Arg Tyr
290 295 300

Ala Asp Arg Ala Lys His Ile Val Asn His Ala Val Val Asn Glu Asp
305 310 315 320

Pro Asn Ala Arg Ile Ile Arg Asp Leu Arg Glu Glu Val Glu Lys Leu
325 330 335

Arg Glu Gln Leu Thr Lys Ala Glu Ala Met Lys Ser Pro Glu Leu Lys
340 345 350

Asp Arg Leu Glu Glu Ser Glu Lys Leu Ile Gln Glu Met Thr Val Thr
355 360 365

Trp Glu Glu Lys Leu Arg Lys Thr Glu Glu Ile Ala Gln Glu Arg Gln
370 375 380

Lys Gln Leu Glu Ser Leu Gly Ile Ser Leu Gln Ser Ser Gly Ile Lys
 385 390 395 400

Val Gly Asp Asp Lys Cys Phe Leu Val Asn Leu Asn Ala Asp Pro Ala
 405 410 415

Leu Asn Glu Leu Leu Val Tyr Tyr Leu Lys Glu His Thr Leu Ile Gly
 420 425 430

Ser Ala Asn Ser Gln Asp Ile Gln Leu Cys Gly Met Gly Ile Leu Pro
 435 440 445

Glu His Cys Ile Ile Asp Ile Thr Ser Glu Gly Gln Val Met Leu Thr
 450 455 460

Pro Gln Lys Asn Thr Arg Thr Phe Val Asn Gly Ser Ser Val Ser Ser
 465 470 475 480

Pro Ile Gln Leu His His Gly Asp Arg Ile Leu Trp Gly Asn Asn His
 485 490 495

Phe Phe Arg Leu Asn Leu Pro
 500

<210> 117

<211> 358

<212> PRT

<213> Homo sapiens

<400> 117

Arg His Pro Val Cys Leu Leu Val Leu Gly Met Ala Gly Ser Gly Lys
 1 5 10 15

Thr Thr Phe Val Gln Arg Leu Thr Gly His Leu His Ala Gln Gly Thr
 20 25 30

Pro Pro Tyr Val Ile Asn Leu Asp Pro Ala Val His Glu Val Pro Phe
 35 40 45

Pro Ala Asn Ile Asp Ile Arg Asp Thr Val Lys Tyr Lys Glu Val Met
 50 55 60

Lys Gln Tyr Gly Leu Gly Pro Asn Gly Gly Ile Val Thr Ser Leu Asn
 65 70 75 80

Leu Phe Ala Thr Arg Phe Asp Gln Val Met Lys Phe Ile Glu Lys Ala
 85 90 95

Gln Asn Met Ser Lys Tyr Val Leu Ile Asp Thr Pro Gly Gln Ile Glu
 100 105 110

Val Phe Thr Trp Ser Ala Ser Gly Thr Ile Ile Thr Glu Ala Leu Ala
115 120 125

Ser Ser Phe Pro Thr Val Val Ile Tyr Val Met Asp Thr Ser Arg Ser
130 135 140

Thr Asn Pro Val Thr Phe Met Ser Asn Met Leu Tyr Ala Cys Ser Ile
145 150 155 160

Leu Tyr Lys Thr Lys Leu Pro Phe Ile Val Val Met Asn Lys Thr Asp
165 170 175

Ile Ile Asp His Ser Phe Ala Val Glu Trp Met Gln Asp Phe Glu Ala
180 185 190

Phe Gln Asp Ala Leu Asn Gln Glu Thr Thr Tyr Val Ser Asn Leu Thr
195 200 205

Arg Ser Met Ser Leu Val Leu Asp Glu Phe Tyr Ser Ser Leu Arg Val
210 215 220

Val Gly Val Ser Ala Val Leu Gly Thr Gly Leu Asp Glu Leu Phe Val
225 230 235 240

Gln Val Thr Ser Ala Ala Glu Glu Tyr Glu Arg Glu Tyr Arg Pro Glu
245 250 255

Tyr Glu Arg Leu Lys Lys Ser Leu Ala Asn Ala Glu Ser Gln Gln Gln
260 265 270

Arg Glu Gln Leu Glu Arg Leu Arg Lys Asp Met Gly Ser Val Ala Leu
275 280 285

Asp Ala Gly Thr Ala Lys Asp Ser Leu Ser Pro Val Leu His Pro Ser
290 295 300

Asp Leu Ile Leu Thr Arg Gly Thr Leu Asp Glu Glu Asp Glu Glu Ala
305 310 315 320

Asp Ser Asp Thr Asp Asp Ile Asp His Arg Val Thr Glu Glu Ser His
325 330 335

Glu Glu Pro Ala Phe Gln Asn Phe Met Gln Glu Ser Met Ala Gln Tyr
340 345 350

Trp Lys Arg Asn Asn Lys
355

<211> 358

<212> PRT

<213> Homo sapiens

<400> 118

```

Arg His Pro Val Cys Leu Leu Val Leu Gly Met Ala Gly Ser Gly Lys
 1             5             10             15
-----
Thr Thr Phe Val Gln Arg Leu Thr Gly His Leu His Ala Gln Gly Thr
 20             25             30
Pro Pro Tyr Val Ile Asn Leu Asp Pro Ala Val His Glu Val Pro Phe
 35             40             45
Pro Ala Asn Ile Asp Ile Arg Asp Thr Val Lys Tyr Lys Glu Val Met
 50             55             60
Lys Gln Tyr Gly Leu Gly Pro Asn Gly Gly Ile Val Thr Ser Leu Asn
 65             70             75             80
Leu Phe Ala Thr Arg Phe Asp Gln Val Met Lys Phe Ile Glu Lys Ala
 85             90             95
Gln Asn Met Ser Lys Tyr Val Leu Ile Asp Thr Pro Gly Gln Ile Glu
100             105             110
Val Phe Thr Trp Ser Ala Ser Gly Thr Ile Ile Thr Glu Ala Leu Ala
115             120             125
Ser Ser Phe Pro Thr Val Val Ile Tyr Val Met Asp Thr Ser Arg Ser
130             135             140
Thr Asn Pro Val Thr Phe Met Ser Asn Met Leu Tyr Ala Cys Ser Ile
145             150             155             160
Leu Tyr Lys Thr Lys Leu Pro Phe Ile Val Val Met Asn Lys Thr Asp
165             170             175
Ile Ile Asp His Ser Phe Ala Val Glu Trp Met Gln Asp Phe Glu Ala
180             185             190
Phe Gln Asp Ala Leu Asn Gln Glu Thr Thr Tyr Val Ser Asn Leu Thr
195             200             205
Arg Ser Met Ser Leu Val Leu Asp Glu Phe Tyr Ser Ser Leu Arg Val
210             215             220
Val Gly Val Ser Ala Val Leu Gly Thr Gly Leu Asp Glu Leu Phe Val
225             230             235             240
Gln Val Thr Ser Ala Ala Glu Glu Tyr Glu Arg Glu Tyr Arg Pro Glu

```

245 250 255
 Tyr Glu Arg Leu Lys Lys Ser Leu Ala Asn Ala Glu Ser Gln Gln Gln
 260 265 270
 Arg Glu Gln Leu Glu Arg Leu Arg Lys Asp Met Gly Ser Val Ala Leu
 275 280 285
 Asp Ala Gly Thr Ala Lys Asp Ser Leu Ser Pro Val Leu His Pro Ser
 290 295 300
 Asp Leu Ile Leu Thr Arg Gly Thr Leu Asp Glu Glu Asp Glu Glu Ala
 305 310 315 320
 Asp Ser Asp Thr Asp Asp Ile Asp His Arg Val Thr Glu Glu Ser His
 325 330 335
 Glu Glu Pro Ala Phe Gln Asn Phe Met Gln Glu Ser Met Ala Gln Tyr
 340 345 350
 Trp Lys Arg Asn Asn Lys
 355

<210> 119

<211> 179

<212> PRT

<213> Homo sapiens

<400> 119

Gln Asn Leu Leu Lys Leu Ile Ser Asn Phe Ser Lys Val Ser Gly Tyr
 1 5 10 15
 Lys Ile Asn Val Gln Lys Ser Gln Ala Phe Leu Tyr Thr Asn Asn Arg
 20 25 30
 Gln Thr Glu Ser Gln Ile Met Gly Glu Leu Pro Phe Thr Ile Ala Ser
 35 40 45
 Lys Arg Ile Lys Tyr Leu Gly Ile Gln Leu Thr Arg Asp Val Lys Asp
 50 55 60
 Leu Phe Lys Glu Asn Tyr Lys Pro Leu Leu Lys Glu Ile Lys Glu Asp
 65 70 75 80
 Thr Asn Lys Trp Lys Asn Ile Pro Cys Ser Trp Val Gly Arg Ile Asn
 85 90 95
 Ile Val Lys Met Ala Ile Leu Pro Lys Val Ile Tyr Arg Phe Asn Ala
 100 105 110

Ile Pro Ile Lys Leu Pro Met Thr Phe Phe Thr Glu Leu Glu Lys Thr
115 120 125

Thr Leu Lys Phe Ile Trp Asn Gln Lys Arg Ala Arg Ile Ala Lys Ser
130 135 140

Ile Leu Ser Gln Lys Asn Lys Ala Gly Gly Ile Thr Leu Leu Asp Phe
145 150 155 160

Lys Leu Tyr Tyr Lys Ala Thr Val Thr Lys Thr Ala Trp Tyr Trp Tyr
165 170 175

Gln Asn Arg

<210> 120
<211> 174
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (12)
<223> Xaa equals stop translation

<220>
<221> SITE
<222> (22)
<223> Xaa equals stop translation

<220>
<221> SITE
<222> (24)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (32)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (42)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (45)
<223> Xaa equals stop translation

<220>
<221> SITE
<222> (46)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (55)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (63)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (65)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (78)
<223> Xaa equals stop translation

<220>
<221> SITE
<222> (85)
<223> Xaa equals stop translation

<220>
<221> SITE
<222> (92)
<223> Xaa equals stop translation

<220>
<221> SITE
<222> (108)
<223> Xaa equals stop translation

<220>
<221> SITE
<222> (116)
<223> Xaa equals stop translation

<220>
<221> SITE
<222> (126)
<223> Xaa equals stop translation

<220>

<221> SITE
 <222> (128)
 <223> Xaa equals stop translation

<220>
 <221> SITE
 <222> (171)
 <223> Xaa equals stop translation

<400> 120
 Gln Thr Asn Leu Glu Leu Ile Ser Ser Arg Leu Xaa Gln Gly Cys Arg
 1 5 10 15
 Ile Lys Leu Asn Thr Xaa Lys Xaa Ile Pro Phe Leu Tyr Thr Ser Xaa
 20 25 30
 Glu Pro Leu Glu Phe Glu Ile Lys Ile Xaa His His Xaa Xaa Tyr Tyr
 35 40 45
 Gln Lys Arg Glu Arg Glu Xaa Ile Cys Ile Met Leu Thr Lys Xaa Val
 50 55 60
 Xaa Lys Val Cys Glu Lys Asn Tyr Lys Ser Leu Met Lys Xaa Ile Lys
 65 70 75 80
 Gly Asp Leu Asn Xaa Trp Lys Asp Lys Leu Cys Xaa Trp Ile Arg Lys
 85 90 95
 Leu Asn Leu Val Met Cys Gln Phe Ile Pro Ile Xaa Ser Ile Asp Ser
 100 105 110
 Met Gln Ser Xaa Lys Ala Thr Leu Trp Thr Ser Ala Asn Xaa Phe Xaa
 115 120 125
 Gly Leu His Glu Lys Ala Lys Arg Cys Asn Ser Arg Asn Asn Ile Glu
 130 135 140
 Glu Glu Gln Arg Ser Arg Thr Leu Leu Asp Phe Lys Ser Phe Tyr Lys
 145 150 155 160
 Ala Thr Ile Ile Lys Ile Val Trp His Trp Xaa Lys Asn Arg
 165 170

<210> 121
 <211> 201
 <212> PRT
 <213> Homo sapiens

<400> 121
 Glu Leu Met Ser Thr His Glu Leu Glu Lys Lys Glu Leu Glu Glu Asn

1	5	10	15
Phe Glu Lys Leu Arg Leu Ser Leu Gln Asp Gln Val Asp Thr Leu Thr	20	25	30
Phe Gln Ser Gln Ser Leu Arg Asp Arg Ala Arg Arg Phe Glu Glu Ala	35	40	45
Leu Arg Lys Asn Thr Glu Glu Gln Leu Glu Ile Ala Leu Ala Pro Tyr	50	55	60
Gln His Leu Glu Glu Asp Met Lys Ser Leu Lys Gln Val Leu Glu Met	65	70	75
Lys Asn Gln Gln Ile His Glu Gln Glu Lys Lys Ile Leu Glu Leu Glu	85	90	95
Lys Leu Ala Glu Lys Asn Ile Ile Leu Glu Glu Lys Ile Gln Val Leu	100	105	110
Gln Gln Gln Asn Glu Asp Leu Lys Ala Arg Ile Asp Gln Asn Thr Val	115	120	125
Val Thr Arg Gln Leu Ser Glu Glu Asn Ala Asn Leu Gln Glu Tyr Val	130	135	140
Glu Lys Glu Thr Gln Glu Lys Lys Arg Leu Ser Arg Thr Asn Glu Glu	145	150	155
Leu Leu Trp Lys Leu Gln Thr Gly Asp Pro Thr Ser Pro Ile Lys Leu	165	170	175
Ser Pro Thr Ser Pro Val Tyr Arg Gly Ser Ser Ser Gly Pro Ser Ser	180	185	190
Pro Ala Arg Val Ser Thr Thr Pro Arg	195	200	

<210> 122

<211> 199

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (49)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (50)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (106)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (118)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 122

Glu	Ile	Lys	Lys	Gly	His	Glu	Ile	Glu	Lys	Lys	Ser	Leu	Glu	Asp	Leu
1				5					10					15	

Leu	Ser	Glu	Lys	Gln	Glu	Ser	Leu	Glu	Lys	Gln	Ile	Asn	Asp	Leu	Lys
		20						25					30		

Ser	Glu	Asn	Asp	Ala	Leu	Asn	Glu	Lys	Leu	Lys	Ser	Glu	Glu	Gln	Lys
		35					40					45			

Xaa	Xaa	Ala	Arg	Glu	Lys	Ala	Asn	Leu	Lys	Asn	Pro	Gln	Ile	Met	Tyr
	50						55				60				

Leu	Glu	Gln	Glu	Leu	Glu	Ser	Leu	Lys	Ala	Val	Leu	Glu	Ile	Lys	Asn
65					70					75					80

Glu	Lys	Leu	His	Gln	Gln	Asp	Ile	Lys	Leu	Met	Lys	Met	Glu	Lys	Leu
			85						90					95	

Val	Asp	Asn	Asn	Thr	Ala	Leu	Val	Asp	Xaa	Leu	Lys	Arg	Phe	Gln	Gln
		100						105					110		

Glu	Asn	Glu	Glu	Leu	Xaa	Ala	Arg	Met	Asp	Lys	His	Met	Ala	Ile	Ser
	115							120				125			

Arg	Gln	Leu	Ser	Thr	Glu	Gln	Ala	Val	Leu	Gln	Glu	Ser	Leu	Glu	Lys
	130					135					140				

Glu	Ser	Lys	Val	Asn	Lys	Arg	Leu	Ser	Met	Glu	Asn	Glu	Glu	Leu	Leu
145					150					155				160	

Trp	Lys	Leu	His	Asn	Gly	Asp	Leu	Cys	Ser	Pro	Lys	Arg	Ser	Pro	Thr
			165						170					175	

Ser	Ser	Ala	Ile	Pro	Leu	Gln	Ser	Pro	Arg	Asn	Ser	Gly	Ser	Phe	Pro
			180					185					190		

Ser	Pro	Ser	Ile	Ser	Pro	Arg
-----	-----	-----	-----	-----	-----	-----

195

<210> 123

<211> 280

<212> PRT

<213> Homo sapiens

<400> 123

Gln Gly Gly Ser Ser Asp Asn Gly Gly Gln Gln Gln Asn Asn Asp Trp
 1 5 10 15

Asn Gln Gln Asn Asn Asn Gln Gln Gln Asn Asn Asp Trp Asn Asn Trp
 20 25 30

Gly Gln Gln Asn Asn Asp Trp Asn Gln Trp Asn Asn Gln Gly Gln Gln
 35 40 45

Asn Asn Asp Trp Asn Asn Trp Gly Gln Gln Asn Asn Asp Trp Asn Gln
 50 55 60

Trp Asn Asn Gln Gly Gln Gln Gln Asn Asn Asp Trp Asn Asn Trp Gly
 65 70 75 80

Gln Gln Asn Asn Asp Trp Asn Gln Trp Asn Asn Gln Gly Gln Gln Gln
 85 90 95

Asn Asn Asp Trp Asn Asn Trp Gly Gln Gln Asn Asn Asp Trp Asn Gln
 100 105 110

Trp Asn Asn Gln Gly Gln Gln Gln Asn Asn Asp Trp Asn Asn Trp Gly
 115 120 125

Gln Gln Asn Asn Asp Trp Asn Gln Trp Asn Asn Gln Asn Asn Asn Gln
 130 135 140

Gln Asn Ala Trp Asn Gly Trp Asp Asn Asn Asn Asn Trp Asn Gln Asn
 145 150 155 160

Asn Gln Gln Gln Asn Asn Trp Asp Trp Asn Asn Gln Asn Asn Trp Asn
 165 170 175

Asn Asn Gln Gln Gln Asn Asn Asp Trp Asn Gln Trp Asn Asn Gln Asn
 180 185 190

Asn Trp Asn Asn Asn Gln Gln Gln Asn Asn Asp Trp Asn Gln Trp Asn
 195 200 205

Asn Gln Gly Gln Gln Asn Asn Asp Trp Asn Gln Trp Asn Asn Gln Asn
 210 215 220

Asn Trp Asn Gln Asn Asn Asn Gln Gln Asn Ala Trp Asn Gly Trp Asp
 225 230 235 240

Asn Asn Asn Asn Trp Asn Gln Trp Asp Gln Asn Asn Gln Trp Asn Asn
 245 250 255

Gln Gln Gln Asn Asn Thr Trp Asp Trp Asn Asn Gln Asn Asn Trp Asn
 -----260-----265-----270-----

Asn Asn Gln Gln Asn Asn Asp Trp
 275 280

<210> 124

<211> 285

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (107)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (122)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 124

Lys Gly Ala Ser Val Gln Lys Ser Thr Gly Ser Lys Asn Asp Ser Trp
 1 5 10 15

Asp Asn Asn Asn Arg Ser Thr Gly Gly Ser Trp Asn Phe Gly Pro Gln
 20 25 30

Asp Ser Asn Asp Asn Lys Trp Gly Glu Gly Asn Lys Met Thr Ser Gly
 35 40 45

Val Ser Gln Gly Glu Trp Lys Gln Pro Thr Gly Ser Asp Glu Leu Lys
 50 55 60

Ile Gly Glu Trp Ser Gly Pro Asn Gln Pro Asn Ser Ser Thr Gly Ala
 65 70 75 80

Trp Asp Asn Gln Lys Gly His Pro Leu Pro Glu Asn Gln Gly Asn Ala
 85 90 95

Gln Ala Pro Cys Trp Gly Arg Ser Ser Xaa Thr Gly Ser Glu Val
 100 105 110

Gly Gly Gln Ser Thr Gly Ser Asn His Xaa Ala Gly Ser Ser Asp Ser

115		120		125
His Asn Ser Gly Arg Arg Ser Tyr Arg Pro Thr His Pro Asp Cys Gln				
130		135		140
Ala Val Leu Gln Thr Leu Leu Ser Arg Thr Asp Leu Asp Pro Arg Val				
145		150		155
Leu Ser Asn Thr Gly Trp Gly Gln Thr Gln Ile Lys Gln Asp Thr Val				
	165		170	175
Trp Asp Ile Glu Glu Val Pro Arg Pro Glu Gly Lys Ser Asp Lys Gly				
	180		185	190
Thr Glu Gly Trp Glu Ser Ala Ala Thr Gln Thr Lys Asn Ser Gly Gly				
	195		200	205
Trp Gly Asp Ala Pro Ser Gln Ser Asn Gln Met Lys Ser Gly Trp Gly				
	210		215	220
Glu Leu Ser Ala Ser Thr Glu Trp Lys Asp Pro Lys Asn Thr Gly Gly				
	225		230	235
Trp Asn Asp Tyr Lys Asn Asn Asn Ser Ser Asn Trp Gly Gly Gly Arg				
	245		250	255
Pro Asp Glu Lys Thr Pro Ser Ser Trp Asn Glu Asn Pro Ser Lys Asp				
	260		265	270
Gln Gly Trp Gly Gly Gly Arg Gln Pro Asn Gln Gly Trp				
	275		280	285

<210> 125

<211> 213

<212> PRT

<213> Homo sapiens

<400> 125

Arg Asp Cys Ala Asp Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly Ile
1 5 10 15

Tyr Thr Ile Tyr Ile Asn Asn Met Pro Glu Pro Lys Lys Val Phe Cys
20 25 30

Asn Met Asp Val Asn Gly Gly Gly Trp Thr Val Ile Gln His Arg Glu
35 40 45

Asp Gly Ser Leu Asp Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met Gly
50 55 60

Phe Gly Asn Pro Ser Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile Phe
65 70 75 80

Ala Ile Thr Ser Gln Arg Gln Tyr Met Leu Arg Ile Glu Leu Met Asp
85 90 95

Trp Glu Gly Asn Arg Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile Gly
100 105 110

Asn Glu Lys Gln Asn Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly Thr
115 120 125

Ala Gly Lys Gln Ser Ser Leu Ile Leu His Gly Ala Asp Phe Ser Thr
130 135 140

Lys Asp Ala Asp Asn Asp Asn Cys Met Cys Lys Cys Ala Leu Met Leu
145 150 155 160

Thr Gly Gly Trp Trp Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly
165 170 175

Met Phe Tyr Thr Ala Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys
180 185 190

Trp His Tyr Phe Lys Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr Met
195 200 205

Met Ile Arg Pro Leu
210

<210> 126

<211> 215

<212> PRT

<213> Homo sapiens

<400> 126

Arg Asp Cys Gln Glu Leu Phe Gln Val Gly Glu Arg Gln Ser Gly Leu
1 5 10 15

Phe Glu Ile Gln Pro Gln Gly Ser Pro Pro Phe Leu Val Asn Cys Lys
20 25 30

Met Thr Ser Asp Gly Gly Trp Thr Val Ile Gln Arg Arg His Asp Gly
35 40 45

Ser Val Asp Phe Asn Arg Pro Trp Glu Ala Tyr Lys Ala Gly Phe Gly
50 55 60

Asp Pro His Gly Glu Phe Trp Leu Gly Leu Glu Lys Val His Ser Ile
65 70 75 80

Met Gly Asp Arg Asn Ser Arg Leu Ala Val Gln Leu Arg Asp Trp Asp
 85 90 95

Gly Asn Ala Glu Leu Leu Gln Phe Ser Val His Leu Gly Gly Glu Asp
 100 105 110

Thr Ala Tyr Ser Leu Gln Leu Thr Ala Pro Val Ala Gly Gln Leu Gly
 115 120 125

Ala Thr Thr Val Pro Pro Ser Gly Leu Ser Val Pro Phe Ser Thr Trp
 130 135 140

Asp Gln Asp His Asp Leu Arg Arg Asp Lys Asn Cys Ala Lys Ser Leu
 145 150 155 160

Ser Gly Gly Trp Trp Phe Gly Thr Cys Ser His Ser Asn Leu Asn Gly
 165 170 175

Gln Tyr Phe Arg Ser Ile Pro Gln Gln Arg Gln Lys Leu Lys Lys Gly
 180 185 190

Ile Phe Trp Lys Thr Trp Arg Gly Arg Tyr Tyr Pro Leu Gln Ala Thr
 195 200 205

Thr Met Leu Ile Gln Pro Met
 210 215

<210> 127

<211> 239

<212> PRT

<213> Homo sapiens

<400> 127

Leu Leu Glu Ile Cys Cys Tyr Ser Met Glu Cys Ala Leu Thr Ala Gln
 1 5 10 15

Gln Asn Gly Ala Asp Arg Val Glu Leu Cys Ala Ala Pro Lys Glu Gly
 20 25 30

Gly Leu Thr Pro Ser Leu Gly Val Leu Lys Ser Val Arg Gln Arg Val
 35 40 45

Thr Ile Pro Val His Pro Ile Ile Arg Pro Arg Gly Gly Asp Phe Cys
 50 55 60

Tyr Ser Asp Gly Glu Phe Ala Ala Ile Leu Glu Asp Val Arg Thr Val
 65 70 75 80

Arg Glu Leu Gly Phe Pro Gly Leu Val Thr Gly Val Leu Asp Val Asp

	85		90		95
Gly Asn Val Asp Met Pro Arg Met Glu Lys Ile Met Ala Ala Ala Gly	100		105		110
Pro Leu Ala Val Thr Phe His Arg Ala Phe Asp Met Cys Ala Asn Pro	115		120		125
Leu Tyr Thr Leu Asn Asn Leu Ala Glu Leu Gly Ile Ala Arg Val Leu	130		135		140
Thr Ser Gly Gln Lys Ser Asp Ala Leu Gln Gly Leu Ser Lys Ile Met	145		150		155
Glu Leu Ile Ala His Arg Asp Ala Pro Ile Ile Met Ala Gly Ala Gly	165		170		175
Val Arg Ala Glu Asn Leu His His Phe Leu Asp Ala Gly Val Leu Glu	180		185		190
Val His Ser Ser Ala Gly Ala Trp Gln Ala Ser Pro Met Arg Tyr Arg	195		200		205
Asn Gln Gly Leu Ser Met Ser Ser Asp Glu His Ala Asp Glu Tyr Ser	210		215		220
Arg Tyr Ile Val Asp Gly Ala Ala Val Ala Glu Met Lys Gly Ile	225		230		235
<210> 128					
<211> 241					
<212> PRT					
<213> Homo sapiens					
<400> 128					
Leu Met Glu Val Cys Val Asp Ser Val Glu Ser Ala Val Asn Ala Glu	1		5		10
					15
Arg Gly Gly Ala Asp Arg Ile Glu Leu Cys Ser Gly Leu Ser Glu Gly	20		25		30
Gly Thr Thr Pro Ser Met Gly Val Leu Gln Val Val Lys Gln Ser Val	35		40		45
Gln Ile Pro Val Phe Val Met Ile Arg Pro Arg Gly Gly Asp Phe Leu	50		55		60
Tyr Ser Asp Arg Glu Ile Glu Val Met Lys Ala Asp Ile Arg Leu Ala	65		70		75
					80

Ile

<213> Homo sapiens

<400> 129

Leu Ser Ser Val Ile Asn Pro Leu Leu Tyr Thr Val Ser Ser Gln Gln
50 55 60

Phe Arg Arg Val Phe Val Gln Val Leu Cys Cys Arg Leu Ser Leu Gln
65 70 75 80

His Ala Asn His Glu Lys Arg Leu Arg Val His Ala His Ser Thr Thr
85 90 95

Asp Ser Ala Arg Phe Val Gln Arg Pro Leu Leu Phe Ala Ser Arg Arg
100 105 110

Gln Ser Ser Ala Arg Arg Thr Glu Lys Ile Phe Leu Ser Thr Phe Gln
115 120 125

Ser Glu Ala Glu Pro Gln Ser Lys Ser Gln Ser Leu Ser Leu Glu Ser
130 135 140

Leu Glu Pro Asn Ser Gly Ala Lys Pro Ala Asn Ser Ala Ala Glu Asn
145 150 155 160

Gly Phe Gln Glu His Glu Val
165

<210> 130

<211> 167

<212> PRT

<213> Homo sapiens

<400> 130

Leu Ile Val Val Thr Leu Ala Val Cys Trp Met Pro Asn Gln Ile Arg
1 5 10 15

Arg Ile Met Ala Ala Ala Lys Pro Lys His Asp Trp Thr Arg Ser Tyr
20 25 30

Phe Arg Ala Tyr Met Ile Leu Leu Pro Phe Ser Glu Thr Phe Phe Tyr
35 40 45

Leu Ser Ser Val Ile Asn Pro Leu Leu Tyr Thr Val Ser Ser Gln Gln
50 55 60

Phe Arg Arg Val Phe Val Gln Val Leu Cys Cys Arg Leu Ser Leu Gln
65 70 75 80

His Ala Asn His Glu Lys Arg Leu Arg Val His Ala His Ser Thr Thr
85 90 95

Asp Ser Ala Arg Phe Val Gln Arg Pro Leu Leu Phe Ala Ser Arg Arg
100 105 110

Gln Ser Ser Ala Arg Arg Thr Glu Lys Ile Phe Leu Ser Thr Phe Gln

115	120	125
Ser Glu Ala Glu Pro Gln Ser Lys Ser Gln Ser Leu Ser Leu Glu Ser		
130	135	140
Leu Glu Pro Asn Ser Gly Ala Lys Pro Ala Asn Ser Ala Ala Glu Asn		
145	150	155
		160
Gly Phe Gln Glu His Glu Val		
165		

<210> 131
 <211> 312
 <212> PRT
 <213> Homo sapiens

<400> 131
Leu Asn His Ala Val Gly Phe Ala Ser Arg Thr Ser Lys Ala Phe Ser
1 5 10 15
Asn Lys Gln Thr Val Lys Gln Cys Gly Cys Ser Glu Val Tyr Leu Asp
20 25 30
Cys Leu Gln Thr Phe Leu Pro Ala Leu Ser Cys Pro Leu Gln Lys Asp
35 40 45
Ile Leu Arg Ser Gly Val Arg Thr Phe Leu His Arg Met Ile Ile Cys
50 55 60
Leu Glu Glu Glu Val Leu Pro Phe Ile Pro Ser Ala Ser Glu His Met
65 70 75 80
Leu Lys Asp Cys Glu Ala Lys Asp Leu Gln Glu Phe Ile Pro Leu Ile
85 90 95
Asn Gln Ile Thr Ala Lys Phe Lys Ile Gln Val Ser Pro Phe Leu Gln
100 105 110
Gln Met Phe Met Pro Leu Leu His Ala Ile Phe Glu Val Leu Leu Arg
115 120 125
Pro Ala Glu Glu Asn Asp Gln Ser Ala Ala Leu Glu Lys Gln Met Leu
130 135 140
Arg Arg Ser Tyr Phe Ala Phe Leu Gln Thr Val Thr Gly Ser Gly Met
145 150 155 160
Ser Glu Val Ile Ala Asn Gln Gly Ala Glu Asn Val Glu Arg Val Leu
165 170 175

Val Thr Val Ile Gln Gly Ala Val Glu Tyr Pro Asp Pro Ile Ala Gln
 180 185 190

Lys Thr Cys Phe Ile Ile Leu Ser Lys Leu Val Glu Leu Trp Gly Gly
 195 200 205

Lys Asp Gly Pro Val Gly Phe Ala Asp Phe Val Tyr Lys His Ile Val
 210 215 220

Pro Ala Cys Phe Leu Ala Pro Leu Lys Gln Thr Phe Asp Leu Ala Asp
 225 230 235 240

Ala Gln Thr Val Leu Ala Leu Ser Glu Cys Ala Val Thr Leu Lys Thr
 245 250 255

Ile His Leu Lys Arg Gly Pro Glu Cys Val Gln Tyr Leu Gln Gln Glu
 260 265 270

Tyr Leu Pro Ser Leu Gln Val Ala Pro Glu Ile Ile Gln Glu Phe Cys
 275 280 285

Gln Ala Leu Gln Gln Pro Asp Ala Lys Val Phe Lys Asn Tyr Leu Lys
 290 295 300

Val Phe Phe Gln Arg Ala Lys Pro
 305 310

<210> 132

<211> 312

<212> PRT

<213> Homo sapiens

<400> 132

Leu Asn His Ala Val Gly Phe Ala Ser Arg Thr Ser Lys Ala Phe Ser
 1 5 10 15

Asn Lys Gln Thr Val Lys Gln Cys Gly Cys Ser Glu Val Tyr Leu Asp
 20 25 30

Cys Leu Gln Thr Phe Leu Pro Ala Leu Ser Cys Pro Leu Gln Lys Asp
 35 40 45

Ile Leu Arg Ser Gly Val Arg Thr Phe Leu His Arg Met Ile Ile Cys
 50 55 60

Leu Glu Glu Glu Val Leu Pro Phe Ile Pro Ser Ala Ser Glu His Met
 65 70 75 80

Leu Lys Asp Cys Glu Ala Lys Asp Leu Gln Glu Phe Ile Pro Leu Ile
 85 90 95

Asn Gln Ile Thr Ala Lys Phe Lys Ile Gln Val Ser Pro Phe Leu Gln
 100 105 110

Gln Met Phe Met Pro Leu Leu His Ala Ile Phe Glu Val Leu Leu Arg
 115 120 125

Pro Ala Glu Glu Asn Asp Gln Ser Ala Ala Leu Glu Lys Gln Met Leu
 130 135 140

Arg Arg Ser Tyr Phe Ala Phe Leu Gln Thr Val Thr Gly Ser Gly Met
 145 150 155 160

Ser Glu Val Ile Ala Asn Gln Gly Ala Glu Asn Val Glu Arg Val Leu
 165 170 175

Val Thr Val Ile Gln Gly Ala Val Glu Tyr Pro Asp Pro Ile Ala Gln
 180 185 190

Lys Thr Cys Phe Ile Ile Leu Ser Lys Leu Val Glu Leu Trp Gly Gly
 195 200 205

Lys Asp Gly Pro Val Gly Phe Ala Asp Phe Val Tyr Lys His Ile Val
 210 215 220

Pro Ala Cys Phe Leu Ala Pro Leu Lys Gln Thr Phe Asp Leu Ala Asp
 225 230 235 240

Ala Gln Thr Val Leu Ala Leu Ser Glu Cys Ala Val Thr Leu Lys Thr
 245 250 255

Ile His Leu Lys Arg Gly Pro Glu Cys Val Gln Tyr Leu Gln Gln Glu
 260 265 270

Tyr Leu Pro Ser Leu Gln Val Ala Pro Glu Ile Ile Gln Glu Phe Cys
 275 280 285

Gln Ala Leu Gln Gln Pro Asp Ala Lys Val Phe Lys Asn Tyr Leu Lys
 290 295 300

Val Phe Phe Gln Arg Ala Lys Pro
 305 310

<210> 133

<211> 441

<212> PRT

<213> Homo sapiens

<400> 133

Leu Lys Leu Pro Arg Leu Lys Leu Glu Val Met Leu Glu Asp Asn Val

1	5	10	15
Cys Leu Pro Ser Asn Gly Lys Leu Tyr Thr Lys Val Ile Asn Trp Val	20	25	30
Gln Arg Ser Ile Trp Glu Asn Gly Asp Ser Leu Glu Glu Leu Met Glu	35	40	45
Glu Val Gln Thr Leu Tyr Tyr Ser Ala Asp His Lys Leu Leu Asp Gly	50	55	60
Asn Leu Leu Asp Gly Gln Ala Glu Val Phe Gly Ser Asp Asp Asp His	65	70	75
Ile Gln Phe Val Gln Lys Lys Pro Pro Arg Glu Asn Gly His Lys Gln	85	90	95
Ile Ser Ser Ser Ser Thr Gly Cys Leu Ser Ser Pro Asn Ala Thr Val	100	105	110
Gln Ser Pro Lys His Glu Trp Lys Ile Val Ala Ser Glu Lys Thr Ser	115	120	125
Asn Asn Thr Tyr Leu Cys Leu Ala Val Leu Asp Gly Ile Phe Cys Val	130	135	140
Ile Phe Leu His Gly Arg Asn Ser Pro Gln Ser Ser Pro Thr Ser Thr	145	150	155
Pro Lys Leu Ser Lys Ser Leu Ser Phe Glu Met Gln Gln Asp Glu Leu	165	170	175
Ile Glu Lys Pro Met Ser Pro Met Gln Tyr Ala Arg Ser Gly Leu Gly	180	185	190
Thr Ala Glu Met Asn Gly Lys Leu Ile Ala Ala Gly Gly Tyr Asn Arg	195	200	205
Glu Glu Cys Leu Arg Thr Val Glu Cys Tyr Asn Pro His Thr Asp His	210	215	220
Trp Ser Phe Leu Ala Pro Met Arg Thr Pro Arg Ala Arg Phe Gln Met	225	230	235
Ala Val Leu Met Gly Gln Leu Tyr Val Val Gly Gly Ser Asn Gly His	245	250	255
Ser Asp Asp Leu Ser Cys Gly Glu Met Tyr Asp Ser Asn Ile Asp Asp	260	265	270
Trp Ile Pro Val Pro Glu Leu Arg Thr Asn Arg Cys Asn Ala Gly Val			

100

275 280 285
 Cys Ala Leu Asn Gly Lys Leu Tyr Ile Val Gly Gly Ser Asp Pro Tyr
 290 295 300
 Gly Gln Lys Gly Leu Lys Asn Cys Asp Val Phe Asp Pro Val Thr Lys
 305 310 315 320
 Leu Trp Thr Ser Cys Ala Pro Leu Asn Ile Arg Arg His Gln Ser Ala
 325 330 335
 Val Cys Glu Leu Gly Gly Tyr Leu Tyr Ile Ile Gly Gly Ala Glu Ser
 340 345 350
 Trp Asn Cys Leu Asn Thr Val Glu Arg Tyr Asn Pro Glu Asn Asn Thr
 355 360 365
 Trp Thr Leu Ile Ala Pro Met Asn Val Ala Arg Arg Gly Ala Gly Val
 370 375 380
 Ala Val Leu Asn Gly Lys Leu Phe Val Cys Gly Gly Phe Asp Gly Ser
 385 390 395 400
 His Ala Ile Ser Cys Val Glu Met Tyr Asp Pro Thr Arg Asn Glu Trp
 405 410 415
 Lys Met Met Gly His Met Thr Ser Pro Arg Ser Asn Ala Gly Ile Ala
 420 425 430
 Thr Val Gly Asn Thr Ile Tyr Ala Val
 435 440

<210> 134

<211> 441

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (44)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (45)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 134

Leu Lys Leu Pro Arg Leu Lys Leu Glu Val Met Leu Glu Asp Asn Val
 1 5 10 15

Cys Leu Pro Ser Asn Gly Lys Leu Tyr Thr Lys Val Ile Asn Trp Val
 20 25 30
 Gln Arg Ser Ile Trp Glu Asn Gly Asp Ser Leu Xaa Xaa Leu Met Glu
 35 40 45
 Glu Val Gln Thr Leu Tyr Tyr Ser Ala Asp His Lys Leu Leu Asp Gly
 50 55 60
 Asn Leu Leu Asp Gly Gln Ala Glu Val Phe Gly Ser Asp Asp Asp His
 65 70 75 80
 Ile Gln Phe Val Gln Lys Lys Pro Pro Arg Glu Asn Gly His Lys Gln
 85 90 95
 Ile Ser Ser Ser Ser Thr Gly Cys Leu Ser Ser Pro Asn Ala Thr Val
 100 105 110
 Gln Ser Pro Lys His Glu Trp Lys Ile Val Ala Ser Glu Lys Thr Ser
 115 120 125
 Asn Asn Thr Tyr Leu Cys Leu Ala Val Leu Asp Gly Ile Phe Cys Val
 130 135 140
 Ile Phe Leu His Gly Arg Asn Ser Pro Gln Ser Ser Pro Thr Ser Thr
 145 150 155 160
 Pro Lys Leu Ser Lys Ser Leu Ser Phe Glu Met Gln Gln Asp Glu Leu
 165 170 175
 Ile Glu Lys Pro Met Ser Pro Met Gln Tyr Ala Arg Ser Gly Leu Gly
 180 185 190
 Thr Ala Glu Met Asn Gly Lys Leu Ile Ala Ala Gly Gly Tyr Asn Arg
 195 200 205
 Glu Glu Cys Leu Arg Thr Val Glu Cys Tyr Asn Pro His Thr Asp His
 210 215 220
 Trp Ser Phe Leu Ala Pro Met Arg Thr Pro Arg Ala Arg Phe Gln Met
 225 230 235 240
 Ala Val Leu Met Gly Gln Leu Tyr Val Val Gly Gly Ser Asn Gly His
 245 250 255
 Ser Asp Asp Leu Ser Cys Gly Glu Met Tyr Asp Ser Asn Ile Asp Asp
 260 265 270
 Trp Ile Pro Val Pro Glu Leu Arg Thr Asn Arg Cys Asn Ala Gly Val
 275 280 285

Cys Ala Leu Asn Gly Lys Leu Tyr Ile Val Gly Gly Ser Asp Pro Tyr
 290 295 300

Gly Gln Lys Gly Leu Lys Asn Cys Asp Val Phe Asp Pro Val Thr Lys
 305 310 315 320

Leu Trp Thr Ser Cys Ala Pro Leu Asn Ile Arg Arg His Gln Ser Ala
 325 330 335

Val Cys Glu Leu Gly Gly Tyr Leu Tyr Ile Ile Gly Gly Ala Glu Ser
 340 345 350

Trp Asn Cys Leu Asn Thr Val Glu Arg Tyr Asn Pro Glu Asn Asn Thr
 355 360 365

Trp Thr Leu Ile Ala Pro Met Asn Val Ala Arg Arg Gly Ala Gly Val
 370 375 380

Ala Val Leu Asn Gly Lys Leu Phe Val Cys Gly Gly Phe Asp Gly Ser
 385 390 395 400

His Ala Ile Ser Cys Val Glu Met Tyr Asp Pro Thr Arg Asn Glu Trp
 405 410 415

Lys Met Met Gly Asn Met Thr Ser Pro Arg Ser Asn Ala Gly Ile Ala
 420 425 430

Thr Val Gly Asn Thr Ile Tyr Ala Val
 435 440

<210> 135

<211> 236

<212> PRT

<213> Homo sapiens

<400> 135

Met Ser Pro Met Gln Tyr Ala Arg Ser Gly Leu Gly Thr Ala Glu Met
 1 5 10 15

Asn Gly Lys Leu Ile Ala Ala Gly Gly Tyr Asn Arg Glu Glu Cys Leu
 20 25 30

Arg Thr Val Glu Cys Tyr Asn Pro His Thr Asp His Trp Ser Phe Leu
 35 40 45

Ala Pro Met Arg Thr Pro Arg Ala Arg Phe Gln Met Ala Val Leu Met
 50 55 60

Gly Gln Leu Tyr Val Val Gly Gly Ser Asn Gly His Ser Asp Asp Leu

103

65 70 75 80

Ser Cys Gly Glu Met Tyr Asp Ser Asn Ile Asp Asp Trp Ile Pro Val

 85 90 95

Pro Glu Leu Arg Thr Asn Arg Cys Asn Ala Gly Val Cys Ala Leu Asn

 100 105 110

Gly Lys Leu Tyr Ile Val Gly Gly Ser Asp Pro Tyr Gly Gln Lys Gly

 115 120 125

Leu Lys Asn Cys Asp Val Phe Asp Pro Val Thr Lys Leu Trp Thr Ser

 130 135 140

Cys Ala Pro Leu Asn Ile Arg Arg His Gln Ser Ala Val Cys Glu Leu

 145 150 155 160

Gly Gly Tyr Leu Tyr Ile Ile Gly Gly Ala Glu Ser Trp Asn Cys Leu

 165 170 175

Asn Thr Val Glu Arg Tyr Asn Pro Glu Asn Asn Thr Trp Thr Leu Ile

 180 185 190

Ala Pro Met Asn Val Ala Arg Arg Gly Ala Gly Val Ala Val Leu Asn

 195 200 205

Gly Lys Leu Phe Val Cys Gly Gly Phe Asp Gly Ser His Ala Ile Ser

 210 215 220

Cys Val Glu Met Tyr Asp Pro Thr Arg Asn Glu Trp

 225 230 235

<210> 136

<211> 236

<212> PRT

<213> Homo sapiens

<400> 136

Leu Ala Pro Met Arg Thr Pro Arg Ala Arg Phe Gln Met Ala Val Leu

 1 5 10 15

Met Gly Gln Leu Tyr Val Val Gly Gly Ser Asn Gly His Ser Asp Asp

 20 25 30

Leu Ser Cys Gly Glu Met Tyr Asp Ser Asn Ile Asp Asp Trp Ile Pro

 35 40 45

Val Pro Glu Leu Arg Thr Asn Arg Cys Asn Ala Gly Val Cys Ala Leu

 50 55 60

Asn Gly Lys Leu Tyr Ile Val Gly Gly Ser Asp Pro Tyr Gly Gln Lys
65 70 75 80

Gly Leu Lys Asn Cys Asp Val Phe Asp Pro Val Thr Lys Leu Trp Thr
85 90 95

Ser Cys Ala Pro Leu Asn Ile Arg Arg His Gln Ser Ala Val Cys Glu
100 105 110

Leu Gly Gly Tyr Leu Tyr Ile Ile Gly Gly Ala Glu Ser Trp Asn Cys
115 120 125

Leu Asn Thr Val Glu Arg Tyr Asn Pro Glu Asn Asn Thr Trp Thr Leu
130 135 140

Ile Ala Pro Met Asn Val Ala Arg Arg Gly Ala Gly Val Ala Val Leu
145 150 155 160

Asn Gly Lys Leu Phe Val Cys Gly Gly Phe Asp Gly Ser His Ala Ile
165 170 175

Ser Cys Val Glu Met Tyr Asp Pro Thr Arg Asn Glu Trp Lys Met Met
180 185 190

Gly Asn Met Thr Ser Pro Arg Ser Asn Ala Gly Ile Ala Thr Val Gly
195 200 205

Asn Thr Ile Tyr Ala Val Gly Gly Phe Asp Gly Asn Glu Phe Leu Asn
210 215 220

Thr Val Glu Val Tyr Asn Leu Glu Ser Asn Glu Trp
225 230 235

<210> 137

<211> 72

<212> PRT

<213> Homo sapiens

<400> 137

Phe Lys Glu Asn Tyr Lys Pro Leu Leu Lys Glu Ile Lys Glu Asp Thr
1 5 10 15

Asn Lys Trp Lys Asn Ile Pro Cys Ser Trp Val Gly Arg Ile Asn Ile
20 25 30

Val Lys Met Ala Ile Leu Pro Lys Val Ile Tyr Arg Phe Asn Ala Ile
35 40 45

Pro Ile Lys Leu Pro Met Thr Phe Phe Thr Glu Leu Glu Lys Thr Thr
50 55 60

Leu Lys Phe Ile Trp Asn Gln Lys
65 70

<210> 138

<211> 71

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (59)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (67)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (69)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 138

Tyr Lys Glu Asn Leu Ser Leu Gln Lys Lys Lys Lys Glu Asp Thr
1 5 10 15

Thr Lys Trp Lys Asn Ile Pro Cys Ser Trp Val Gly Arg Ile Asn Ile
20 25 30

Val Lys Met Ala Ile Leu Pro Lys Val Ile Tyr Arg Phe Ser Ala Ile
35 40 45

Pro Ile Lys Leu Pro Cys Leu Ser Ser Gln Xaa Gly Lys Asn Tyr Phe
50 55 60

Lys Val Xaa Trp Xaa Gln Lys
65 70

<210> 139

<211> 201

<212> PRT

<213> Homo sapiens

<400> 139

Ala Pro Ser Arg Thr Gly Glu Pro Glu Gln Glu Ala Val Ser Arg Thr
1 5 10 15

Arg Gln Glu Trp Glu Ser Ala Gly Gln Gln Ala Pro His Pro Arg Glu
 20 25 30

Ile Phe Lys Gln Lys Glu Arg Ala Met Ser Thr Thr Ser Val Thr Ser
 35 40 45

Ser Gln Pro Gly Lys Leu Arg Ser Pro Phe Leu Gln Lys Gln Leu Thr
 50 55 60

Gln Pro Glu Thr Ser Tyr Gly Arg Glu Pro Thr Ala Pro Val Ser Arg
 65 70 75 80

Pro Ala Ala Gly Val Cys Glu Glu Pro Ala Pro Ser Thr Leu Ser Ser
 85 90 95

Ala Gln Thr Glu Glu Glu Pro Thr Tyr Glu Val Pro Pro Glu Gln Asp
 100 105 110

Thr Leu Tyr Glu Glu Pro Pro Leu Val Gln Gln Gln Gly Ala Gly Ser
 115 120 125

Glu His Ile Asp Asn Tyr Met Gln Ser Gln Gly Phe Ser Gly Gln Gly
 130 135 140

Leu Cys Ala Arg Ala Leu Tyr Asp Tyr Gln Ala Ala Asp Asp Thr Glu
 145 150 155 160

Ile Ser Phe Asp Pro Glu Asn Leu Ile Thr Gly Ile Glu Val Ile Asp
 165 170 175

Glu Gly Trp Trp Arg Gly Tyr Gly Pro Asp Gly His Phe Gly Met Phe
 180 185 190

Pro Ala Asn Tyr Val Glu Leu Ile Glu
 195 200

<210> 140

<211> 199

<212> PRT

<213> Homo sapiens

<400> 140

Ser Pro Gln Arg Thr Trp Glu Gln Gln Gln Glu Val Val Ser Arg Asn
 1 5 10 15

Arg Asn Glu Gln Glu Ser Ala Val His Pro Arg Glu Ile Phe Lys Gln
 20 25 30

Lys Glu Arg Ala Met Ser Thr Thr Ser Ile Ser Ser Pro Gln Pro Gly
 35 40 45

Lys Leu Arg Ser Pro Phe Leu Gln Lys Gln Leu Thr Gln Pro Glu Thr
 50 55 60

His Phe Gly Arg Glu Pro Ala Ala Ala Ile Ser Arg Pro Arg Ala Asp
 65 70 75 80

Leu Pro Ala Glu Glu Pro Ala Pro Ser Thr Pro Pro Cys Leu Val Gln
 85 90 95

Ala Glu Glu Glu Ala Val Tyr Glu Glu Pro Pro Glu Gln Glu Thr Phe
 100 105 110

Tyr Glu Gln Pro Pro Leu Val Gln Gln Gln Gly Ala Gly Ser Glu His
 115 120 125

Ile Asp His His Ile Gln Gly Gln Gly Leu Ser Gly Gln Gly Leu Cys
 130 135 140

Ala Arg Ala Leu Tyr Asp Tyr Gln Ala Ala Asp Asp Thr Glu Ile Ser
 145 150 155 160

Phe Asp Pro Glu Asn Leu Ile Thr Gly Ile Glu Val Ile Asp Glu Gly
 165 170 175

Trp Trp Arg Gly Tyr Gly Pro Asp Gly His Phe Gly Met Phe Pro Ala
 180 185 190

Asn Tyr Val Glu Leu Ile Glu
 195

<210> 141

<211> 221

<212> PRT

<213> Homo sapiens

<400> 141

Gln Ser Leu Ser Thr Phe Leu Tyr Ile Gly Leu Leu Gly Ser Val Gly
 1 5 10 15

Glu Arg Met Ala Arg Arg Met Arg Ile Gln Leu Phe Arg Lys Leu Val
 20 25 30

Tyr Gln Asp Val Ala Tyr Phe Asp Val His Ser Ser Gly Lys Leu Val
 35 40 45

Glu Ile Ile Gly Ser Asp Val Gln Asn Phe Lys Ser Ser Phe Lys Gln
 50 55 60

Cys Ile Ser Gln Gly Leu Arg Asn Gly Ile Gln Val Val Gly Ser Val

65		70		75		80									
Phe	Ala	Leu	Leu	Ser	Ile	Ser	Pro	Thr	Leu	Thr	Ala	Ala	Leu	Ile	Gly
				85					90					95	
Cys	Leu	Pro	Cys	Val	Phe	Leu	Ile	Gly	Ser	Leu	Met	Gly	Thr	Glu	Leu
			100					105					110		
Arg	His	Ile	Ser	Arg	Glu	Val	Gln	Ser	Gln	Asn	Ser	Leu	Phe	Ala	Ser
		115					120					125			
Leu	Ile	Asp	Glu	Ala	Phe	Ser	His	Ile	Arg	Thr	Val	Lys	Ser	Leu	Ala
	130					135					140				
Met	Glu	Asp	Phe	Leu	Ile	Asn	Lys	Ile	Asn	Tyr	Asn	Val	Asp	Lys	Ala
145					150					155				160	
Lys	Met	Leu	Ser	Glu	Lys	Leu	Ser	Phe	Gly	Ile	Gly	Ser	Phe	Gln	Gly
				165					170					175	
Leu	Ser	Asn	Leu	Thr	Leu	Asn	Gly	Val	Val	Leu	Gly	Val	Leu	Tyr	Val
		180					185						190		
Gly	Gly	His	Leu	Met	Ser	Arg	Gly	Glu	Leu	Asp	Ala	Gly	His	Leu	Met
		195					200					205			
Ser	Phe	Leu	Ala	Thr	Thr	Gln	Thr	Leu	Gln	Arg	Ser	Leu			
	210					215					220				

<210> 142
 <211> 221
 <212> PRT
 <213> Homo sapiens

<400> 142
 Glu Gly Leu Leu Thr Phe Gly Tyr Leu Val Leu Leu Ser His Val Gly
 1 5 10 15
 Glu Arg Met Ala Val Asp Met Arg Arg Ala Leu Phe Ser Ser Leu Leu
 20 25 30
 Arg Gln Asp Ile Thr Phe Phe Asp Ala Asn Lys Thr Gly Gln Leu Val
 35 40 45
 Ser Arg Leu Thr Thr Asp Val Gln Glu Phe Lys Ser Ser Phe Lys Leu
 50 55 60
 Val Ile Ser Gln Gly Leu Arg Ser Cys Thr Gln Val Ala Gly Cys Leu
 65 70 75 80

Ala Thr Pro Ala Leu Met Gly Val Gly Thr Leu Met Gly Ser Gly Leu
100 105 110

Arg Lys Leu Ser Arg Gln Cys Gln Glu Gln Ile Ala Arg Ala Met Gly
115 120 125

Val Ala Asp Glu Ala Leu Gly Asn Val Arg Thr Val Arg Ala Phe Ala
130 135 140

Met Glu Gln Arg Glu Glu Glu Arg Tyr Gly Ala Glu Leu Glu Ala Cys
145 150 155 160

Arg Cys Arg Ala Glu Glu Leu Gly Arg Gly Ile Ala Leu Phe Gln Gly
165 170 175

Leu Ser Asn Ile Ala Phe Asn Cys Met Val Leu Gly Thr Leu Phe Ile
180 185 190

Gly Gly Ser Leu Val Ala Gly Gln Gln Leu Thr Gly Gly Asp Leu Met
195 200 205

Ser Phe Leu Val Ala Ser Gln Thr Val Gln Ser Phe Leu
210 215 220

<210> 143

<211> 152

<212> PRT

<213> Homo sapiens

<400> 143

Asp Gln Gly Gly Glu Trp Lys His Gly Arg Ile Ile Leu Pro Ser Tyr
1 5 10 15

Asp Met Glu Tyr Gln Ile Val Phe Glu Gly Val Ile Gly Lys Gly Arg
20 25 30

Ser Gly Glu Ile Ala Ile Asp Asp Ile Arg Ile Ser Thr Asp Val Pro
35 40 45

Leu Glu Asn Cys Met Glu Pro Ile Ser Ala Phe Ala Val Asp Ile Pro
50 55 60

Glu Ile His Glu Arg Glu Gly Tyr Glu Asp Glu Ile Asp Asp Glu Tyr
65 70 75 80

Glu Val Asp Trp Ser Asn Ser Ser Ser Ala Thr Ser Gly Ser Gly Ala
85 90 95

110

Pro Ser Thr Asp Lys Glu Lys Ser Trp Leu Tyr Thr Leu Asp Pro Ile
100 105 110

Leu Ile Thr Ile Ile Ala Met Ser Ser Leu Gly Val Leu Leu Gly Ala
115 120 125

Thr Cys Ala Gly Leu Leu Leu Tyr Cys Thr Cys Ser Tyr Ser Gly Leu
130 135 140

Ser Ser Arg Ser Cys Thr Thr Leu
145 150

<210> 144

<211> 152

<212> PRT

<213> Homo sapiens

<400> 144

Asp Gln Gly Gly Glu Trp Lys His Gly Arg Ile Ile Leu Pro Ser Tyr
1 5 10 15

Asp Met Glu Tyr Gln Ile Val Phe Glu Gly Val Ile Gly Lys Gly Arg
20 25 30

Ser Gly Glu Ile Ala Ile Asp Asp Ile Arg Ile Ser Thr Asp Val Pro
35 40 45

Leu Glu Asn Cys Met Glu Pro Ile Ser Ala Phe Ala Val Asp Ile Pro
50 55 60

Glu Ile His Glu Arg Glu Gly Tyr Glu Asp Glu Ile Asp Asp Glu Tyr
65 70 75 80

Glu Val Asp Trp Ser Asn Ser Ser Ser Ala Thr Ser Gly Ser Gly Ala
85 90 95

Pro Ser Thr Asp Lys Glu Lys Ser Trp Leu Tyr Thr Leu Asp Pro Ile
100 105 110

Leu Ile Thr Ile Ile Ala Met Ser Ser Leu Gly Val Leu Leu Gly Ala
115 120 125

Thr Cys Ala Gly Leu Leu Leu Tyr Cys Thr Cys Ser Tyr Ser Gly Leu
130 135 140

Ser Ser Arg Ser Cys Thr Thr Leu
145 150

<210> 145
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 145

Pro Ser Gly Phe Asn Cys Asn Phe Asp Phe Leu Glu Glu Pro Cys Gly
 1 5 10 15

Trp Met Tyr Asp His Ala Lys Trp Leu Arg Thr Thr Trp Ala Ser Ser
 20 25 30

Ser Ser Pro Asn Asp Arg Thr Phe Pro Asp Asp Arg Asn Phe Leu Arg
 35 40 45

Leu Gln Ser Asp Ser Gln Arg Glu Gly Gln Tyr Ala Arg Leu Ile Ser
 50 55 60

Pro Pro Val His Leu Pro Arg Ser Pro Val Cys Met Glu Phe Gln Tyr
 65 70 75 80

Gln Ala Thr Gly Gly Arg Gly Val Ala Leu Gln Val Val Arg Glu Ala
 85 90 95

Ser Gln Glu Ser
 100

<210> 146
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 146

Pro Ser Gly Phe Asn Cys Asn Phe Asp Phe Leu Glu Glu Pro Cys Gly
 1 5 10 15

Trp Met Tyr Asp His Ala Lys Trp Leu Arg Thr Thr Trp Ala Ser Ser
 20 25 30

Ser Ser Pro Asn Asp Arg Thr Phe Pro Asp Asp Arg Asn Phe Leu Arg
 35 40 45

Leu Gln Ser Asp Ser Gln Arg Glu Gly Gln Tyr Ala Arg Leu Ile Ser
 50 55 60

Pro Pro Val His Leu Pro Arg Ser Pro Val Cys Met Glu Phe Gln Tyr
 65 70 75 80

Gln Ala Thr Gly Gly Arg Gly Val Ala Leu Gln Val Val Arg Glu Ala
 85 90 95

Ala Arg Arg Ala
100

<210> 147
<211> 61
<212> PRT
<213> Homo sapiens

<400> 147
Pro Ala Gly Ile Gly Met Arg Leu Glu Val Leu Gly Cys Asp Trp Thr
1 5 10 15
Asp Ser Lys Pro Thr Val Lys Thr Leu Gly Pro Thr Val Lys Ser Glu
20 25 30
Glu Thr Thr Thr Pro Tyr Pro Thr Glu Glu Glu Ala Thr Glu Cys Gly
35 40 45
Glu Asn Cys Ser Phe Glu Asp Asp Lys Asp Leu Gln Leu
50 55 60

<210> 148
<211> 65
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (6)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 148
Pro Ala Gly Leu Gln Xaa Arg Leu Leu Gln His Ser Leu Ile Phe Leu
1 5 10 15
Cys Pro Tyr Thr Asp Ser Lys Pro Thr Val Glu Thr Leu Gly Pro Thr
20 25 30
Val Lys Ser Glu Glu Thr Thr Thr Pro Tyr Pro Thr Glu Glu Glu Ala
35 40 45
Thr Glu Cys Gly Glu Asn Cys Ser Phe Glu Asp Asp Lys Asp Leu Gln
50 55 60
Leu
65

<210> 149
<211> 63
<212> PRT
<213> Homo sapiens

<400> 149
His Phe Gly Arg Pro Arg Arg Ala Asp Tyr Leu Arg Ile Gly Val Pro
1 5 10 15

Asp Gln Arg Gly Gln Arg Gly Glu Ser Pro Ser Leu Leu Lys Asn Thr
20 25 30

Lys Ile Ser Trp Ala Trp Trp Val Pro Val Ile Pro Ala Ile Arg Glu
35 40 45

Gly Glu Ala Gly Glu Ser Leu Glu Pro Gly Arg Gln Arg Leu Gln
50 55 60

<210> 150
<211> 64
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (7)
<223> Xaa equals stop translation

<220>
<221> SITE
<222> (16)
<223> Xaa equals stop translation

<220>
<221> SITE
<222> (36)
<223> Xaa equals stop translation

<400> 150
His Val Gly Arg Pro Arg Xaa Val Asp Leu Leu Ser Pro Arg Val Xaa
1 5 10 15

Asp Gln Pro Gly Gln His Gly Lys Met Pro Phe Leu Leu Lys Ile Gln
20 25 30

Lys Cys Ser Xaa Met Trp Trp Arg Met Pro Val Val Leu Ala Thr Gln
35 40 45

Glu Ala Glu Val Gly Gly Ser Lys Pro Arg Lys Leu Arg Leu Gln
50 55 60

<210> 151
 <211> .180
 <212> PRT
 <213> Homo sapiens

<400> 151
 Pro Gly Ala Gly Pro Gly Pro Ala Ala Gly Ala Ala Leu Pro Asp Gln
 1 5 10 15
 Ser Phe Leu Trp Asn Val Phe Gln Arg Val Asp Lys Asp Arg Ser Gly
 20 25 30
 Val Ile Ser Asp Thr Glu Leu Gln Gln Ala Leu Ser Asn Gly Thr Trp
 35 40 45
 Thr Pro Phe Asn Pro Val Thr Val Arg Ser Ile Ile Ser Met Phe Asp
 50 55 60
 Arg Glu Asn Lys Ala Gly Val Asn Phe Ser Glu Phe Thr Gly Val Trp
 65 70 75 80
 Lys Tyr Ile Thr Asp Trp Gln Asn Val Phe Arg Thr Tyr Asp Arg Asp
 85 90 95
 Asn Ser Gly Met Ile Asp Lys Asn Glu Leu Lys Gln Ala Leu Ser Gly
 100 105 110
 Phe Gly Tyr Arg Leu Ser Asp Gln Phe His Asp Ile Leu Ile Arg Lys
 115 120 125
 Phe Asp Arg Gln Gly Arg Gly Gln Ile Ala Phe Asp Asp Phe Ile Gln
 130 135 140
 Gly Cys Ile Val Leu Gln Arg Leu Thr Asp Ile Phe Arg Arg Tyr Asp
 145 150 155 160
 Thr Asp Gln Asp Gly Trp Ile Gln Val Ser Tyr Glu Gln Tyr Leu Ser
 165 170 175
 Met Val Phe Ser
 180

<210> 152
 <211> 179
 <212> PRT

<213> Homo sapiens

<400> 152

Pro Gly Leu Tyr Gly Gln Gly Gly Ala Pro Pro Asn Val Asp Pro Glu
 1 5 10 15

Ala Tyr Ser Trp Phe Gln Ser Val Asp Ser Asp His Ser Gly Tyr Ile
 20 25 30

Ser Met Lys Glu Leu Lys Gln Ala Leu Val Asn Cys Asn Trp Ser Ser
 35 40 45

Phe Asn Asp Glu Thr Cys Leu Met Met Ile Asn Met Phe Asp Lys Thr
 50 55 60

Lys Ser Gly Arg Ile Asp Val Tyr Gly Phe Ser Ala Leu Trp Lys Phe
 65 70 75 80

Ile Gln Gln Trp Lys Asn Leu Phe Gln Gln Tyr Asp Arg Asp Arg Ser
 85 90 95

Gly Ser Ile Ser Tyr Thr Glu Leu Gln Gln Ala Leu Ser Gln Met Gly
 100 105 110

Tyr Asn Leu Ser Pro Gln Phe Thr Gln Leu Leu Val Ser Arg Tyr Cys
 115 120 125

Pro Arg Ser Ala Asn Pro Ala Met Gln Leu Asp Arg Phe Ile Gln Val
 130 135 140

Cys Thr Gln Leu Gln Val Leu Thr Glu Ala Phe Arg Glu Lys Asp Thr
 145 150 155 160

Ala Val Gln Gly Asn Ile Arg Leu Ser Phe Glu Asp Phe Val Thr Met
 165 170 175

Thr Ala Ser

<210> 153

<211> 129

<212> PRT

<213> Homo sapiens

<400> 153

Ile Thr Arg Glu Glu Trp Glu Lys Lys Leu Asn Ala Val Lys Leu Arg
 1 5 10 15

Lys Glu Asp Met Asn Thr Leu Val Met Asn Phe Leu Val Thr Glu Gly
 20 25 30

Tyr Val Glu Ala Ala Glu Lys Phe Gln Arg Glu Ser Gly Thr Lys Pro
 35 40 45
 Glu Ile Asp Leu Ala Thr Ile Thr Asp Arg Met Ala Val Lys Lys Ala
 50 55 60
 Val Gln Asn Gly Asn Val Glu Asp Ala Ile Glu Lys Val Asn Asp Leu
 65 70 75 80
 Asn Pro Glu Ile Leu Asp Thr Asn Pro Glu Leu Phe Phe His Leu Gln
 85 90 95
 Gln Gln Arg Leu Ile Glu Leu Ile Arg Gln Gly Lys Thr Glu Glu Ala
 100 105 110
 Leu Glu Phe Ala Gln Glu Glu Leu Ala Pro Arg Gly Glu Glu Asn Gln
 115 120 125

Ala

<210> 154

<211> 129

<212> PRT

<213> Homo sapiens

<400> 154

Ile Thr Lys Asp Glu Trp Met Glu Lys Leu Asn Asn Leu His Val Gln
 1 5 10 15
 Arg Ala Asp Met Asn Arg Leu Ile Met Asn Tyr Leu Val Thr Glu Gly
 20 25 30
 Phe Lys Glu Ala Ala Glu Lys Phe Arg Met Glu Ser Gly Ile Glu Pro
 35 40 45
 Ser Val Asp Leu Glu Thr Leu Asp Glu Arg Ile Lys Ile Arg Glu Met
 50 55 60
 Ile Leu Lys Gly Gln Ile Gln Glu Ala Ile Ala Leu Ile Asn Ser Leu
 65 70 75 80
 His Pro Glu Leu Leu Asp Thr Asn Arg Tyr Leu Tyr Phe His Leu Gln
 85 90 95
 Gln Gln His Leu Ile Glu Leu Ile Arg Gln Arg Glu Thr Glu Ala Ala
 100 105 110
 Leu Glu Phe Ala Gln Thr Gln Leu Ala Asp Arg Ala Arg Arg Ala Glu

117

115

120

125

Ser

<210> 155

<211> 91

<212> PRT

<213> Homo sapiens

<400> 155

Arg Gly Glu Glu Asn Gln Ala Phe Leu Glu Glu Leu Glu Lys Thr Val
 1 5 10 15

Ala Leu Leu Val Phe Asp Asp Ala Ser Thr Cys Pro Val Lys Glu Leu
 20 25 30

Leu Asp Leu Ser His Arg Leu Lys Thr Ala Ser Glu Val Asn Ala Ala
 35 40 45

Ile Leu Thr Ser Gln Ser His Glu Lys Asp Pro Lys Leu Pro Ser Leu
 50 55 60

Leu Lys Met Leu Ile Trp Ala Gln Thr Gln Leu Asp Glu Lys Ala Val
 65 70 75 80

Tyr Pro His Ile Asn Asp Leu Ser Thr Ala Ile
 85 90

<210> 156

<211> 92

<212> PRT

<213> Homo sapiens

<400> 156

Gln Gly Glu Glu Ser Arg Glu Cys Leu Thr Glu Met Glu Arg Thr Leu
 1 5 10 15

Ala Leu Leu Ala Phe Asp Ser Pro Glu Glu Ser Pro Phe Gly Asp Leu
 20 25 30

Leu His Thr Met Gln Arg Gln Lys Val Trp Ser Glu Val Asn Gln Ala
 35 40 45

Val Leu Asp Tyr Glu Asn Arg Glu Ser Thr Pro Lys Leu Ala Lys Leu
 50 55 60

Leu Lys Leu Leu Leu Trp Ala Gln Asn Glu Leu Asp Gln Lys Lys Val
 65 70 75 80

Lys Tyr Pro Lys Met Thr Asp Leu Ser Lys Gly Val
85 90

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/09071

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) :C07K 14/47; C12N 5/10, 5/16, 15/12, 15/63, 15/64

US CL :Please See Extra Sheet.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 530/350; 536/23.1, 23.5, 24.3, 24.31; 435/69.1, 71.1, 71.2, 471, 325, 252.3, 254.11, 320.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

NONE

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

WEST, CAS ONLINE, CAPLUS, MEDLINE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 96/09386 A2 (THE GOVERNMENT OF THE UNITED STATES OF AMERICA) 28 March 1996 (28-03-96), see entire document.	1-12, 14-16, 21

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
E earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*G* document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means	
P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

23 JUNE 2000

Date of mailing of the international search report

24 JUL 2000

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

Facsimile No. (703) 305-3230

Authorized officer

PREMA MERTZ

Telephone No. (703) 308-0196

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/09071**Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-12, 14-16, 21

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/09071

A. CLASSIFICATION OF SUBJECT MATTER:

US CL :

530/350; 536/23.1, 23.5, 24.3, 24.31; 435/69.1, 71.1, 71.2, 471, 325, 252.3, 254.11, 320.1

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claims 1-12, 14-16, 21, drawn to a nucleic acid of SEQ ID NO:11 encoding a protein of SEQ ID NO:60, a vector, a host cell, a method of making the protein and the protein of SEQ ID NO:60.

Group II, claim 13, drawn to an antibody that binds the protein of SEQ ID NO:60.

Group III, claim 17, drawn to a method of treating a condition comprising administering the protein of SEQ ID NO:60.

Group IV, claim 18, drawn to a method of diagnosing a pathological condition using the polynucleotide encoding a protein of SEQ ID NO:60.

Group V, claim 19, drawn to a method of diagnosing a pathological condition by determining the amount of protein of SEQ ID NO:60.

Group VI, claim 20, drawn to a method of identifying a binding partner of the protein of SEQ ID NO:60.

Group VII, claims 22-23, drawn to a method of identifying an activity in a biological assay.

Group VIII, claim 17, drawn to a method for treating a condition comprising administering the nucleic acid of SEQ ID NO:11.

The inventions listed as Groups I-VIII do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

Pursuant to 37 C.F.R. § 1.475 (d), the ISA/US considers that where multiple products and processes are claimed, the main invention shall consist of the first invention of the category first mentioned in the claims and the first recited invention of each of the other categories related thereto. Accordingly, the main invention (Group I) comprises the first-recited product, a nucleic acid encoding a protein of SEQ ID NO:60, a vector, a host cell, a method of making the protein of SEQ ID NO:60, and the protein of SEQ ID NO:60. Further pursuant to 37

C.F.R. § 1.475 (d), the ISA/US considers that any feature which the subsequently recited products and methods share with the main invention does not constitute a special technical feature within the meaning of PCT Rule 13.2 and that each of such products and methods accordingly defines a separate invention.

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack Unity of Invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows:

the polynucleotides set forth in SEQ ID NO:11-59 encoding the polypeptides set forth in SEQ ID NO:60-108.

